

GenCore version 5.1.6
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ON protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 42.7959 Seconds

(without alignments)

118.840 Million cell updates/sec

Title: US-10-084-813-11

Perfect score: 94

Sequence: 1 LPFLYSLVFIFGVGNWL 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	94	100.0	18	4	AAB88916
2	94	100.0	18	4	AAB88993
3	94	100.0	27	2	AAW33994
4	94	100.0	27	2	AAW33961
5	94	100.0	29	2	AAW40023
6	94	100.0	83	2	AAW01249
7	94	100.0	100	2	AAW88231
8	94	100.0	184	2	AAW27406
9	94	100.0	215	2	AAW27408
10	94	100.0	215	2	AAW88238
11	94	100.0	329	4	ABA46859
12	94	100.0	329	5	ABE81055
13	94	100.0	332	2	AAW26766
14	94	100.0	344	5	ABG32881
15	94	100.0	344	6	ABU61655
16	94	100.0	352	2	AAW27407
17	94	100.0	352	2	AAW27123
18	94	100.0	352	2	AAW07602
19	94	100.0	352	2	AAW23835
20	94	100.0	352	2	AAW88232
21	94	100.0	352	3	AAW80128
22	94	100.0	352	4	AAW9089
23	94	100.0	352	4	AAE07046
24	94	100.0	352	4	AAE07048
25	94	100.0	352	4	AAG80111

26	94	100.0	352	4	AAE04321
27	94	100.0	352	4	AAE07037
28	94	100.0	352	4	AAE07039
29	94	100.0	352	4	ABA46858
30	94	100.0	352	4	ABB56342
31	94	100.0	352	4	ABB83354
32	94	100.0	352	4	AAAB82948
33	94	100.0	352	5	AAU97150
34	94	100.0	352	5	AAU97152
35	94	100.0	352	5	AAU52829
36	94	100.0	352	5	AAU52828
37	94	100.0	352	5	ABG70597
38	94	100.0	352	5	ABG92883
39	94	100.0	352	5	ABG92880
40	94	100.0	352	5	AAE25808
41	94	100.0	352	5	AAE25811
42	94	100.0	352	5	ABB81054
43	94	100.0	352	5	ABB08343
44	94	100.0	352	6	ABG75540
45	94	100.0	352	6	ABR58602
46	94	100.0	352	6	AAO29514
47	94	100.0	352	6	ABU61654
48	94	100.0	352	6	ABP97728
49	94	100.0	352	6	ABP81933
50	94	100.0	352	7	ADC03341
51	94	100.0	360	2	AAW79166
52	94	100.0	360	2	AAW35833
53	94	100.0	360	4	AAW80108
54	94	100.0	360	4	AAU07613
55	94	100.0	360	4	AAU07614
56	94	100.0	360	4	ABR56340
57	94	100.0	360	6	ABP97725
58	94	100.0	360	6	ABP81987
59	94	100.0	371	2	AAW23834
60	94	100.0	371	2	AAW79165
61	94	100.0	374	4	AAW80107
62	94	100.0	374	6	ABU09083
63	94	100.0	374	7	ADD44861
64	94	100.0	374	7	ADD44865
65	94	100.0	439	2	AAW41280
66	94	100.0	439	2	AAW41280
67	92	97.9	354	7	ADD44859
68	90	95.7	268	7	ADC10142
69	90	95.7	268	7	ADC10144
70	90	95.7	352	7	AAW27125
71	90	95.7	352	7	ADC03359
72	88	93.6	354	2	AAW54037
73	77	81.9	31	2	AAW39995
74	77	81.9	355	2	AAW52749
75	77	81.9	355	2	AAW25751
76	77	81.9	355	2	AAW26588
77	77	81.9	355	3	AAW20571
78	77	81.9	355	6	ABU09082
79	77	81.9	355	6	ABP97724
80	77	81.9	355	6	ABP81790
81	75	79.8	360	2	AAW99274
82	75	79.8	360	3	AAW07498
83	75	79.8	360	4	AAW80110
84	75	79.8	360	4	AAW80110
85	75	79.8	360	6	ABR40283
86	75	79.8	360	6	ABU09085
87	75	79.8	360	6	ABP97727
88	75	79.8	360	6	ABP81792
89	75	79.8	360	7	ADE27676
90	75	79.8	361	4	ABB11966
91	73	77.7	18	4	ABR88915
92	73	77.7	355	2	AAW29179
93	73	77.7	355	7	ADD45360
94	72	76.6	18	4	ABR88917
95	70	74.5	355	2	AAW51744
96	67	71.3	13	2	AAW33968
97	63	67.0	332	5	ABJ03698
98	63	67.0	355	2	AAW03376

AAE04321	Human che
AAE07037	Human G-p
AAE07039	Human G-p
ABA46858	Human HDG
ABB56342	Non-endog
ABB83354	Human CCR
AAAB82948	Human HIV
AAU97150	Human G-p
AAU97152	Human G-p
AAU52829	Human CCR
AAU52828	Human CC
ABG70597	Human G-p
ABG92883	Human imm
ABG92880	Human G-p
AAE25808	Human G-p
AAE25811	Human G-p
ABB81054	G-protein
ABB08343	Human che
ABG75540	Human G-p
ABR58602	Human can
AAO29514	Human C-C
ABU61654	Human G-p
ABP97728	Amino aci
ABP81933	Human C-C
ADC03341	Human che
AAW79166	Human mon
AAW35833	Human mon
AAW80108	Human CCR
AAU07613	Human CCR
AAU07614	Human wil
ABR56340	Non-endog
ABP97725	Amino aci
ABP81987	Human C-C
AAW23834	Human CC
AAW79165	Human mon
AAW80107	Human CCR
ABU09083	Human che
ADD44861	Human Pro
ADD44865	Human Pro
AAW41280	Fusion pr
ADD44859	Rat Prote
ADD44863	Rat Prote
ADC10142	Human NOV
ADC10144	Human NOV
AAW27125	Macaque c
ADC03359	Macaque c
AAW54037	Mouse CC-
AAW39995	Peptide e
AAW52749	C-C chemo
AAW25751	Human MIP
AAW26588	Human MIP
AAW20571	Human CC-
ABU09082	Human che
ABP97724	Amino aci
ABP81790	Human C-C
AAW99274	Chemokine
AAW07498	A human C
AAW80110	Human CCR
ABR40283	Amino aci
ABU09085	Human che
ABP97727	Amino aci
ABP81792	Human C-C
ADE27676	Human seg
ABB11966	Human CCR
ABR88915	HIV gp120
AAW29179	Rat CC ch
ADD45360	Rat Prote
ABR88917	HIV gp120
AAW51744	Human C-C
AAW33968	CCR5 rece
ABJ03698	Human ova
AAW03376	CC-chemok

99 63 67.0 355 2 AAW03377 CC-Chemok
100 63 67.0 355 2 AAW03378 CC-Chemok

ALIGNMENTS

```

RESULT 1
AAB88916
ID AAB88916 standard; peptide; 18 AA.
AC AAB88916;
XX
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #9.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PS Claim 21; Page 38; 114pp; English.
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 94; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
Db 1 LPPLYSLVFIFGVGNML 18

RESULT 2
AAB88993
ID AAB88993 standard; peptide; 18 AA.
AC AAB88993;
XX
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #86.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX

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XX WO200116182-A2.
XX
XX 08-MAR-2001.
XX
XX 25-AUG-2000; 2000WO-US023505.
XX
XX 27-AUG-1999; 99US-0151270P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Saxinger C;
XX
XX WPI; 2001-244398/25.
XX
XX Novel polypeptides useful for treating HIV infection, have homology to
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
PT and binds to HIV gp120 under physiological conditions.
XX
XX Claim 21; Page 38; 114pp; English.
XX
XX The present invention describes a number of peptides which are able to
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
CC useful in the treatment of HIV, as they prevent replication of the virus.
CC The present sequence is an example of a peptide of the invention
XX
XX Sequence 18 AA;

Query Match 100.0%; Score 94; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18
Db 1 LPPLYSLVFIFGVGNML 18

RESULT 3
AAB33994
ID AAB33994 standard; peptide; 27 AA.
XX
XX AAB33994;
XX
XX 28-MAY-1998 (first entry)
XX
XX CCR5 receptor antagonist.
XX
XX Antagonist; integral membrane protein; inhibitor; transmembrane domain;
KW therapy; psychotic disorder; Huntington's disease; Parkinson's disease;
KW post-myocardial infarction; HIV infection; cell proliferation disorder;
KW peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;
KW antibacterial; CCR5 receptor.
XX
XX Homo sapiens.
XX
XX WO9735881-A2.
XX
XX 02-OCT-1997.
XX
XX 26-MAR-1997; 97WO-CA000203.
XX
XX 27-MAR-1996; 96US-0014306P.
XX
XX 25-JUN-1996; 96US-00670119.
XX
XX 20-AUG-1996; 96US-0024240P.
XX
XX (NGGY/) NG G Y K.
XX (SEEM/) SEEMAN P.
XX (GEOR/) GEORGE S R.
XX (ODOW/) O'DOWD B F.
XX
XX Ng GYK, Seeman P, George SR, Odowd BF;
XX

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DR WPI; 1997-489566/45.
 XX Inhibitor of integral membrane protein - used to treat e.g.
 PT schizophrenia, hypertension, viral infection, cancer etc.
 XX Disclosure; Page 88; 127pp; English.
 XX
 CC This sequence represents a CCR5 receptor antagonist, and is an antagonist
 CC of the invention. The antagonists (A) are for inhibiting the function of
 CC a prokaryotic or eukaryotic integral membrane protein (IMP) having at
 CC least one transmembrane domain (TMD), comprises a peptide including at
 CC least 4 consecutive amino acids (aa) from the sequence of the TMD. (A)
 CC are used to treat or prevent disorders in mammals that involve
 CC disturbances of IMP, and the same effect is achieved by inserting a
 CC nucleic acid encoding (A) into the cells of the mammal. Specified
 CC conditions that can be treated are schizophrenia, psychotic disorders,
 CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial
 CC infarction, tachyarrhythmia, human immunodeficiency virus infection,
 CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug
 CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,
 CC renal disease, Parkinson's disease, congestive heart failure, migraine,
 CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune
 CC diseases, graft rejection etc. (A) can be used as diuretics and
 CC antibacterials. (A) may also be used to determine function of orphan
 CC receptors and, when attached to a marker, for tissue imaging to
 CC localise/quantify specific receptors. The transgenic animals are used to
 CC test efficacy/toxicity of (A) and as models of diseases. (A) are very
 CC specific and selective, against the IMP from which they are derived, so
 CC should have few side effects
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 94; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIPIFGVGNML 18
 Db 2 LPPLSLVFIPIFGVGNML 19
 RESULT 4
 AAW33961
 ID AAW33961 standard; peptide; 27 AA.
 AC AAW33961;
 XX
 DT 28-MAY-1998 (first entry)
 DE CCR5 receptor antagonist.
 XX
 KW Antagonist; integral membrane protein; inhibitor; transmembrane domain;
 KW therapy; psychotic disorder; Huntington's disease; Parkinson's disease;
 KW post-myocardial infarction; HIV infection; cell proliferation disorder;
 KW peptic ulcer; glaucoma; asthma; renal disease; autoimmune disease;
 KW antibacterial; CCR5 receptor.
 XX
 OS Homo sapiens.
 XX
 FN WO9735881-A2.
 XX
 PD 02-OCT-1997.
 XX
 PF 26-MAR-1997; 97WO-CA000203.
 XX
 PR 27-MAR-1996; 96US-0014306P.
 PR 25-JUN-1996; 96US-00670119.
 PR 20-AUG-1996; 96US-0024240P.
 XX
 XX (NGY/) NG G Y K.
 PA (SEEM/) SEEMAN P.
 PA (GEOR/) GEORGE S R.
 PA (ODOW/) O'DOWD B F.

XX Ng GYK, Seeman P, George SR, Odowd BF;
 XX WPI; 1997-489566/45.
 XX
 PT Inhibitor of integral membrane protein - used to treat e.g.
 PT schizophrenia, hypertension, viral infection, cancer etc.
 XX Claim 22; Page 96; 127pp; English.
 XX
 CC This sequence represents a CCR5 receptor antagonist, and is an antagonist
 CC of the invention. The antagonists (A) are for inhibiting the function of
 CC a prokaryotic or eukaryotic integral membrane protein (IMP) having at
 CC least one transmembrane domain (TMD), comprises a peptide including at
 CC least 4 consecutive amino acids (aa) from the sequence of the TMD. (A)
 CC are used to treat or prevent disorders in mammals that involve
 CC disturbances of IMP, and the same effect is achieved by inserting a
 CC nucleic acid encoding (A) into the cells of the mammal. Specified
 CC conditions that can be treated are schizophrenia, psychotic disorders,
 CC Huntington's disease, Tourette's syndrome, hypertension, post-myocardial
 CC infarction, tachyarrhythmia, human immunodeficiency virus infection,
 CC AIDS, cell proliferation (cancer, psoriasis or hyperkeratosis), and drug
 CC abuse. (A) can also be used to treat peptic ulcer, glaucoma, asthma,
 CC renal disease, Parkinson's disease, congestive heart failure, migraine,
 CC depression, obesity, diabetic neuropathy/retinopathy, autoimmune
 CC diseases, graft rejection etc. (A) can be used as diuretics and
 CC antibacterials. (A) may also be used to determine function of orphan
 CC receptors and, when attached to a marker, for tissue imaging to
 CC localise/quantify specific receptors. The transgenic animals are used to
 CC test efficacy/toxicity of (A) and as models of diseases. (A) are very
 CC specific and selective, against the IMP from which they are derived, so
 CC should have few side effects
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 94; DB 2; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIPIFGVGNML 18
 Db 2 LPPLSLVFIPIFGVGNML 19
 RESULT 5
 AAW40023
 ID AAW40023 standard; peptide; 29 AA.
 AC AAW40023;
 XX
 DT 18-JUN-1998 (first entry)
 DE Peptide effecting G-protein-coupled receptor activity.
 XX
 KW G-protein-coupled receptor; GPCR; transmembrane domain; oligomerisation;
 KW therapeutic composition; GPCR function; receptor monomeric form;
 KW multimeric form; inhibition; GPCR-mediated process; GPCR binding;
 KW treatment; disease.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO9800538-A2.
 XX
 PD 08-JAN-1998.
 XX
 PF 01-JUL-1997; 97WO-IB000814.
 XX
 PR 01-JUL-1996; 96US-0021031P.
 XX
 PA (BIOS-) BIOSIGNAL INC.
 PA (UTMO-) UNIV MONTREAL.
 XX

```
Query Match      100.0%; Score 94; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 7	
AAW88231	
ID	AAW88231 standard; protein; 100 AA.
XX	
XX	AAW88231;
XX	
XX	15-MAR-1999 (first entry)
XX	
XX	HIV-1 co-receptor CCR5 variant CCR5m303.
XX	
XX	HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
KW	gene therapy; human.
KW	
XX	
OS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
FH	32..56
FT	/note= "transmembrane domain 1"
FT	67..87
FT	/note= "transmembrane domain 2"
FT	
FT	
FT	
FT	
PN	W09854317-A1.
XX	
XX	03-DEC-1998.
XX	
XX	29-MAY-1998; 98WO-EP003437.
XX	
XX	30-MAY-1997; 97US-0048057P.
XX	
XX	(MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
PA	
XX	
XX	Beretta A, Quillient C, Arenzana Siesdedos F, Braun J;
PI	
PI	
PI	WPI; 1999-059835/05.
DR	N-PSDB; AAW88231.
DR	
XX	
XX	
XX	New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
PT	resistance of CCR5-expressing cells to HIV-1 infection.
PT	
PT	
PS	Claim 2; Page 37; 55pp; English.
PS	
XX	
XX	
CC	This is the amino acid sequence of a CCR5 variant protein, designated
CC	CCR5m303, that comprises the first two transmembrane domains of wild-type
CC	CCR5 (see AAW88232), but lacks transmembrane domains 3-7. CCR5 serves as
CC	a co-receptor for infection by macrophage-tropic (M-tropic) strains of

CC HIV-1. The presence of the CCR5m303 variant allele (see AAV84125) with
 CC the wild type CCR5 allele in an individual shows a positive correlation
 CC with resistance to infection with M-tropic HIV-1 strains, and may
 CC indicate slower progression of the disease. The detection of CCR5
 CC variants may be used to identify individuals at lower risk of infection
 CC relative to the general population who, if infected, may exhibit slower
 CC progression to AIDS. Probes and primers (see AAV84127-36) are provided
 CC for use in diagnostic methods for detecting the presence of such
 CC variants. A method is provided for inhibiting HIV-1 infection of a cell
 CC expressing the CCR5 receptor. This involves introducing a nucleic acid
 CC encoding a CCR5 variant into the cell, thereby reducing the number of
 CC functional CCR5 molecules present on the cell surface
 CC XX

SQ Sequence 100 AA;

Query Match 100.0%; Score 94; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 7.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
 |||||
 Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 8

AAW27406
 ID AAW27406 standard; protein; 184 AA.

XX AC AAW27406;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor-5; CCR5;
 KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
 KW predisposition; resistance; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.

XX OS Homo sapiens.

XX PN WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX XX (EURO-) EUROSREEN SA.

XX FI Samson M, Parmentier M, Vassart G, Libert F;

XX DR WPI; 1997-479829/44.

XX DR N-PSDB; AAT90116.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 XX disease and viral infection.

XX PS Claim 1; Fig 1a; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
 CC 5 (CCR5), which is not a receptor of human immunodeficiency virus type 1
 CC or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat
 CC and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
 CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
 CC viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders. Subjects that express the
 CC inactive receptor have a predisposition, or resistance to HIV-1 and/or

CC HIV-2
 XX
 SQ Sequence 184 AA;

Query Match 100.0%; Score 94; DB 2; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
 |||||
 Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 9

AAW27408
 ID AAW27408 standard; protein; 215 AA.

XX AC AAW27408;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;
 KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;
 KW predisposition; resistance; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.

XX OS Homo sapiens.

XX PN WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX XX (EURO-) EUROSREEN SA.

XX FI Samson M, Parmentier M, Vassart G, Libert F;

XX DR WPI; 1997-479829/44.

XX DR N-PSDB; AAT90118.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 XX to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 XX disease and viral infection.

XX PS Claim 7; Fig 1d-e; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
 CC 5 (CCR5), which lacks the last 3 transmembrane regions and the regions
 CC involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,
 CC treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
 CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
 CC viral infections, especially human immunodeficiency virus type 1 or type
 CC 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune
 CC disorders. Subjects that express the inactive receptor have a
 CC predisposition, or resistance to HIV-1 and/or HIV-2

XX SQ Sequence 215 AA;

Query Match 100.0%; Score 94; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
 |||||
 Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 10
AAW88238
ID AAW88238 standard; protein; 215 AA.
XX
AC AAW88238;
XX
DT 15-MAR-1999 (first entry)
XX
DE HIV-1 co-receptor CCR5 variant CCR5-delta32.
XX
KW HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
KW gene therapy; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 32..56
FT FT /note= "transmembrane domain 1"
FT Domain 67..87
FT FT /note= "transmembrane domain 2"
FT Domain 103..124
FT FT /note= "transmembrane domain 3"
FT Domain 142..167
FT FT /note= "transmembrane domain 4"
XX
FN W09854317-A1.
XX
PD 03-DEC-1998.
XX
PF 29-MAY-1998; 98WO-EP003437.
XX
PR 30-MAY-1997; 97US-0048057P.
XX
PA (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX
PI Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
XX WPI; 1999-059835/05.
DR N-PSDB; AAW84159.
XX
PT New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
PT resistance of CCR5-expressing cells to HIV-1 infection.
XX
PS Disclosure; Page 38-39; 55pp; English.
XX
CC This is the amino acid sequence of a CCR5 variant protein, designated
CC CCR5-delta32, that includes the first 4 transmembrane domains of wild-
CC type CCR5 (see AAW88232), but lacks transmembrane domains 5-7. CCR5
CC serves as a co-receptor for infection by macrophage-tropic (M-tropic)
CC strains of HIV-1. Individuals homozygous for the CCR5-delta32 mutation
CC are resistant to HIV-1 infection, but heterozygous individuals are
CC susceptible. The invention additionally relates to the identification of
CC variant CCR5m303 (see AAW88231), which lacks transmembrane domains 3-7 of
CC CCR5. The detection of CCR5 variants may be used to identify individuals
CC at lower risk of infection relative to the general population who, if
CC infected, may exhibit slower progression to AIDS. Probes and primers (see
CC AAW84127-36) are provided for use in diagnostic methods for detecting the
CC presence of such variants. A method is provided for inhibiting HIV-1
CC infection of a cell expressing the CCR5 receptor. This involves
CC introducing a nucleic acid encoding a CCR5 variant into the cell, thereby
CC reducing the number of functional CCR5 molecules present on the cell
CC surface
XX
SQ Sequence 215 AA;
Query Match 100.0%; Score 94; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LPPLYSLVIFGFGVGNML 18
|||||

Db 33 LPPLYSLVIFGFGVGNML 50
RESULT 11
AAB46859
ID AAB46859 standard; protein; 329 AA.
XX
AC AAB46859;
XX
DT 16-AUG-2001 (revised)
DT 02-AUG-2001 (revised)
DT 04-MAY-2001 (first entry)
XX
XX Human MCP-1 receptor protein fragment.
XX
KW HDGMR10; human; G-protein chemokine receptor; antiinflammatory;
KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;
KW cytostatic; antiparasitic; antipsoiatic; antirheumatic; antiarthritic;
KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;
KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;
KW T-cell mediated autoimmune disease; psoriasis; allergy; atherosclerosis;
KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;
KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;
KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;
KW hyper-eosinophilic syndrome; vulneryary.
XX
OS Homo sapiens.
XX
FN US2001000241-A1.
XX
PD 12-APR-2001.
XX
PF 29-NOV-2000; 2000US-00725285.
XX
PR 06-JUN-1995; 95US-00466343.
PR 18-NOV-1998; 98US-00195662.
PR 25-JUN-1999; 99US-00339912.
XX
XX (LIYY/) LI Y.
PA (RUBE/) RUBEN S M.
XX
PI Li Y, Ruben SM;
XX
XX WPI; 2001-226317/23.
XX
PT New human G-protein chemokine receptor polypeptides and polynucleotides,
PT useful for identifying (ant)agonists to the G-protein chemokine receptor.
XX
PS Disclosure; Page 16-17; 22pp; English.
XX
CC This invention describes a novel receptor polypeptide (I) selected from
CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the
CC specification; and (ii) a polypeptide encoded by the cDNA contained in a
CC plasmid, and fragments, analogs and derivatives of the polypeptide. The
CC products of the invention have antiinflammatory, immunomodulatory,
CC anticoagulant, antiallergic, immunosuppressive, vulneryary, cytostatic,
CC antiparasitic, antipsoiatic, antirheumatic, antiarthritic and vasotropic
CC activity and can be used for gene therapy. The G-protein chemokine
CC receptors, HDGMR10, (I) are useful for screening for compounds which
CC activate or inhibit activation of (I). The products of the invention can
CC also be used for stimulating haematopoiesis, wound healing, coagulation,
CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-
CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and
CC stimulating growth factor activity. HDGMR10 is useful for treating
CC allergy, atherosclerosis, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic
CC reactions, prostaglandin-independent fever, bone marrow failure,
CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-
CC eosinophilic syndrome. (N.B. This record was resubmitted to correct
CC errors in the keyword formatting)
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 94; DB 4; Length 329;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFGVGNML 18
 DB 28 LPPLYSLVFIFGFGVGNML 45

RESULT 12
 ABB81055
 ID ABB81055 standard; protein; 329 AA.
 XX
 AC ABB81055;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human MCP-1 receptor.
 XX
 KW 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNER10;
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;
 KW antiparasitic; antipsoriatic; antiallergic; antiinflammatory; cytostatic;
 KW antirheumatic; antiarthritic; gene therapy; human; MCP-1; receptor.
 XX
 OS Homo sapiens.
 XX
 PN US2002076745-A1.
 XX
 PD 20-JUN-2002.
 XX
 PF 18-NOV-1998; 98US-00195662.
 XX
 PR 06-JUN-1995; 95US-00466343.
 XX
 PA (LIYY/) LI Y.
 PA (RUBE/) RUBEN S M.
 XX
 PI Li Y, Ruben SM;
 XX
 DR WPI; 2002-598724/64.
 XX
 PT New polynucleotide encoding a human G protein chemokine receptor HDGNER10,
 useful e.g. for treating tumors.
 XX
 PS Example; Fig 2; 22pp; English.
 XX
 CC The invention relates to a novel human 7-transmembrane receptor, HDGNER10,
 CC which has been identified as a G-protein chemokine receptor. The GPCR
 CC HDGNER10 polypeptide can be expressed by standard recombinant methodology.
 CC Compounds that activate or inhibit the receptor polypeptide, optionally
 CC expressed from DNA in gene therapy vectors, are used to treat diseases
 CC that require: (a) activation of the receptor (e.g. stimulation of
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis
 CC etc). The present sequence represents a human MCP-1 receptor used in
 CC comparison studies with the HDGNER10 receptor
 XX
 SQ Sequence 329 AA;

Query Match 100.0%; Score 94; DB 5; Length 329;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFGVGNML 18
 DB 28 LPPLYSLVFIFGFGVGNML 45

RESULT 13
 AAW26766
 ID AAW26766 standard; protein; 332 AA.
 XX

AC AAW26766;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Human chemokine receptor MMLR-CCR.
 XX
 DE Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;
 KW monocyte; macrophage; chemotaxis; haematopoiesis; infection;
 KW inflammation; proliferative disease; cardiovascular disease; tumour;
 KW rheumatoid arthritis; alveolitis; atherosclerosis;
 KW chronic granulomatous disease; asthma; myasthenia gravis; diabetes;
 KW inflammatory bowel disease; toxic shock syndrome; septic shock;
 KW Chediak-Higashi syndrome; therapy; diagnosis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 107..128
 FT /note= "conserved peptide"
 FT Misc-difference 121
 FT /note= "a claimed polypeptide has isoleucine at residue
 FT 121"
 XX
 PN W09741225-A2.
 XX
 PD 06-NOV-1997.
 XX
 PF 25-APR-1997; 97WO-US006993.
 XX
 PR 26-APR-1996; 96US-00638081.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Au-Young J, Bandman O, Coleman R, Wilde CG;
 XX
 DR WPI; 1997-549729/50.
 DR N-PSDB; AAT99542.
 XX
 PT Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful
 to study, diagnose and treat, e.g. infection, inflammation, solid tumour
 and proliferative and cardiovascular disease.
 XX
 PS Claim 8; Page 37-38; 59pp; English.
 XX
 CC This protein comprises human MMLR-CCR, a novel C-C chemokine receptor
 CC associated with monocyte/macrophage infiltration and chemotaxis and
 CC haematopoiesis. The amino acid sequence was deduced from a cDNA clone
 CC (see AAT99542) obtained from a cDNA library made from mononuclear cells
 CC collected on day 2 of a mixed lymphocyte culture, i.e. cells associated
 CC with inflammation and immunomodulation. Another novel chemokine receptor,
 CC MPHG-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7
 CC transmembrane spanning segments connected by a series of intracellular
 CC and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study,
 CC diagnose and treat disease states in which normal leukocyte function is
 CC perturbed by normal leukopoiesis or inappropriate activation via
 CC chemokine agonists or antagonists, such as infection, inflammation,
 CC proliferative disease, tumorigenesis, autoimmune disease, abnormal cell
 CC proliferation, solid tumours, cardiovascular disease, rheumatoid
 CC arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,
 CC asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic
 CC shock syndrome, septic shock and Chediak-Higashi syndrome
 XX
 SQ Sequence 332 AA;

Query Match 100.0%; Score 94; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFGVGNML 18
 DB 24 LPPLYSLVFIFGFGVGNML 41

RESULT 14

ABC92881
ID ABC92881 standard; peptide; 344 AA.

XX
AC ABC92881;

XX
DT 19-NOV-2002 (first entry)

XX
DE Class I receptors WSXWS motif.

XX Immunoglobulin; variable heavy chain; variable light chain; human;
KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;
KW immunologic deficiency syndrome; blood protein disorder; nephritis;
KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;
KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;
KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;
KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;
KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;
KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;
KW lymphocytopenia.

XX
OS Synthetic.

XX
PN WO200264612-A2.

XX
PD 22-AUG-2002.

XX
PF 08-FEB-2002; 2002WO-US003634.

XX
PR 09-FEB-2001; 2001US-00779880.

XX
PR 09-FEB-2001; 2001WO-US004153.

XX
PR 12-JUN-2001; 2001US-0297257P.

XX
PR 08-AUG-2001; 2001US-0310458P.

XX
PR 12-OCT-2001; 2001US-0328447P.

XX
PR 21-DEC-2001; 2001US-0341725P.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Roschke V, Rosen CA, Ruben SM;

XX
DR WPI; 2002-643455/69.

XX
PT New human G-protein Chemokine Receptor gene (HDGNR10) useful for
PT treating, preventing, ameliorating or monitoring diseases or disorders
PT associated with aberrant expression of HDGNR10 e.g. cancer.

XX
PS Example 17; Page 386; 562pp; English.

XX
CC The invention describes an isolated polynucleotide encoding a first
CC antibody at least 95-100% identical to a second antibody consisting of an
CC amino acid sequence comprising at least one, two or three CDR regions of
CC a variable heavy (VH) or variable light (VL) domain of the antibody
CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,
CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.926, XF27/28.7D5, XF27/28.18B5,
CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody
CC is useful treating, preventing, ameliorating, prognosing or monitoring
CC cancers or other diseases or disorders e.g. immunologic deficiency
CC syndromes such as blood protein disorders and ataxia telangiectasia,
CC inflammation associated disorders such as endotoxin lethality, nephritis
CC and inflammatory bowel disease, conditions associated with an increase in
CC certain haematopoietic cells such as histiocytosis, defective or aberrant
CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,
CC an infectious disease, an autoimmune disease such as Addison's disease,
CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative
CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or
CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,
CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a
CC disease or disorder associated with aberrant expression of novel human G-
CC protein chemokine receptor (CCR5) HDGNR10. This is the amino acid
CC sequence of the WSXWS motif found in class I receptors

XX
SQ Sequence 344 AA;

Query Match 100.0%; Score 94; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNNML 18
| | | | | | | | | | | | | | | | | |
DB 28 LPPLYSLVFIQFVGNNML 45

RESULT 15

ABU61655
ID ABU61655 standard; protein; 344 AA.

XX
AC ABU61655;

XX
DT 08-AUG-2003 (first entry)

XX Human monocyte chemoattractant protein 1 (MCP-1) receptor.

XX Human; G-protein chemokine receptor; receptor; HDGNR10; MCP-1;
KW 7-transmembrane receptor; monocyte chemoattractant protein 1.

XX
OS Homo sapiens.

XX
PN US2003023044-A1.

XX
PD 30-JAN-2003.

XX
PF 03-SEP-2002; 2002US-00232686.

XX
PR 06-JUN-1995; 95US-00466343.

XX
PR 18-NOV-1998; 98US-00195662.

XX
PR 25-JUN-1999; 99US-00339912.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Li Y, Ruben SM;

XX
DR WPI; 2003-456307/43.

XX
PT Producing an antibody, involves immunizing an animal with a polypeptide
PT or with a polypeptide encoded by the human G-protein chemokine receptor
PT clone in ARCC 97183, and recovering the antibody.

XX
PS Disclosure; Fig 2; 23pp; English.

XX
CC The invention relates to a method of producing an antibody, involving
CC immunising an animal with a human G-protein chemokine receptor (HDGNR10)
CC polypeptide (also referred to as a human 7-transmembrane receptor) and
CC recovering an antibody which binds the polypeptide. The method is useful
CC for producing an antibody which binds specifically to the human G-protein
CC chemokine receptor polypeptide. This sequence represents the monocyte
CC chemoattractant protein 1 (MCP-1) receptor which shares homology with the
CC HDGNR10 polypeptide of the invention

XX
SQ Sequence 344 AA;

Query Match 100.0%; Score 94; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFVGNNML 18
| | | | | | | | | | | | | | | | | |
DB 28 LPPLYSLVFIQFVGNNML 45

RESULT 16

AAW27407
ID AAW27407 standard; protein; 352 AA.

XX
AC AAW27407;

XX
DT 14-APR-1998 (first entry)

XX DE Human CCR5.
 XX KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
 KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
 KW atherosclerosis; autoimmune disorder.
 XX OS Homo sapiens.
 XX FN WO9732019-A2.
 XX PD 04-SEP-1997.
 XX PF 28-FEB-1997; 97WO-BE000023.
 XX PR 01-MAR-1996; 96EP-00870021.
 XX PR 06-AUG-1996; 96EP-00870102.
 XX PA (EURO-) EUROSCREEN SA.
 XX PI Samson M, Parmentier M, Vassart G, Libert F;
 XX DR WPI; 1997-479829/44.
 XX DR N-PSDB; AAT90117.
 XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
 PT disease and viral infection.
 XX PS Claim 4; Fig 1b-c; 94pp; English.
 XX CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but
 CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,
 CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,
 CC atherosclerosis and autoimmune disorders
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 94; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIPIFGVGNML 18
 Db 33 LPPLYSLVFIPIFGVGNML 50
 RESULT 17
 AAW27123
 ID AAW27123 standard; protein; 352 AA.
 XX AC AAW27123;
 XX DT 14-DEC-1997 (first entry)
 XX DE Human chemokine receptor 88C.
 XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
 KW modulator; antibody; human.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers

FT Domain 1..32
 FT /label= Extracellular_domain
 FT Domain 56..67
 FT /label= Intracellular_domain
 FT Domain 89..112
 FT /label= Extracellular_domain
 FT Domain 125..145
 FT /label= Intracellular_domain
 FT Domain 166..191
 FT /label= Extracellular_domain
 FT Domain 213..235
 FT /label= Intracellular_domain
 FT Domain 259..280
 FT /label= Extracellular_domain
 FT Domain 301..352
 FT /label= Intracellular_domain
 XX WO9722698-A2.
 FN 26-JUN-1997.
 XX PD 20-DEC-1996; 96WO-US020759.
 XX PF 20-DEC-1995; 95US-00575967.
 XX PR 07-JUN-1996; 96US-00661393.
 XX PA (ICOS-) ICOS CORP.
 XX PI Gray PW, Schweickart VL, Raport CJ;
 XX DR WPI; 1997-341689/31.
 XX DR N-PSDB; AAT85161.
 XX PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
 PT modulate leukocyte trafficking, e.g. for treatment of inflammation,
 PT tumours, viral infections, auto-immune diseases, etc.
 XX PS Claim 16; Page 47-48; 65pp; English.
 XX CC This polypeptide sequence comprises novel human chemokine receptor 88C, a
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
 CC macrophage library. It shows 62% identity to CCRRL1. Chemokine receptor
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
 CC and their polypeptide fragments can be produced in transformed host
 CC cells. The receptors, peptides comprising one or more of the
 CC extracellular or intracellular domains, and anti-receptor antibodies can
 CC be used to modulate receptor activities, particularly ligand and G
 CC protein binding, and are potentially useful in the treatment
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
 CC infection, AIDS, inflammatory conditions, pathological immune response,
 CC abnormal haematopoietic processes etc
 XX SQ Sequence 352 AA;
 Query Match 100.0%; Score 94; DB 2; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIPIFGVGNML 18
 Db 33 LPPLYSLVFIPIFGVGNML 50
 RESULT 18
 AAW07602
 ID AAW07602 standard; protein; 352 AA.
 XX AC AAW07602;
 XX DT 26-FEB-1997 (first entry)
 XX DE Human G-protein chemokine receptor HDGNR10.

```

XX G-protein chemokine receptor; HDGMR10; signal transduction;
KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
KW therapy.
XX
OS Homo sapiens.
XX
XX WO9639437-A1.
XX
XX 12-DEC-1996.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 1997-043072/04.
XX
XX N-PSDB; AAT44042.
XX
XX Human G-protein chemokine receptor, HDGMR10 - useful to identify
PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and
PT acute inflammation, rheumatoid arthritis, etc.
XX
XX Claim 1; Page 44-46; 61pp; English.
XX
XX Novel human mature G-protein chemokine receptor HDGMR10 (AAW07602) is a 7
CC -transmembrane protein involved in signal transduction. Its amino acid
CC sequence was deduced from a cDNA clone (AAT44042) isolated from a human
CC monocyte library. Isolation of the cDNA allows prodn. of recombinant
CC HDGMR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant
CC receptor can be used to identify agonists or antagonists of the receptor;
CC such cpds. can be used to treat conditions related to the under- and over
CC -expression of G-protein chemokine receptors
XX
XX Sequence 352 AA;
XX
Query Match 100.0%; Score 94; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
Db 33 LPPLYSLVIFGFVGNML 50

RESULT 19
AAW23835
ID AAW23835 standard; protein; 352 AA.
XX
XX AAW23835;
XX
XX 08-JUN-1998 (first entry)
XX
XX Human CC chemokine receptor 5 (CCR5).
XX
XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;
KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 29..55
XX /label= I
XX /note= "transmembrane domain"
XX Domain 104..126
XX /label= III
XX /note= "transmembrane domain"
XX Region 109..120
XX /note= "extracellular loop-1 (Claim 19)"
XX Domain 143..171

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FT /label= IV
FT Region /note= "transmembrane domain"
FT 187..210
FT /note= "extracellular loop-2 (Claim 19)"
FT Domain 194..219
FT /label= V
FT /note= "transmembrane domain"
FT 238..258
FT /label= VI
FT /note= "transmembrane domain"
FT 261..276
FT /note= "extracellular loop-3 (Claim 19)"
FT Domain 277..300
FT /label= VII
FT /note= "transmembrane domain"
XX
XX WO9745543-A2.
XX
XX 04-DEC-1997.
XX
XX 28-MAY-1997; 97WO-US009586.
XX
XX 28-MAY-1996; 96US-0018508P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Combadriere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;
XX Broder CC, Kennedy PE;
XX WPI; 1998-032650/03.
XX N-PSDB; AAT76920.
XX
XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion
PT between HIV and a target cell.
XX
XX Claim 68; Fig 1C; 70pp; English.
XX
XX This protein sequence comprises of a novel human macrophage-selective CC
XX chemokine receptor that has been designated CCR5. The sequence was
XX deduced from an isolated cDNA clone (see AAT76920). An Ala127Leu variant
XX (see W238340 of CCR5 was also identified. The susceptibility of human
XX macrophages to HIV infection depends on cell surface expression of CD4
XX and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-
XX protein coupled cell surface molecules. It plays an essential role in the
XX membrane fusion step of infection by some HIV isolates. The establishment
XX of stable, non-human cell lines and transgenic mammals having cells that
XX coexpress human CD4 and CCR5 provides valuable tools for research of HIV
XX infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding
XX agents capable of blocking membrane fusion between HIV and target cells
XX represent potential anti-HIV therapeutics for macrophage tropic strains
XX of HIV
XX
XX Sequence 352 AA;
XX
Query Match 100.0%; Score 94; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
Db 33 LPPLYSLVIFGFVGNML 50

RESULT 20
AAW88232
ID AAW88232 standard; protein; 352 AA.
XX
XX AAW88232;
XX
XX 15-MAR-1999 (first entry)
XX
XX HIV-1 co-receptor CCR5.
XX

```

KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;
KW gene therapy; human.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Domain 32..56

FT Domain /note= "transmembrane domain 1"

FT Domain 67..87

FT Domain /note= "transmembrane domain 2"

FT Misc-difference 101

FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA

FT (Stop) in CCR5m303"

FT Domain 103..124

FT Domain /note= "transmembrane domain 3"

FT Domain 142..167

FT Domain /note= "transmembrane domain 4"

FT Domain 200..223

FT Domain /note= "transmembrane domain 5"

FT Domain 236..260

FT Domain /note= "transmembrane domain 6"

FT Domain 275..301

FT Domain /note= "transmembrane domain 7"

XX WO9854317-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-EP003437.

XX 30-MAY-1997; 97US-0048057P.

XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;

XX WPI; 1999-059835/05.

XX N-PSDB; AAV84126.

XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
XX resistance of CCR5-expressing cells to HIV-1 infection.

XX Disclosure; Page 34-35; 55pp; English.

XX This is the amino acid sequence of wild-type human CCR5, which serves as
XX a co-receptor for infection by macrophage-tropic (M-tropic) strains of
XX HIV-1. The invention relates to the identification of a CCR5 variant (see
XX AAV84127), designated CCR5m303, comprising the first two transmembrane
XX domains of wild-type CCR5, but lacking transmembrane domains 3-7. The
XX presence of the CCR5m303 variant with the wild type CCR5 allele shows a
XX positive correlation with resistance to infection with M-tropic HIV-1
XX strains, and may indicate slower progression of the disease. The
XX detection of CCR5 variants may be used to identify individuals at lower
XX risk of infection relative to the general population who, if infected,
XX may exhibit slower progression to AIDS. Probes and primers (see AAV84127-
XX 36) are provided for use in diagnostic methods for detecting the presence
XX of such variants. A method is provided for inhibiting HIV-1 infection of
XX a cell expressing the CCR5 receptor. This involves introducing a nucleic
XX acid encoding a CCR5 variant into the cell, thereby reducing the number
XX of functional CCR5 molecules present on the cell surface

XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18

DB 33 LPPLYSLVFIQFGVGNML 50

RESULT 21

AAV80128

ID AAV80128 standard; protein; 352 AA.

XX AC AAV80128;

XX 19-MAY-2000 (first entry)

XX Human G-protein chemokine receptor HDGMR10 SEQ ID NO:2.
XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGMR10;
XX diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;
XX tumour; infection; leukaemia; psoriasis; allergy;
XX T-cell mediated autoimmune disease; atherogenesis; anaphylaxis;
XX inflammation; allergic reaction; silicosis; sarcoidosis;
XX rheumatoid arthritis; hyper-eosinophilia syndrome.

XX Homo sapiens.

XX US6025154-A.

XX 15-FEB-2000.

XX 06-JUN-1995; 95US-00466343.

XX 06-JUN-1995; 95US-00466343.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI; 2000-181807/16.

XX N-PSDB; AAZ91481.

XX Isolated nucleic acid encoding human G-protein chemokine receptor useful
XX for diagnostic assays, scientific research and screening for compounds
XX which bind to and activate or inhibit activation of the receptor
XX polypeptides.
XX Claim 1; Fig 1; 22pp; English.

XX The present sequence represents a human G-protein chemokine receptor
XX designated HDGMR10. HDGMR10 polynucleotides are useful in methods of
XX screening for compounds which bind to and either: (1) activate the
XX HDGMR10 polypeptides causing stimulation of haematopoiesis, wound
XX healing, coagulation, and angiogenesis; treatment of solid tumours,
XX chronic infections, leukaemia, T-cell mediated autoimmune diseases,
XX parasitic infections, psoriasis, and to stimulate growth factor activity;
XX or (2) inhibit activation of the HDGMR10 polypeptides which is useful for
XX preventing and/or treating allergy, atherogenesis, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and immunoglobulin
XX E-mediated allergic reactions, prostaglandin-independent fever, bone
XX marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and
XX hyper-eosinophilia syndrome. The polynucleotides are also useful for
XX diagnostic assays for detecting diseases related to mutations in the
XX nucleic acid sequences encoding the polypeptides and for detecting an
XX altered level of the soluble form of the receptor polypeptides. The
XX polynucleotides are also useful for in vitro purposes related to
XX scientific research, synthesis of DNA and manufacture of DNA vectors

XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18

DB 33 LPPLYSLVFIQFGVGNML 50

RESULT 22

AAV79089

ID AAV79089 standard; protein; 352 AA.

XX AAG79089;
 XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;
 XX C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.
 XX Homo sapiens.
 XX WO200164752-A2.
 XX 07-SEP-2001.
 XX 28-FEB-2001; 2001WO-US006322.
 XX 02-MAR-2000; 2000US-00517605.
 XX (UJNY) UNIV NEW YORK STATE.
 XX (UJNY) UNIV NJMEGEN.
 XX Litman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;
 XX WPI; 2001-602565/68.
 XX An antibody for the treatment or prevention of HIV-infection comprises a
 XX gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of
 XX DC-SIGN due to concomitant conformational change.
 XX Disclosure; Page 118-119; 131pp; English.
 XX The specification describes an antibody which is specific for an
 XX antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or
 XX is exposed upon gp120 binding of DC-SIGN due to concomitant
 XX conformational change. DC-SIGN is a receptor that is specifically
 XX expressed on dendritic cells and facilitates infection of T lymphocytes
 XX with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC
 XX -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)
 XX with high affinity. The antibody of the invention inhibits the trans
 XX enhancement of HIV entry into a T cell or macrophage facilitated by
 XX dendritic cells. The antibody is useful to treat or prevent HIV
 XX infection. The present sequence represents a human CCR5 protein, which is
 XX a translocation promoting agent that interacts with CD4. This receptor
 XX functions in HIV-1 entry into cells
 XX Sequence 352 AA;
 XX
 XX Query Match 100.0%; Score 94; DB 4; Length 352;
 XX Best Local Similarity 100.0%; Pred. No. 3e-07;
 XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 LPPLSLVFIQGVGNML 18
 XX
 XX Db 33 LPPLSLVFIQGVGNML 50
 XX
 XX RESULT 23
 XX AAE07046
 XX ID AAE07046 standard; protein; 352 AA.
 XX
 XX AAE07046;
 XX
 XX 16-OCT-2001 (first entry)
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 XX human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 XX cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 XX neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 XX Rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;

KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Domain 1..36 /label= Extracellular_domain
 XX Domain 37..305 /label= Transmembrane_domain
 XX Domain 37..58 /label= Transmembrane_domain
 XX /note= "Segment 1"
 XX Domain 59..67 /label= Intracellular_loop_1
 XX Domain 68..88 /label= Transmembrane_domain
 XX /note= "Segment 2"
 XX Domain 89..102 /label= Extracellular_loop_1
 XX Domain 103..124 /label= Transmembrane_domain
 XX /note= "Segment 3"
 XX Domain 125..141 /label= Intracellular_loop_2
 XX Domain 142..166 /label= Transmembrane_domain
 XX /note= "Segment 4"
 XX Domain 167..195 /label= Extracellular_loop_2
 XX Domain 196..223 /label= Transmembrane_domain
 XX /note= "Segment 5"
 XX Domain 224..235 /label= Intracellular_loop_3
 XX Domain 236..260 /label= Transmembrane_domain
 XX /note= "Segment 6"
 XX Domain 261..274 /label= Extracellular_loop_3
 XX Domain 287..305 /label= Transmembrane_domain
 XX /note= "Segment 7"
 XX Domain 306..352 /label= Intracellular_domain
 XX
 XX WO200158916-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US004153.
 XX 09-FEB-2000; 2000US-0181258P.
 XX 03-MAR-2000; 2000US-0187999P.
 XX 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2001-488966/53.
 XX N-PSDB; AAD13282.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 XX (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
 XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 XX neurodegenerative disorders.
 XX Claim 102; Fig 1; 518pp; English.
 XX The invention relates to human G-protein chemokine receptor (CCR5)

CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGMR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein
 XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFVGNML 18
 DB 33 LPPLYSLVIFGFVGNML 50

RESULT 24
 ID AAE07048
 AC AAE07048; protein; 352 AA.

16-OCT-2001 (first entry)

Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.

Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;
 neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 cardiovascular disorder; myocardial ischaemia.

Homo sapiens.

WO200158916-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US0004153.

09-FEB-2000; 2000US-0181258P.

09-MAR-2000; 2000US-0187999P.

22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Roschke V, Li Y, Ruben SM;

WFI; 2001-488966/53.

N-PSDB; AAD13299.

PT Isolated nucleic acid encoding a human G-protein chemokine receptor
 PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 PT neurodegenerative disorders.

XX Example 40; Page 504-505; 518pp; English.

CC The invention relates to human G-protein chemokine receptor (CCR5)
 CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are
 CC useful for treating, preventing or ameliorating a disease or disorder
 CC associated with inflammation, defective or aberrant chemotaxis of immune
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell
 CC interaction. The disease or disorder may also be an infectious disease
 CC (e.g. a viral infection such as an early stage HIV infection, a
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
 CC function. CCR5 HDGMR10 protein is used as a food additive or preservative
 CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful
 CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,
 CC protein, antibodies, agonists and antagonists are also useful in the
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
 CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
 CC present sequence is human CCR5 HDGMR10 protein
 XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFVGNML 18
 DB 33 LPPLYSLVIFGFVGNML 50

RESULT 25

AAAG80111

ID AAG80111 standard; protein; 352 AA.

AC AAG80111;

17-JAN-2002 (first entry)

Human CCR5 protein.

Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 antirheumatic; antiarthritic.

Homo sapiens.

WO200172830-A2.

04-OCT-2001.

02-APR-2001; 2001WO-EP003708.

31-MAR-2000; 2000DE-01016013.

(IPFP-) IPF PHARM GMBH.

(FORS/) FORSMANN U.

Forssmann W, Adermann K, Heitland A, Spodberg N;

DR WPI; 2001-626256/72.
 XX
 XX Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.
 XX
 XX Disclosure; Page 10; 26pp; German.
 XX
 XX This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antirheumatic, antiarthritic,
 CC immunosuppressive, dermatological, antitumor, antiproliferative and
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AG8004S-AG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
 |||||
 DB 33 LPPLYSLVIFGFGVGNML 50

RESULT 26

AAE04321
 ID AAE04321 standard; protein; 352 AA.

AC AAE04321;

DT 04-SEP-2001 (first entry)

XX Human chemokine receptor (CCR), CC-CR-5 related protein #2.

XX Human; transformed mammalian cell; CD4; reporter gene; translocation;
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;
 KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;
 KW CC-CR-5; envelope glycoprotein; anti-HIV.

OS Homo sapiens.

XX US6258527-B1.

XX 10-JUL-2001.

XX 21-MAY-1997; 97US-00861105.

XX 20-MAY-1996; 96US-0017157P.

XX 19-JUN-1996; 96US-0020043P.

XX 19-MAY-1997; 97US-00858660.

XX (AARO-) AARON DIAMOND AIDS RES CENT.
 PA (UUNY) UNIV NEW YORK STATE.

XX Littnan DR, Deng H, Ellmeier W, Landau NR, Liu R;

XX WPI; 2001-417127/44.

XX N-PSDB; AAD08577.

XX Transformed mammalian cell (I) that contains a CD4 gene, reporter gene
 PT and HIV LTR for identification of drugs and antibodies for treatment of

PT HIV.
 XX
 XX Disclosure; Col 47-50; 37pp; English.
 XX
 CC The present invention relates to a transformed mammalian cell that
 CC contains a gene encoding CD4, a construct encoding a reporter gene under
 CC the regulation of an human immuno deficiency virus (HIV) long terminal
 CC repeat (LTR) and that has been transduced with a vector encoding a human
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the
 CC cell surface of transformed mammalian cell. The invention is useful for
 CC identifying drugs or antibodies that interfere with the translocation of
 CC HIV into transformed mammalian cell or for identifying a human chemokine
 CC receptor that facilitates the infection of a particular HIV strain into
 CC the transformed mammalian cell. Compounds identified can be used to treat
 CC cellular dysfunction and to prevent or combat HIV infection. The present
 CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.
 CC CC-CR-5 is the principal cofactor for entry mediated by the envelope
 CC glycoproteins of primary macrophage-tropic strains of HIV-1
 XX
 SQ Sequence 352 AA;

Query Match 100.0%; Score 94; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18

|||||

DB 33 LPPLYSLVIFGFGVGNML 50

RESULT 27

AAE07037

ID AAE07037 standard; protein; 352 AA.

XX AAE07037;

DT 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytostatic; immunosuppressive; neotropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..36 /label= Extracellular_domain

FT Domain 37..305 /label= Transmembrane_domain

FT Domain 37..58 /label= Transmembrane_domain

FT Domain /note= "Segment 1"

FT Domain 59..67 /label= Intracellular_loop_1

FT Domain 68..88 /label= Transmembrane_domain

FT Domain /note= "Segment 2"

FT Domain 89..102 /label= Extracellular_loop_1

FT Domain 103..124 /label= Transmembrane_domain

FT Domain /note= "Segment 3"

FT Domain 125..141 /label= Intracellular_loop_2

FT Domain 142..166

FT /label= Transmembrane_domain
 FT /note= "Segment 4"
 FT Domain 167..195
 FT /label= Extracellular_loop_2
 FT Domain 196..223
 FT /label= Transmembrane_domain
 FT /note= "Segment 5"
 FT Domain 224..235
 FT /label= Intracellular_loop_3
 FT Domain 236..260
 FT /label= Transmembrane_domain
 FT /note= "Segment 6"
 FT Domain 261..274
 FT /label= Extracellular_loop_3
 FT Domain 287..305
 FT /label= Transmembrane_domain
 FT /note= "Segment 7"
 FT Domain 306..352
 FT /label= Intracellular_domain
 FT
 PN WO200158915-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-US0004152.
 XX 09-FEB-2000; 2000US-0181258P.
 XX 09-MAR-2000; 2000US-0187999P.
 XX 22-SEP-2000; 2000US-0234336P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2001-488965/53.
 XX N-PSDB; AAD13181.
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 neurodegenerative disorders.
 XX Claim 102; Fig 1; 495pp; English.
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10
 protein. CCR5 HDGMR10 cDNA is included in ATCC Deposit No: 97183. CCR5
 HDGMR10 antibodies are useful for treating, preventing or ameliorating a
 disease or disorder associated with inflammation, defective or aberrant
 chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii
 pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen
 presenting cell interaction. The disease or disorder may also be an
 infectious disease (e.g. a viral infection such as an early stage HIV
 infection, a cytomegalovirus infection, or a poxvirus infection), an
 autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative
 disorder. The disease or disorder may be associated with aberrant CCR5
 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or
 lack of CCR5 ligand function. CCR5 HDGMR10 protein is used as a food
 additive or preservative to increase or decrease storage capabilities.
 CCR5 HDGMR10 DNA are useful for chromosome identification and in gene
 therapy. CCR5 HDGMR10 DNA, protein, antibodies, agonists and antagonists
 are also useful in the diagnosis, treatment and prevention of cancer
 (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,
 liver, lung, urogenital); immune disorders (Addison's disease, allergies,
 autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
 Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 colitis); cardiovascular disorders (myocardial ischaemias) and wound
 healing
 XX Sequence 352 AA;
 SQ Query Match 100.0%; Score 94; DB 4; Length 352;
 Best Local Similarity 100.0%; Pred. No. 3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVFIKFGVGNML 18
 |||||
 Db 33 LPPLSLVFIKFGVGNML 50
 RESULT 28
 AAE07039
 ID AAE07039 standard; protein; 352 AA.
 XX
 AC AAE07039;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.
 XX
 KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;
 KW cytotatic; immunosuppressive; neutropic; neuroprotective; gene therapy;
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
 KW cardiovascular disorder; myocardial ischaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200158915-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US0004152.
 XX
 PR 09-FEB-2000; 2000US-0181258P.
 PR 09-MAR-2000; 2000US-0187999P.
 PR 22-SEP-2000; 2000US-0234336P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Roschke V, Li Y, Ruben SM;
 XX WPI; 2001-488965/53.
 XX N-PSDB; AAD13198.
 DR
 DR Isolated nucleic acid encoding a human G-protein chemokine receptor
 (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
 neurodegenerative disorders.
 XX
 XX Example 40; Page 486-487; 495pp; English.
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10
 protein. CCR5 HDGMR10 antibodies are useful for treating, preventing or
 ameliorating a disease or disorder associated with inflammation,
 defective or aberrant chemotaxis of immune cells, HIV infection (such as
 Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or
 aberrant T-cell antigen presenting cell interaction. The disease or
 disorder may also be an infectious disease (e.g. a viral infection such
 as an early stage HIV infection, a cytomegalovirus infection, or a
 poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or
 a neurodegenerative disorder. The disease or disorder may be associated
 with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5
 ligand expression, or lack of CCR5 ligand function. CCR5 HDGMR10 protein
 is used as a food additive or preservative to increase or decrease
 storage capabilities. CCR5 HDGMR10 DNA are useful for chromosome
 identification and in gene therapy. CCR5 HDGMR10 DNA, protein,
 antibodies, agonists and antagonists are also useful in the diagnosis,
 treatment and prevention of cancer (breast, ovary, adrenal gland, bone,
 bone marrow, gastrointestinal tract, liver, lung, urogenital); immune
 disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,
 autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular

CC disorders (myocardial ischaemias) and wound healing

XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGFGVGNML 18

|||||

Db 33 LPPLSLVIFGFGVGNML 50

RESULT 29

AAB46858

ID AAB46858 standard; protein; 352 AA.

XX AAB46858;

XX 16-AUG-2001 (revised)

DT 02-AUG-2001 (revised)

DT 04-MAY-2001 (first entry)

XX Human HDGMR10 protein.

XX HDGMR10; human; G-protein chemokine receptor; antiinflammatory;

KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;

KW cytostatic; antiparasitic; antipsoptic; antirheumatic; antiarthritic;

KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;

KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;

KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;

KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;

KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;

KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;

KW hyper-eosinophilic syndrome; vulnery.

XX Homo sapiens.

XX US2001000241-A1.

XX 12-APR-2001.

XX 29-NOV-2000; 2000US-00725285.

XX 06-JUN-1995; 95US-00466343.

XX 18-NOV-1998; 98US-00195662.

XX 25-JUN-1999; 99US-00339912.

XX (LIYY/) LI Y.

PA (RUBE/) RUBEN S M.

XX Li Y, Ruben SM;

XX WPI: 2001-226317/23.

XX N-PSDB; AAF26390.

XX New human G-protein chemokine receptor polypeptides and polynucleotides,

PT useful for identifying (ant)agonists to the G-protein chemokine receptor.

XX Claim 1a; Page 15; 22pp; English.

XX This invention describes a novel receptor polypeptide (I) selected from

CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the

CC specification; and (ii) a polypeptide encoded by the cDNA contained in a

CC plasmid, and fragments, analogs and derivatives of the polypeptide. The

CC products of the invention have antiinflammatory, immunomodulatory,

CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic,

CC antiparasitic, antipsoptic, antirheumatic, antiarthritic and vasotropic

CC activity and can be used for gene therapy. The G-protein chemokine

CC receptors, HDGMR10, (I) are useful for screening for compounds which

CC activate or inhibit activation of (I). The products of the invention can

CC also be used for stimulating haematopoiesis, wound healing, coagulation,

CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-

CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and

CC stimulating growth factor activity. HDGMR10 is useful for treating

CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute

CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic

CC reactions, prostaglandin-independent fever, bone marrow failure,

CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-

CC eosinophilic syndrome. (N.B. This record was resubmitted to correct

CC errors in the keyword formatting)

XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGFGVGNML 18

|||||

Db 33 LPPLSLVIFGFGVGNML 50

RESULT 30

ABB56342

ID ABB56342 standard; protein; 352 AA.

XX ABB56342;

XX 18-FEB-2002 (first entry)

XX Non-endogenous human GPCR protein, SEQ ID NO: 477.

XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;

KW constitutively activated GPCR; agonist; disease.

XX Homo sapiens.

XX Synthetic.

XX WO200177172-A2.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-US011098.

XX 07-APR-2000; 2000US-0195747P.

XX (AREN-) ARENA PHARM INC.

XX Lehmann-Bruinsma K, Liaw CW, Lin I;

XX WPI: 2001-648759/74.

XX N-PSDB; ABI97978.

XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in

XX disease treatment, comprises contacting candidate compounds with versions

XX of GPCRs.

XX Claim 1; Page 277-278; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which

XX the endogenous ligand has been identified. Non-endogenous constitutively

XX activated versions of known GPCRs are used in the invention for the

XX direct identification of candidate compounds as receptor agonists,

XX inverse agonists or partial agonists. Such agonists are useful as

XX therapeutic agents for diseases or disorders associated with GPCRs. The

XX present sequence is a non-endogenous version of a known human GPCR

XX Sequence 352 AA;

Query Match 100.0%; Score 94; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 3e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGFGVGNML 18

|||||

Db 33 LPPLYSLVFIFGFVGNML 50

Search completed: March 4, 2004, 17:59:20
Job time : 45.7959 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 9.18367 Seconds
(without alignments)
188.535 Million cell updates/sec

Title: US-10-084-813-11
Perfect score: 94
Sequence: 1 LPPLYSILVFIFGVGNML 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	100.0	352	2 J03113	chemokine (C-C) re
2	94	100.0	360	2 J02443	chemokine (C-C) re
3	94	100.0	374	2 J38450	chemokine (C-C) re
4	77	81.9	355	2 A51177	chemokine (C-C) re
5	77	81.9	355	2 I49339	macrophage inflam
6	77	81.9	359	2 I49341	MIP-1 alpha recept
7	75	79.8	360	2 A57160	chemokine (C-C) re
8	66	70.2	360	2 J04587	chemokine (C-C) re
9	63	67.0	355	2 G02436	chemokine (C-C) re
10	62	66.0	383	2 S55594	G protein-coupled
11	60	63.8	356	2 I49340	G protein-coupled
12	60	63.8	361	2 B45680	MIP-1 alpha recept
13	59	62.8	373	2 J04162	G protein-coupled
14	59	62.8	373	2 J04737	P2Y receptor - bov
15	58	61.7	354	2 I58186	G protein-coupled
16	57	60.6	352	2 G00048	probable G protein
17	57	60.6	352	2 A45747	fusin (FUSRA) - c
18	57	60.6	362	2 S33733	neuropeptide Y/pep
19	57	60.6	367	2 J03049	G protein-coupled
20	56	59.6	316	2 T23640	interferon-inducib
21	56	59.6	327	2 S56162	hypothetical prote
22	56	59.6	333	2 S28787	MDCK15 protein - h
23	56	59.6	359	2 J01104	neuropeptide Y/pep
24	56	59.6	359	2 J04425	angiotensin II rec
25	56	59.6	359	2 J01194	angiotensin II rec
26	56	59.6	359	2 A48857	angiotensin II rec
27	56	59.6	359	2 A42656	angiotensin II rec
28	56	59.6	359	2 I54003	angiotensin II rec
29	56	59.6	359	2 I39418	angiotensin II rec

30	56	59.6	359	2 JH0621	angiotensin II rec
31	56	59.6	359	2 JC2134	angiotensin II rec
32	56	59.6	372	2 S26667	G protein-coupled
33	56	59.6	374	2 S42628	G protein-coupled
34	56	59.6	374	2 S32785	G protein-coupled
35	56	59.6	387	2 I69202	G protein-coupled
36	54	57.4	359	2 J01516	angiotensin II rec
37	54	57.4	359	2 I51372	angiotensin II rec
38	53	56.4	323	1 Q08ED3	HHRF3 protein - hu
39	53	56.4	354	2 T09353	G protein-coupled
40	53	56.4	369	2 JC5068	G protein-coupled
41	52	55.3	326	2 T25301	hypothetical prote
42	52	55.3	416	2 S68822	neurotensin recept
43	50	53.2	175	2 C63198	conserved hypothet
44	50	53.2	380	2 JC2434	kappa opioid recep
45	50	53.2	380	2 A48227	kappa opioid recep
46	50	53.2	380	2 JC2338	kappa opioid recep
47	50	53.2	380	2 S36143	kappa opioid recep
48	50	53.2	380	2 A55259	kappa opioid recep
49	50	53.2	387	2 JC5949	galanin receptor 2
50	50	53.2	821	2 E95245	penicillin-binding
51	50	53.2	821	2 E95110	peptidoglycan glyc
52	49	52.1	380	2 I38435	angiotensin recept
53	48	51.1	355	2 JC4304	orphan G protein-c
54	48	51.1	384	2 A39003	bombesin/gastrin-r
55	48	51.1	384	2 I57682	bombesin/GRP rece
56	48	51.1	425	2 T15959	hypothetical prote
57	48	51.1	584	2 JC7809	sulfakinin recepto
58	47	50.0	360	2 G02064	G protein-coupled
59	47	50.0	363	2 I48261	angiotensin II rec
60	47	50.0	363	2 A49092	angiotensin II rec
61	47	50.0	363	2 JC2543	angiotensin II rec
62	47	50.0	370	1 I52315	G protein-coupled
63	46.5	49.5	376	2 T24368	hypothetical prote
64	46	48.9	362	2 JN0694	angiotensin II rec
65	46	48.9	560	2 H71712	60 kd inner-membra
66	46	48.9	560	2 B97709	60K inner-membra
67	45.5	48.4	472	2 F90078	hypothetical prote
68	45	47.9	174	2 T11400	NADH2 dehydrogenas
69	45	47.9	177	2 D72512	hypothetical prote
70	45	47.9	213	2 E64030	probable holoctoc
71	45	47.9	333	2 I65989	G protein-coupled
72	45	47.9	341	2 S63666	platelet activatin
73	45	47.9	342	2 S13638	platelet-activatin
74	45	47.9	420	2 I51667	thrombin receptor
75	45	47.9	427	2 S50150	gastric CCK-A rece
76	45	47.9	428	2 JN0692	cholecystokinin ty
77	45	47.9	430	2 I51898	cholecystokinin A
78	44	46.8	323	2 S61919	B-alpha pheromone
79	44	46.8	328	2 I55450	G protein-coupled
80	44	46.8	341	2 S43252	platelet-activatin
81	44	46.8	342	2 A40191	platelet-activatin
82	44	46.8	350	2 JN0621	G protein-coupled
83	44	46.8	384	2 A41007	gastrin-releasing
84	44	46.8	390	2 B41007	bombesin receptor,
85	44	46.8	444	2 T27866	hypothetical prote
86	44	46.8	455	2 T15622	hypothetical prote
87	43.5	46.3	411	2 A82492	hypothetical prote
88	43	45.7	178	2 A64399	hypothetical prote
89	43	45.7	241	2 S01147	H+-transporting tw
90	43	45.7	295	2 AD3552	high-affinity bran
91	43	45.7	295	2 AH3063	hypothetical prote
92	43	45.7	295	2 H98222	hypothetical prote
93	43	45.7	295	2 H86907	transporter yxfa l
94	43	45.7	351	1 A46525	complement C5a ana
95	43	45.7	355	2 JC5067	G protein-coupled
96	43	45.7	373	2 J00087	delta opioid recep
97	43	45.7	378	2 A45680	G protein-coupled
98	43	45.7	378	2 B55735	lymphocyte-specific
99	43	45.7	444	2 A42685	cholecystokinin re
100	43	45.7	488	2 A53572	prostaglandin E2 r

chemokine (C-C) receptor 5 - human
N:Alternate names: C-C CKR-5; CCR5
C:Species: Homo sapiens (man)
C:Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000
C:Accession: A43113; S71808; A58832; G02653; A58833
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.
Biochemistry 35, 3362-3367, 1996
A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor
A:Reference number: A43113; MUID:96241590; PMID:8639485
A:Accession: A43113
A:Molecule type: mRNA
A:Residues: 1-352 <SAM1>
A:Cross-references: GB:X91492; NID:gl262810; PIDN:CAAG2796.1; PID:gl262811
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Llesnard, C.; Barber, C.M.; Sargost
M.; Inai, T.; Rana, S.; Yi, Y.; Smyth, R.G.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.; Nature 382, 722-725, 1996
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the A/A, A/R, and R/R genotypes of the CC chemokine receptor 5 gene
A:Reference number: S71808; MUID:96345670; PMID:8751444
A:Accession: S71808
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 182-206; 207-230 <SAM2>
A:Accession: A58833
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-184; 'IKDSHLGAGPAAACHGILLGNPKNSASVSK' <SAM3>
A:Cross-references: GB:X99393; NID:gl524062; PIDN:CAAG7767.1; PID:gl524063
A:Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection and may have had a selective advantage by conferring resistance to Yersinia plague infection
R:Combadieere, C.; Anujya, S.K.; Tiffany, H.L.; Murphy, P.M.; J. Leukoc. Biol. 60, 147-152, 1996
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor
A:Reference number: A58832; MUID:96295970; PMID:8699119
A:Accession: A58832
A:Molecule type: mRNA
A:Residues: 1-352 <COM1>
A:Cross-references: GB:U57840; NID:gl502408; PIDN:AAB17071.1; PID:gl502409
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes
R:Combadieere, C. submitted to the EMBL Data Library, May 1996
A:Reference number: H01541
A:Accession: G02653
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-89, 'L', 91-352 <COM2>
A:Cross-references: EMBL:U57840
R:Raport, C.J.; Goelling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.
J. Biol. Chem. 271, 17161-17166, 1996
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor
A:Reference number: A58833; MUID:96291862; PMID:8663314
A:Accession: A58833
A:Molecule type: mRNA
A:Residues: 1-352 <RAP>
A:Cross-references: GB:U54994; NID:gl457945; PIDN:AACS0598.1; PID:gl457946
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30574) and dual-tropic strains of HIV-1 bind to a complex of chemokine C-C Genetics.
A:Gene: GGB:CKR5; CCR5; CC-CKR-5; CCR5; ChemR13
A:Cross-references: GDB:I230510; OMIM:601373
A:Map position: 3p21-3p21
C:Function:
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES
A:Note: probably acts to control granulocyte proliferation and differentiation
C:Superfamily: vertebrate rhodopsin
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
F:32-56/Domain: transmembrane #status predicted <TM1>
F:67-87/Domain: transmembrane #status predicted <TM2>
F:103-124/Domain: transmembrane #status predicted <TM3>

C:Accession: I38450
 R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994
 A:Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2
 A:Reference number: A53477; MUID:94195821; PMID:8146186
 A:Accession: I38450
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-374 <RES>
 A:Cross-references: EMBL:U03882; NID:g472555; PIDN:AAAL9119.1; PID:g472556
 C:Genetics:
 A:Gene: GDB:CMKBR2
 A:Cross-references: GDB:337364; OMIM:601267
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein
 F:44-68/Domain: transmembrane #status predicted <TM1>
 F:79-99/Domain: transmembrane #status predicted <TM2>
 F:115-136/Domain: transmembrane #status predicted <TM3>
 F:154-178/Domain: transmembrane #status predicted <TM4>
 F:208-226/Domain: transmembrane #status predicted <TM5>
 F:244-265/Domain: transmembrane #status predicted <TM6>
 F:282-309/Domain: transmembrane #status predicted <TM7>
 F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:32-277,113-190/Disulfide bonds: #status predicted
 Query Match 100.0%; Score 94; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIFGVGNML 18
 Db 45 LPPLYSLVFIFGVGNML 62
 RESULT 4
 A45177
 chemokine (C-C) receptor 1 - human
 N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
 C:Accession: A45177; I55671
 R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
 Cell 72, 415-425, 1993
 A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-C chemokine receptor
 A:Reference number: A45177; MUID:93161416; PMID:7679328
 A:Accession: A45177
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-355 <NEO>
 A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 A:Experimental source: HL60 cells
 A:Note: sequence extracted from NCBI backbone (NCBI:124876)
 R:Gao, J.
 J. Exp. Med. 177, 1421-1427, 1993
 A:Title: Structure and functional expression of the human macrophage inflammatory protein 1 alpha
 A:Reference number: I55671; MUID:93240122; PMID:7683036
 A:Accession: I55671
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-355 <RES>
 A:Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
 C:Genetics:
 A:Gene: GDB:CMKBR1; CMKR-1
 A:Cross-references: GDB:138446; OMIM:601159
 A:Map position: 3p21-3p21
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
 F:36-60/Domain: transmembrane #status predicted <TM1>
 F:71-91/Domain: transmembrane #status predicted <TM2>
 F:108-129/Domain: transmembrane #status predicted <TM3>
 F:147-171/Domain: transmembrane #status predicted <TM4>
 F:205-223/Domain: transmembrane #status predicted <TM5>

F:240-264/Domain: transmembrane #status predicted <TM6>
 F:288-305/Domain: transmembrane #status predicted <TM7>
 F:5/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:24-273,106-183/Disulfide bonds: #status predicted
 F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 Query Match 81.9%; Score 77; DB 2; Length 355;
 Best Local Similarity 77.8%; Pred. No. 6.4e-05;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIFGVGNML 18
 Db 37 LPPLYSLVFIFGVGNML 54
 RESULT 5
 I49339
 macrophage inflammatory protein-1 alpha receptor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
 C:Accession: I49339
 R:Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine genes
 A:Reference number: I49339; MUID:95340546; PMID:7542241
 A:Accession: I49339
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-355 <RES>
 A:Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548
 C:Superfamily: vertebrate rhodopsin
 Query Match 81.9%; Score 77; DB 2; Length 355;
 Best Local Similarity 83.3%; Pred. No. 6.4e-05;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIFGVGNML 18
 Db 37 LPPLYSLVFIFGVGNML 54

RESULT 6
 I49341
 MIP-1 alpha receptor like-2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 02-Jul-1998
 C:Accession: I49341
 R:Gao, J.L.; Murphy, P.M.
 J. Biol. Chem. 270, 17494-17501, 1995
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine genes
 A:Reference number: I49341; MUID:95340546; PMID:7542241
 A:Accession: I49341
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-355 <RES>
 A:Cross-references: EMBL:U28406; NID:g881551; PID:g881552
 C:Superfamily: vertebrate rhodopsin
 Query Match 81.9%; Score 77; DB 2; Length 359;
 Best Local Similarity 77.8%; Pred. No. 6.4e-05;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIFGVGNML 18
 Db 41 LPPLYSLVFIFGVGNML 58

RESULT 7
 A57160
 chemokine (C-C) receptor 4 - human
 N:Alternate names: C-C CKR-4
 C:Species: Homo sapiens (man)
 C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000

C;Accession: A57160
 R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.; W
 J. Biol. Chem. 270, 19495-19500, 1995
 A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor c
 C;Date: 21-Dec-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 A;Reference number: A57160; MUID:95370289; PMID:7642634
 A;Accession: A57160
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-360 <POW>
 A;Cross-references: GB:X85740; NID:gl370103; PIDN:CAA59743.1; PID:g971452
 A;Note: source clone K5-5
 C;Genetics:
 A;Gene: GDB:CMKBR4
 A;Cross-references: GDB:677463
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F;40-65/Domain: transmembrane #status predicted <TM1>
 F;76-97/Domain: transmembrane #status predicted <TM2>
 F;112-133/Domain: transmembrane #status predicted <TM3>
 F;151-175/Domain: transmembrane #status predicted <TM4>
 F;208-226/Domain: transmembrane #status predicted <TM5>
 F;243-264/Domain: transmembrane #status predicted <TM6>
 F;291-308/Domain: transmembrane #status predicted <TM7>
 F;29-276,110-187/Disulfide bonds: #status predicted
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 Query Match 79.8%; Score 75; DB 2; Length 360;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIPIFGVGN 16
 |||||:|:|:|
 DB 42 LPPLSLVFIPIFGVGN 57
 RESULT 8
 JC4587
 chemokine (C-C) receptor 4 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
 C;Accession: JC4587
 R;Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996
 A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to
 A;Reference number: JC4587; MUID:96136324; PMID:8573157
 A;Accession: JC4587
 A;Molecule type: mRNA
 A;Residues: 1-360 <HOO>
 A;Cross-references: EMBL:X90862; NID:gl167851; PIDN:CAA62372.1; PID:gl167852
 A;Experimental source: thymus
 C;Genetics:
 A;Gene: cc ckr-4
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
 F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 Query Match 70.2%; Score 66; DB 2; Length 360;
 Best Local Similarity 75.0%; Pred. No. 0.0041;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIPIFGVGN 16
 |||||:|:|:|
 DB 42 LPPLSLVFIPIFGVGN 57
 RESULT 9
 JC4587
 chemokine (C-C) receptor 3 - human
 N;Alternate names: C-C CKR-3
 C;Species: Homo sapiens (man)
 C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 04-Mar-2000
 C;Accession: G02436; A57237
 R;Ponath, P.D.
 submitted to the EMBL Data Library, February 1996
 A;Reference number: H01272
 A;Accession: G02436
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-355 <PON>
 A;Cross-references: EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477561
 R;Comadriere, C.; Abuja, S.K.; Murphy, P.M.
 J. Biol. Chem. 270, 16491-16494, 1995
 A;Title: Cloning and functional expression of a human eosinophil CC chemokine receptor.
 A;Reference number: A57237; MUID:95348056; PMID:7622448
 A;Accession: A57237
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>
 A;Cross-references: GB:U28694; NID:gl199579; PIDN:AAC50469.1; PID:gl199580
 A;Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC50469.
 C;Genetics:
 A;Gene: GDB:CMKBR3
 A;Cross-references: GDB:579624; OMIM:601268
 A;Map position: 3p21-3p21
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
 F;36-60/Domain: transmembrane #status predicted <TM1>
 F;71-91/Domain: transmembrane #status predicted <TM2>
 F;108-129/Domain: transmembrane #status predicted <TM3>
 F;147-171/Domain: transmembrane #status predicted <TM4>
 F;205-223/Domain: transmembrane #status predicted <TM5>
 F;240-261/Domain: transmembrane #status predicted <TM6>
 F;288-305/Domain: transmembrane #status predicted <TM7>
 F;24-273,106-183/Disulfide bonds: #status predicted
 F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
 Query Match 67.0%; Score 63; DB 2; Length 355;
 Best Local Similarity 61.1%; Pred. No. 0.012;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIPIFGVGNML 18
 |||||:|:|:|
 DB 37 VPPLSLVFIPIFGVGNV 54
 RESULT 10
 S55594
 G protein-coupled receptor E1 - equine herpesvirus 2
 C;Species: equine herpesvirus 2
 C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
 C;Accession: S55594
 R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.
 J. Mol. Biol. 249, 520-528, 1995
 A;Title: The DNA sequence of equine herpesvirus 2.
 A;Reference number: S55594; MUID:95302501; PMID:7783207
 A;Accession: S55594
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-383 <TEL>
 A;Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: G protein-coupled receptor
 Query Match 66.0%; Score 62; DB 2; Length 383;
 Best Local Similarity 61.1%; Pred. No. 0.02;
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LPPLSLVFIPIFGVGNML 18
 |||||:|:|:|

P2Y receptor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
 C:Accession: JCA162
 R:Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
 Biochem. Biophys. Res. Commun. 212, 648-656, 1995
 A:Title: Cloning and characterisation of a bovine P2Y receptor.
 A:Reference number: JCA162, PMID:9532058; PMID:7626079
 A:Accession: JCA162
 A:Molecule type: mRNA
 A:Residues: 1-373 <HEN>
 A:Cross-references: EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g1032485
 A:Experimental source: aortic endothelial cell

C/Accession: AF0574; AF3103; AF3006; L39444; U82461
R/Federiciel, B.; Melhado, I.G.; Duncan, A.N.V.; Delaney, A.; Schappert, K.; Clark-Lewis,
I. Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a putative

Query Match 60.6%; Score 57; DB 2; Length 362;
 Best Local Similarity 68.8%; Pred. No. 0.12;
 Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNL 16
 ||:|||||:|:|
 Db 43 LPTVYILVITGFLGN 58

RESULT 19
 JE0349
 interferon-inducible protein 10 (IP-10) receptor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
 C:Accession: JE0349
 R:Tamari, M.; Tomimaga, Y.; Yatsunami, K.; Narumi, S.
 Biochem. Biophys. Res. Commun. 251, 41-48, 1998
 A>Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
 A:Reference number: JE0349; MUID:99009219; PMID:9790904
 A:Accession: JE0349
 A:Molecule type: mRNA
 A:Residues: 1-367 <TAM>
 A:Cross-references: DDBJ:AB031174; NID:93798731; PIDN:BA34045.1; PID:93798732
 C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
 C:Superfamily: vertebrate rhodopsin

Query Match 60.6%; Score 57; DB 2; Length 367;
 Best Local Similarity 62.5%; Pred. No. 0.12;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNL 16
 ||:|||||:|:|
 Db 55 LPALYSLLFLGLGN 70

RESULT 20
 T23640
 hypothetical protein M01B2.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T23640
 R:Lloyd, C.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19776
 A:Accession: T23640
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-316 <WIL>
 A:Cross-references: EMBL:Z83116; PIDN:CAB05565.1; GSPDB:GN00023; CESP:M01B2.7
 A:Experimental source: clone M01B2
 C:Genetics:
 A:Gene: CESP:M01B2.7
 A:Map position: 5
 A:Introns: 34/2; 72/1; 108/2; 160/2; 205/1; 272/2

Query Match 59.6%; Score 56; DB 2; Length 316;
 Best Local Similarity 66.7%; Pred. No. 0.15;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LYSLVIFFGVGNL 18
 ||:|||||:|:|
 Db 11 LYSTIFVGTGNL 25

RESULT 21
 S56162
 MCKR15 protein - human
 C:Species: Homo sapiens (man)
 C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
 C:Accession: S56162
 R:Barella, L.; Loetscher, M.; Tobler, A.; Baggiolini, M.; Moser, B.
 Biochem. J. 309, 773-779, 1995

A>Title: Sequence variation of a novel heptahelical leucocyte receptor through alternati
 A:Reference number: S56162; MUID:95366951; PMID:7639692
 A:Accession: S56162
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-327 <BAR>
 A:Cross-references: EMBL:X68829; NID:9840783; PIDN:CAA48723.1; PID:9840784
 C:Superfamily: vertebrate rhodopsin

Query Match 59.6%; Score 56; DB 2; Length 327;
 Best Local Similarity 50.0%; Pred. No. 0.16;
 Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNL 18
 :|||:|:|:|:|:|
 Db 9 VPVAYSLIFLLGVGNL 26

RESULT 22
 S28787
 neuropeptide Y/peptide YY receptor Y3 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-Aug-1999
 C:Accession: S28787
 R:Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.
 Mol. Pharmacol. 40, 869-875, 1991
 A>Title: Sequence and expression of a neuropeptide Y receptor cDNA.
 A:Reference number: S28787; MUID:92100053; PMID:1661837
 A:Accession: S28787
 A:Molecule type: mRNA
 A:Residues: 1-353 <RIM>
 A:Cross-references: EMBL:M86739
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 59.6%; Score 56; DB 2; Length 353;
 Best Local Similarity 55.6%; Pred. No. 0.17;
 Matches 10; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNL 18
 ||:|||||:|:|
 Db 42 LPTVYSILFETGIVGNL 59

RESULT 23
 JC1104
 angiotensin II receptor type 1 - human
 N:Alternate names: angiotensin II receptor 1A
 C:Species: Homo sapiens (man)
 C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jul-2000
 C:Accession: JC1104; JQ1402; JH0574; JH0267; A44014; S18983
 R:Mauzy, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.
 Biochem. Biophys. Res. Commun. 186, 277-284, 1992
 A>Title: Cloning, expression, and characterization of a gene encoding the human angioten
 A:Reference number: JC1104; MUID:92337608; PMID:1378723
 A:Accession: JC1104
 A:Molecule type: DNA
 A:Residues: 1-359 <MAU>
 R:Furuta, H.; Guo, D.F.; Inagami, T.
 Biochem. Biophys. Res. Commun. 183, 8-13, 1992
 A>Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type
 A:Reference number: JQ1402; MUID:92181475; PMID:1543512
 A:Accession: JQ1402
 A:Molecule type: DNA
 A:Residues: 1-359 <FUR>
 A:Cross-references: EMBL:Z11162; NID:928709; PID:928710
 A:Experimental source: lymphocyte
 R:Bergsma, D.J.; Ellis, C.; Kumar, C.; Nuthalaganti, P.; Kersten, H.; Elshourbagy, N.; G.
 Biochem. Biophys. Res. Commun. 183, 989-995, 1992
 A>Title: Cloning and characterization of a human angiotensin II type 1 receptor.
 A:Reference number: JH0574; MUID:92231907; PMID:1567413
 A:Accession: JH0574
 A:Molecule type: mRNA

```

Query Match          59.6%; Score 56; DB 2; Length 359;
Best Local Similarity 50.0%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 LPPLYSILVIFGFGVGNML 18
          :|:|:|:|:|:|:|:|
Db       31 IPTLYSILVFGVFGNSL 48

RESULT 26
A48857
angiotensin II receptor type 1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A48857
R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is present i
A:Reference number: A48857; MUID:193236091; PMID:7916579
A:Accession: A48857
A>Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359 -BUR>
A:Cross-references: GB:S59041; NID:g299614; PIDN:AAB26239.1; PID:g299615
A:Experimental source: proximal tubule cells
A:Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBIPI:129601)
C:Superfamily: vertebrate rhodopsin

```

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Query Match          59.6%; Score 56; DB 2; Length 359;
Best Local Similarity 50.0%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1  LPPLYSLVFIFGVGNML 18
          :|:::|:|
Db      31  IPTLSIIFVGVFGNSL 48

```

RESULT 27

A42656
angiotensin II receptor type 1B (AT3) - rat
N:Alternate names: angiotensin II receptor chain B
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A42656; S20423
R:Sandberg, K.; Ji, H.; Clark, A.J.; Shapira, H.; Catt, K.J.
J. Biol. Chem. 267, 9455-9458, 1992
A:Title: Cloning and expression of a novel angiotensin II receptor subtype.
A:Reference number: A42656; MUID:92250585; PMID:1374402
A:Accession: A42656
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAS>
A:Cross-references: GB:X60065; NID:g202801; PIDN:AAA40704.1; PID:g202802
A:Experimental source: adrenal cortex
A:Note: Sequence extracted from NCBI backbone (NCBIN:100262, NCBIP:100268)
R:Iwai, N.; Inagami, T.
FEBS Lett. 298, 257-260, 1992
A:Title: Identification of two subtypes in the rat type I angiotensin II receptor.
A:Reference number: S20423; MUID:92183879; PMID:1544458
A:Accession: S20423
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <IWA>
A:Cross-references: GB:X64052; NID:g57521; PIDN:CAA45410.1; PID:g57522
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 59.6%; Score 56; DB 2; Length 359;
Best Local Similarity 50.0%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNML 18
:|||||:|
DB 31 IPTLYSIIFVVGIFGNSL 48

RESULT 28

SI5403
angiotensin II receptor type 1 - bovine
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: SI5403
R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Haegawa, M.; Matsuda, Y.
Nature 351, 230-233, 1991
A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiotensin II receptor.
A:Reference number: SI5403; MUID:91251900; PMID:2041569
A:Accession: SI5403
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAS>
A:Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
C:Superfamily: vertebrate rhodopsin

Query Match 59.6%; Score 56; DB 2; Length 359;
Best Local Similarity 50.0%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNML 18
:|||||:|
DB 31 IPTLYSIIFVVGIFGNSL 48

RESULT 29

I39418
angiotensin II receptor type 1b - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Nov-1999
C:Accession: I39418
R:Kuroda, S.
Biochem. Biophys. Res. Commun. 199, 467-474, 1994

A:Title: Novel subtype of human angiotensin II type 1 receptor: cDNA cloning and express
A:Reference number: I39418; MUID:94183213; PMID:8135787
A:Accession: I39418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <RES>
A:Cross-references: GB:D13814; NID:g471120; PIDN:BAA02968.1; PID:g471121
C:Superfamily: vertebrate rhodopsin

Query Match 59.6%; Score 56; DB 2; Length 359;
Best Local Similarity 50.0%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNML 18
:|||||:|
DB 31 IPTLYSIIFVVGIFGNSL 48

RESULT 30

JH0621
angiotensin II receptor 1A - mouse
C:Species: Mus musculus (house mouse)
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Nov-1999
C:Accession: JH0621; JCI193
R:Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Kobilka, B.K.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 185, 253-259, 1992
A:Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1) is
A:Reference number: JH0621; MUID:92287102; PMID:1599461
A:Accession: JH0621
A:Molecule type: DNA
A:Residues: 1-359 <SAS>
A:Cross-references: GB:S37484; NID:g249945; PIDN:AAE22269.1; PID:g249946
A:Experimental source: strain Balb/C
R:Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.; I
Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
A:Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals (mo
A:Reference number: JCI193; MUID:92359981; PMID:1497638
A:Accession: JCI193
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-6, 'I', 8-19, 'IS', 22-37, 'M', 39-133, 'K', 135-359 <YOS>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot-

F:37-57/Domain: transmembrane #status predicted <TM1>
F:65-85/Domain: transmembrane #status predicted <TM2>
F:103-123/Domain: transmembrane #status predicted <TM3>
F:145-165/Domain: transmembrane #status predicted <TM4>
F:201-220/Domain: transmembrane #status predicted <TM5>
F:241-261/Domain: transmembrane #status predicted <TM6>
F:286-306/Domain: transmembrane #status predicted <TM7>
F:4,176,188/Binding site: carbonylate (Aen) (covalent) #status predicted
F:331,338/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 59.6%; Score 56; DB 2; Length 359;
Best Local Similarity 50.0%; Pred. No. 0.18;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFFGVGNML 18
:|||||:|
DB 31 IPTLYSIIFVVGIFGNSL 48

Search completed: March 4, 2004, 18:03:56
Job time : 10.1837 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 5.87755 Seconds
(without alignments)
159.465 Million cell updates/sec

Title: US-10-084-813-11
Perfect score: 94
Sequence: 1 LPPLYSILVIFGFGVGNML 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	94	100.0	352	1	CKR5_GORGO
2	94	100.0	352	1	CKR5_HUMAN
3	94	100.0	352	1	CKR5_HYLLE
4	94	100.0	352	1	CKR5_HYLLM
5	94	100.0	352	1	CKR5_HYLSY
6	94	100.0	352	1	CKR5_PANTR
7	94	100.0	352	1	CKR5_PONPY
8	94	100.0	360	1	CKR2_MACMU
9	94	100.0	373	1	CKR2_MOUSE
10	94	100.0	373	1	CKR2_RAT
11	94	100.0	374	1	CKR2_HUMAN
12	92	97.9	354	1	CKR5_MOUSE
13	92	97.9	354	1	CKR5_RAT
14	90	95.7	352	1	CKR5_CERAE
15	90	95.7	352	1	CKR5_CERPY
16	90	95.7	352	1	CKR5_CERTO
17	90	95.7	352	1	CKR5_MACMU
18	90	95.7	352	1	CKR5_PAPHA
19	90	95.7	352	1	CKR5_PYBHI
20	90	95.7	352	1	CKR5_PYGTH
21	90	95.7	352	1	CKR5_TRAFR
22	90	95.7	352	1	CKR5_TRAPH
23	77	81.9	355	1	CKR1_HUMAN
24	77	81.9	355	1	CKR1_MACMU
25	77	81.9	355	1	CKR1_MOUSE
26	77	81.9	359	1	CKR3_MOUSE
27	76	80.9	359	1	CKR3_RAT
28	75	79.8	360	1	CKR4_HUMAN
29	66	70.2	360	1	CKR4_MOUSE
30	65	69.1	355	1	CKR3_MACMU
31	63	67.0	355	1	CKR3_CERAE
32	63	67.0	355	1	CKR3_HUMAN
33	63	67.0	357	1	CKR9_HUMAN

34	63	67.0	369	1	CKB9_MOUSE
35	61	64.9	378	1	CKD6_MOUSE
36	61	64.9	382	1	CKD6_RAT
37	60	63.8	356	1	CKRV_MOUSE
38	60	63.8	361	1	EBI2_HUMAN
39	59	62.8	373	1	P2YR_BOVIN
40	59	62.8	373	1	P2YR_HUMAN
41	59	62.8	373	1	P2YR_MOUSE
42	59	62.8	373	1	P2YR_RAT
43	58	61.7	354	1	C3X1_RAT
44	58	61.7	358	1	CKR3_CAVPO
45	58	61.7	384	1	CKD6_HUMAN
46	57	60.6	352	1	CCR4_CERTO
47	57	60.6	352	1	CCR4_HUMAN
48	57	60.6	352	1	CCR4_MACFA
49	57	60.6	352	1	CCR4_MACMU
50	57	60.6	362	1	CCR4_PAPAN
51	57	60.6	362	1	P2YR_CHICK
52	57	60.6	362	1	P2YR_MELGA
53	57	60.6	367	1	CKB3_MOUSE
54	57	60.6	368	1	CKB3_HUMAN
55	57	60.6	373	1	P2YR_CAVPO
56	56	59.6	192	1	CCR4_SHEEP
57	56	59.6	353	1	CCR4_BOVIN
58	56	59.6	353	1	CCR4_FELCA
59	56	59.6	354	1	C3X1_MOUSE
60	56	59.6	359	1	AG2R_BOVIN
61	56	59.6	359	1	AG2R_CANFA
62	56	59.6	359	1	AG2R_CAVPO
63	56	59.6	359	1	AG2R_HUMAN
64	56	59.6	359	1	AG2R_MERUN
65	56	59.6	359	1	AG2R_MOUSE
66	56	59.6	359	1	AG2R_PANTR
67	56	59.6	359	1	AG2R_PIG
68	56	59.6	359	1	AG2R_RABIT
69	56	59.6	359	1	AG2R_RAT
70	56	59.6	359	1	AG2R_SHEEP
71	56	59.6	359	1	AG2S_HUMAN
72	56	59.6	359	1	AG2S_MOUSE
73	56	59.6	359	1	AG2S_RAT
74	56	59.6	372	1	CKR5_HUMAN
75	56	59.6	374	1	CKR5_MOUSE
76	56	59.6	374	1	CKR5_RAT
77	56	59.6	387	1	HM74_HUMAN
78	54	57.4	359	1	AG2R_CHICK
79	54	57.4	359	1	AG2R_MELGA
80	53	56.4	354	1	US28_HCMVA
81	53	56.4	374	1	CKR6_HUMAN
82	52	55.3	337	1	GP80_HUMAN
83	52	55.3	342	1	CKR6_CERAE
84	52	55.3	342	1	CKR6_HUMAN
85	52	55.3	342	1	CKR6_MACNE
86	52	55.3	342	1	CKR6_PANTR
87	52	55.3	343	1	CKR6_MACFA
88	52	55.3	343	1	CKR6_MACMU
89	52	55.3	416	1	NTR2_RAT
90	51	54.3	343	1	GP81_MOUSE
91	51	54.3	349	1	CKR4_RAT
92	51	54.3	359	1	CKR4_MOUSE
93	51	54.3	367	1	CKR6_MOUSE
94	50	53.2	322	1	CKC1_MOUSE
95	50	53.2	363	1	AG22_MERUN
96	50	53.2	370	1	GALT_RAT
97	50	53.2	380	1	OPRK_CAVPO
98	50	53.2	380	1	OPRK_HUMAN
99	50	53.2	380	1	OPRK_MOUSE
100	50	53.2	380	1	OPRK_RAT

ALIGNMENTS

RESULT 1

```

CKR5 GORGO
ID CKR5 GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268697; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF005659; AAB62553.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS02662; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40515 MW; D056FCB9FE5EACB4 CRC64;

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Query Match 100.0%; Score 94; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 5; le-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVPIFGVGNML 18

|||||

33 LPPLSLVPIFGVGNML 50

Db

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RESULT 2
CKR5 HUMAN
ID CKR5 HUMAN STANDARD; PRT; 352 AA.
AC P51681; O14692; O14693; O14696; O14697; O14698; O14699;
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;
AC O14708; O15538; O9UPA4;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5)
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).
GN CKR5 OR CMKBR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96241590; PubMed=8639485;
RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;
RT "Molecular cloning and functional expression of a new human
RT CC-chemokine receptor gene.";
RL Biochemistry 35:3362-3367(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96291862; PubMed=8663314;
RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;
RT "Molecular cloning and functional characterization of a novel human
RT CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";
RL J. Biol. Chem. 271:17161-17166(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9625970; PubMed=8699119;
RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;
RT "Cloning and functional expression of CC CKR5, a human monocyte CC
RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and
RT RANTES.";
RL J. Leukoc. Biol. 60:147-152(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Rae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=9343222;
RA Kumann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [6]
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049523; PubMed=9388201;
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;
RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts
RT with 5'-end heterogeneity, dual promoter usage, and evidence for
RT polymorphisms within the regulatory regions and noncoding exons.";
RL J. Biol. Chem. 272:30662-30671(1997).

```


[8] SEQUENCE FROM N.A., AND VARIANT ARG-178.
 RA Magierowska M., Barre-Sinoussi F., Isafras H., Theodorou I.,
 RA Debre P.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 [9]
 RN SEQUENCE FROM N.A.
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
 RA "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 [10]
 RN CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhardt M.,
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;
 RT "Identification of a major co-receptor for primary isolates of
 RT HIV-1.";
 RL Nature 381:661-666 (1996).
 [11]
 RN CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,
 RA Nagaoka K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,
 RA Paxton W.A.;
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor
 RT CC-CKR-5.";
 RL Nature 381:667-673 (1996).
 [12]
 RN SULFATION.
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1
 RT entry.";
 RL Cell 96:667-676 (1999).
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and rantes and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation. Acts as co-receptor with CD4 for primary non-
 CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1
 CC virus. It promotes Env-mediated fusion of the virus.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Found in promyelocytic cells.
 CC -1- PTM: Sulfation contributes to the efficiency of HIV-1 entry.
 CC -1- PTM: Modified by O-linked glycosylation, but not by N-linked
 CC glycosylation.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 DR EMBL; X91492; CAA62796.1; -;
 DR EMBL; U54994; AAC50598.1; -;
 DR EMBL; U57840; AAB17071.1; -;
 DR EMBL; U95626; AAB57793.1; -;
 DR EMBL; U83326; AAC51797.1; -;
 DR EMBL; AF011500; AAB65700.1; -;
 DR EMBL; AF011501; AAB65701.1; -;
 DR EMBL; AF011502; AAB65702.1; -;
 DR EMBL; AF011503; AAB65703.1; -;
 DR EMBL; AF011505; AAB65705.1; -;
 DR EMBL; AF011506; AAB65706.1; -;
 DR EMBL; AF011507; AAB65707.1; -;
 DR EMBL; AF011508; AAB65708.1; -;
 DR EMBL; AF011509; AAB65709.1; -;

DR EMBL; AF011510; AAB65710.1; -;
 DR EMBL; AF011511; AAB65711.1; -;
 DR EMBL; AF011512; AAB65712.1; -;
 DR EMBL; AF011513; AAB65713.1; -;
 DR EMBL; AF011514; AAB65714.1; -;
 DR EMBL; AF011515; AAB65715.1; -;
 DR EMBL; AF011516; AAB65716.1; -;
 DR EMBL; AF011517; AAB65717.1; -;
 DR EMBL; AF011518; AAB65718.1; -;
 DR EMBL; AF011519; AAB65719.1; -;
 DR EMBL; AF011520; AAB65720.1; -;
 DR EMBL; AF011521; AAB65721.1; -;
 DR EMBL; AF011522; AAB65722.1; -;
 DR EMBL; AF011523; AAB65723.1; -;
 DR EMBL; AF011524; AAB65724.1; -;
 DR EMBL; AF011525; AAB65725.1; -;
 DR EMBL; AF011526; AAB65726.1; -;
 DR EMBL; AF011527; AAB65727.1; -;
 DR EMBL; AF011528; AAB65728.1; -;
 DR EMBL; AF011529; AAB65729.1; -;
 DR EMBL; AF011530; AAB65730.1; -;
 DR EMBL; AF011531; AAB65731.1; -;
 DR EMBL; AF011532; AAB65732.1; -;
 DR EMBL; AF011533; AAB65733.1; -;
 DR EMBL; AF011534; AAB65734.1; -;
 DR EMBL; AF011535; AAB65735.1; -;
 DR EMBL; AF011536; AAB65736.1; -;
 DR EMBL; AF011537; AAB65737.1; -;
 DR EMBL; AF031237; AAB94735.1; -;
 DR EMBL; AF052539; AAD18131.1; -;
 DR EMBL; AY221093; AAO65971.1; -;
 DR EMBL; HGNC:1606; CCR5.
 DR MIM; 601373; -;
 DR GO; GO:0005768; C:cytosol; TAS.
 DR GO; GO:0005888; C:integral to plasma membrane; TAS.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; TAS.
 DR GO; GO:0015026; F:coreceptor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0006968; P:cellular defense response; TAS.
 DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR GO; GO:0007125; P:invasive growth; TAS.
 DR GO; GO:0007203; P:phosphatidylinositol-4,5-bisphosphate hydrolysis; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
 KW Polymorphism.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 Query Match 100.0%; Score 94; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 5,1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVFIFGVGNML 18
 Db 33 LPPLYSLVFIFGVGNML 50
 RESULT 3
 ID CKR5_HYLLE STANDARD; PRT; 352 AA.
 AC O97883;
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 GN C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 OS CCR5 OR CKR5.
 OC Hylobates leucogenys (White-cheeked gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=61853;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 DR EMBL; AF075451; RAD19863.1; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PS00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;
 Query Match 100.0%; Score 94; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFGVGNML 18
 |||||
 DB 33 LPPLYSLVIFGFGVGNML 50
 RESULT 4
 ID_CKR5_HYLM ML STANDARD; PRT; 352 AA.
 AC Q95NC0;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CCR5 OR CKR5.
 OS Hylobates moloch (Silvery gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=81572;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 DR EMBL; AF177899; AAK43382.1; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1.1.
 DR PRINTS; PS00237; GPCRHHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;
 Query Match 100.0%; Score 94; DB 1; Length 352;
 Best Local Similarity 100.0%; Pred. No. 5.1e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LPPLYSLVIFGFGVGNML 18
 |||||
 DB 33 LPPLYSLVIFGFGVGNML 50
 RESULT 5
 ID_CKR5_HYLS Y STANDARD; PRT; 352 AA.
 AC Q95NC5;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKERS.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DE EMBL: AF177884; AAC43367.1; -;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7cm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G PROTEIN RECF 1; 1.
DR PROSITE: PS0262; G PROTEIN RECF 2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;
Query Match 100.0%; Score 94; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 5,1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LPPLYSIVFIQGVGNML 18
Db 33 LPPLYSIVFIQGVGNML 50
RESULT 6
ID CCR5_PANTR STANDARD; PRT; 352 AA.
AC P56440; O02778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
KW

GN CCR5 OR CMKERS.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharroon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peller S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC [2]
CC SEQUENCE FROM N.A.
RX Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98022612; PubMed=9359654;
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
CC [4]
CC SEQUENCE FROM N.A.
RX MEDLINE=97426118; PubMed=9282822;
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT HIV type 1 host.";
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
CC [5]
CC SEQUENCE FROM N.A.
RX MEDLINE=98090115; PubMed=9430250;
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
CC [6]
CC SEQUENCE FROM N.A.
RX Zhang Y., Ryder O.A., Zhang Y.;
RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DE EMBL: AF005663; AAB62557.1; -;
DR EMBL: U94329; AAB58446.1; -;
DR EMBL: AF011542; AAB65742.1; -;
DR EMBL: U97666; AAC51670.1; -;
DR EMBL: AF011540; AAB65740.1; -;
DR EMBL: U97937; AAC03717.1; -;
DR EMBL: AF177894; AAK43377.1; -;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7cm.1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G PROTEIN RECF 1; 1.
DR PROSITE: PS0262; G PROTEIN RECF 2; 1.
DE G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF 1).
SQ SEQUENCE 352 AA; 40539 MW; 4A33B68B80FE34C CRC64;

Query Match 100.0%; Score 94; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
|||||
Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 7
CKR5_PONPY
ID CKR5_PONPY STANDARD; PRT; 352 AA.
AC O97881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKRS.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075446; AAD1958.1; -
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEPT_F1_1; 1.

DR PROSITE; PS00262; G_PROTEIN_RECEPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF659A CRC64;

Query Match 100.0%; Score 94; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
|||||
Db 33 LPPLYSLVFIQFGVGNML 50

RESULT 8
CKR2_MACMU
ID CKR2_MACMU STANDARD; PRT; 360 AA.
AC O18793;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN CCR2 OR CMKBR2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=B;
CC IsoId=O18793-1; Sequence-Displayed;
CC Name=A;
CC IsoId=O18793-2; Sequence-Not described;
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC -----
DR EMBL; AF013958; AAD11572.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Alternative splicing.
FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 70 1 (POTENTIAL).
FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 81 100 2 (POTENTIAL).
FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 135 3 (POTENTIAL).
FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 178 4 (POTENTIAL).
FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. .) (POTENTIAL).
FT MOD RES 26 26 SULFATION (BY SIMILARITY).
FT DISULFID 113 190 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 100.0%; Score 94; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGVGNML 18
Db 45 LPPLYSLVFIFGVGNML 62

RESULT 9
CCR2_MOUSE STANDARD; PRT; 373 AA.
AC P51683; Q61172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 2 (C-C CCR-2) (CCR-2) (CCR2)
DE (JE/FIC receptor) (MCP-1 receptor).
GN CCR2 OR CMKR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96205938; PubMed=8631787;
RA Boring L., Goelling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,
RA Charo I.F.;
RT "Molecular cloning and functional expression of murine JE (monocyte
RT chemoattractant protein 1) and murine macrophage inflammatory protein
RT receptors: evidence for two closely linked C-C chemokine
RT receptors on chromosome 9."
RL J. Biol. Chem. 271:7551-7558 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=96216064; PubMed=8662823;
RA Kurihara T., Bravo R.;
RT "Cloning and functional expression of mCCR2, a murine receptor for
RT the C-C chemokines JE and EIC."
RL J. Biol. Chem. 271:11603-11606 (1996).
RN [3]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97026720; PubMed=8872898;
RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,
RA Post T.W., Gerard C., Dorf M.E.;
RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse
RT transcriptase-polymerase chain reaction does not detect mRNA for the
RT KC or new MCP-1 receptor."
RL J. Neurosci. Res. 45:382-391 (1996).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC but not in nonhematopoietic cell lines.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; U47035; AAC52453.1; -.
DR EMBL; U51717; AAC52557.1; -.
DR EMBL; U56819; AAC52784.1; -.
DR MGD; MGI:106185; Ccr2.
DR GO; GO:0016493; P:C-C chemokine receptor activity; IDA.
DR GO; GO:0019955; P:cytokine binding; IPI.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.
DR GO; GO:0030097; P:hemopoiesis; IMP.
DR GO; GO:0006959; P:humoral immune response; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0030334; P:regulation of cell migration; IMP.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G PROTEIN RECP Fl_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP Fl_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 56 83 1 (POTENTIAL).
FT DOMAIN 84 93 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 94 114 2 (POTENTIAL).
FT DOMAIN 115 127 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 128 149 3 (POTENTIAL).
FT DOMAIN 150 166 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 167 191 4 (POTENTIAL).
FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 220 239 5 (POTENTIAL).
FT DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 281 6 (POTENTIAL).
FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 299 322 7 (POTENTIAL).
FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203 BY SIMILARITY.
FT CONFLICT 39 39 Y -> H (IN REF. 1).
FT CONFLICT 184 184 A -> G (IN REF. 1).
FT CONFLICT 264 264 V -> G (IN REF. 1).
SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 100.0%; Score 94; DB 1; Length 373;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGVGNML 18
Db 58 LPPLYSLVFIFGVGNML 75

RESULT 10
CCR2_RAT STANDARD; PRT; 373 AA.
ID CCR2_RAT

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AC 055193;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 2 (CCR-2) (CCR-2) (CCR2)
DE CCR2 OR CMKBR2
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salaferran M.A., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streif W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured gila and rat experimental
RT allergic encephalomyelitis."
RL J. Neuroimmunol. 86:1-12(1998).
CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5
CC chemokines. Transduces a signal by increasing the intracellular
CC calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and
CC macrophages.
CC -!- INDUCTION: In animals in which experimental allergic
CC encephalomyelitis (EAE) has been induced.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: U77349; AAC03242.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR PROSITE: PS00262; G-PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 61 81 POTENTIAL.
FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 92 112 POTENTIAL.
FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 149 POTENTIAL.
FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 POTENTIAL.
FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 221 241 POTENTIAL.
FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 257 277 POTENTIAL.
FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 302 322 POTENTIAL.
FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).
FT DISULFID 126 203 BY SIMILARITY.
SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5DFD09 CRC64;

Query Match 100.0%; Score 94; DB 1; Length 373;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
DB 58 LPPLSLVIFGFVGNML 75

RESULT 11
CCR2_HUMAN
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ID CCR2_HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 2 (CCR-2) (CCR-2) (CCR2)
DE C-C chemokine receptor type 2 (CCR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
GN CCR2 OR CMKBR2
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94195821; PubMed=8146186;
RX Charo I.F., Myers S.J., Herman A., Francis C., Connolly A.J.,
RX Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
RT chemoattractant protein 1 receptors reveals alternative splicing of
RT the carboxyl-terminal tails."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94324942; PubMed=8048929;
RX Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;
RT "cDNA cloning and functional expression of a human monocyte
RT chemoattractant protein 1 receptor."
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97150864; PubMed=8995400;
RX Wong L.-M., Myers S.J., Teou C.-L., Gosling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
RT chemoattractant protein 1 receptor gene. Evidence for the role of the
RT carboxyl-terminal tail in receptor trafficking."
RL J. Biol. Chem. 272:1038-1045(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RX Nhan M., Parnell L., Dedhia N., Ansari A., Mardie E., Schutz K.,
RX Guoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RX Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RX Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,
RX Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RX Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RX Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ILE.64 AND GLU.355.
RX Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldane S.A.,
RX Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RX Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RX MEDLINE=20501139; PubMed=11046064;
RX Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
RX Chakravarty L., Kolattukudy P.E.;
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that
RT has tyrosine sulfation in a conserved extracellular N-terminal
RT region."
RL J. Immunol. 165:5295-5303(2000).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level. Alternative coreceptor with CD4 for HIV-1 infection.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P41597-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P41597-2; Sequence=VSP_001893;
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
```

```

Qy      1 LPELYSLVFIRFGVGNML 18
          |||||
          |||||
Db     45 LPPEYSLVFIRFGVGNML 62

RESULT 12
ID   CKR5_MOUSE STANDARD; PRT; 354 AA.
AC   P51682; O35313; O35891; P97308; P97405; Q61867;
DT   01-OCT-1996 (Rel. 34, Created)
DD   15-JUL-1998 (Rel. 35, Last sequence update)
DI   10-OCT-2003 (Rel. 45, Last annotation update)
DE   C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE   alpha receptor).
GN   CKR5 OR CMKR5.
```

ID	_CKR5 MOUSE	STANDARD;	PRT: 354 AA.
AC	P51682;	O35313;	O35891;
DC	P97308;	P97405;	Q61867;
DT	01-OCT-1996	(Rel. 34, Created)	
DT	15-JUL-1998	(Rel. 36, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1-alpha receptor).		
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1-alpha receptor).		
GN	CKR5	OR	CMKR5.
OS	Mus musculus (Mouse).		
OC	Eukaryota;	Metazoa;	Chordata;
OC	Mammalia;	Eutheria;	Rodentia;
OC	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		

STRAIN=129/SvJ; TISSUE=Spleen;
MEDLINE=96205938; PubMed=8631787;
Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,
Charo I.F.;
"Molecular cloning and functional expression of murine JE (monocyte
chemoattractant protein 1) and murine macrophage inflammatory protein
1alpha receptors: evidence for two closely linked C-C chemokine
receptors on chromosome 9,"
J. Biol. Chem. 271:7551-7558(1996).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
MEDLINE=96278910; PubMed=8662830.

RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Cloning and characterization of a novel murine macrophage
RT inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 271:14445-14451(1996).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=129/Ola;
RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;
RV W607197.00001367. PubMed-9342292

RA. MEDLINE=96001367; PubMed=9583224;
 RA. Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
 RT implicate specific amino acids in infections by simian and human
 RT immunodeficiency viruses."; J. Virol. 71:8642-8656(1997).
 RL [5]
 RL SEQUENCE FROM N.A.
 RP STRAIN=129;
 RP
 RX MEDLINE=97404635; PubMed=9261347;
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human
 RT immunodeficiency virus-1." J. Virol. 71:1003-1011(1997).

RI	Immunodeficiency virus type 1.
RA	J. Virol. 71:6305-6314 (1997).
RP	[6]
RN	SEQUENCE FROM N.A.
RR	Guo B., Kuno K., Harada A., Matsushima K.;
RA	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC	-I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC	MIP-1-beta and RANTES and subsequently transduces a signal by
CC	increasing the intracellular calcium ions level.
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-I- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,
CC	but not in nonhematopoietic cell lines.
CC	-I- SIMILARITY: Belongs to family 1 of G-protein coupled.

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EMBL; X94151; AAC52454.1; -
EMBL; X94151; AAC52454.1; -
EMBL; U68565; AAB37273.1; -
EMBL; U83327; AAC53386.1; -
EMBL; AF022990; AAC53389.1; -
EMBL; AF019772; AAB11183.1; -
EMBL; D83648; BAA12024.1; -
MGD; MGI:107182; Ccr5.
GO; GO:0016493; F-C-C chemokine receptor activity; IDA.
GO; GO:0006952; P:defense response; IMP.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Polymorphism.
DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
TRANSSEM 33 60
DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
DOMAIN 71 91
DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
TRANSSEM 105 126
DOMAIN 127 143
TRANSSEM 144 168
DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
TRANSSEM 201 220
DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
TRANSSEM 238 262
DOMAIN 263 279
TRANSSEM 280 303
DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
DISULFID 103 180 BY SIMILARITY.
CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).
VARIANT 11 11 I -> S.
VARIANT 62 62 K -> R.
VARIANT 66 66 V -> M.
VARIANT 97 97 I -> V.
VARIANT 109 109 V -> L.
VARIANT 156 156 V -> A.
VARIANT 160 160 F -> S.
VARIANT 185 185 P -> L.
VARIANT 213 213 I -> V.
VARIANT 318 318 I -> M.
VARIANT 337 337 V -> A.
CONFLICT 3 3 F -> L (IN REF. 2).
CONFLICT 80 80 L -> F (IN REF. 2).
CONFLICT 145 145 N -> I (IN REF. 5).
CONFLICT 190 190 H -> Y (IN REF. 3).
CONFLICT 208 208 P -> S (IN REF. 1).
SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;

Query Match 97.9%; Score 92; DB 1; Length 354;
Best Local Similarity 94.4%; Pred. No. 1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGFGVGNML 18
|||||
Db 35 LPPLSLVIFGFGVGNMW 52

RESULT 13
CKR5 RAT
ID CKR5 RAT STANDARD; PRT; 354 AA.
AC O08556;
DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
GN CCR5 OR CMGR5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=98334064; PubMed=9670989;
RA Splenis O., Gourmal N., Bodde H.W.G.M., Sauter A., Fiebich B.L.,
RA Berger M., Gebicke-Haerter P.J.;
RT Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
RL J. Neurosci. Res. 53:16-28 (1998).
RN [2]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salazar M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12 (1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

EMBL; Y12009; CAAT2737.1; -
EMBL; U77350; AAC03243.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
TRANSSEM 33 60
DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).
DOMAIN 71 91
DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).
TRANSSEM 105 126
DOMAIN 127 143
TRANSSEM 144 168
DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).
TRANSSEM 201 220
DOMAIN 221 237
TRANSSEM 238 262
DOMAIN 263 279
TRANSSEM 280 303
DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).
DISULFID 103 180 BY SIMILARITY.
CARBOHYD 270 270 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 97.9%; Score 92; DB 1; Length 354;
Best Local Similarity 94.4%; Pred. No. 1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGFGVGNML 18


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Db      35 LPPLSLVFIFGFVGNM 52
|||||
RESULT 14
ID      CKR5 CERAE      STANDARD;      PRT;      352 AA.
AC      P56493;
DT      15-JUL-1998 (Rel. 36, Created)
DT      15-JUL-1998 (Rel. 36, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN      CKR5 OR CMKR5.
OS      Cercopithecus aethiops (Green monkey) (Grivet).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=9534;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RX      MEDLINE=98001387; PubMed=9343222;
RA      Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT      "Polymorphisms in the CKR5 genes of African green monkeys and mice
RT      implicate specific amino acids in infections by simian and human
RT      immunodeficiency viruses.";
RL      J. Virol. 71:8642-8656 (1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT      "CDNA sequence of African green monkey CCR-5 chemokine receptor
RT      gene.";
RL      Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC      -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC      MIP-1-beta and RANTES and subsequently transduces a signal by
CC      increasing the intracellular calcium ions level. May play a role
CC      in the control of granulocytic lineage proliferation or
CC      differentiation.
CC      -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; U83324; AAC51795.1; -
DR      EMBL; U83325; AAC51796.1; -
DR      EMBL; AB015944; BAA31328.1; -
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS; P000237; GPCRHHODPSN.
DR      PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
DR      PROSITE; PS0262; G PROTEIN RECP F1.2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW      Polymorphism.
FT      DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT      TRANSSEM 31 58 1 (POTENTIAL).
FT      DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT      TRANSSEM 69 89 2 (POTENTIAL).
FT      DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT      TRANSSEM 103 124 3 (POTENTIAL).
FT      DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT      TRANSSEM 142 166 4 (POTENTIAL).
FT      DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT      TRANSSEM 199 218 5 (POTENTIAL).
FT      DOMAIN 219 235 EXTRACELLULAR (POTENTIAL).
FT      TRANSSEM 236 260 6 (POTENTIAL).
FT      DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT      TRANSSEM 278 301 7 (POTENTIAL).

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FT      DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT      DISULPID 101 178 BY SIMILARITY.
FT      MOD RES 3 3 SULFATION (BY SIMILARITY).
FT      MOD RES 10 10 SULFATION (BY SIMILARITY).
FT      MOD RES 15 15 SULFATION (BY SIMILARITY).
FT      VARIANT 14 14 N -> Y.
FT      VARIANT 352 352 F -> L.
SQ      SEQUENCE 352 AA; 40561 MW; 7F52B690C72EC29A CRC64;

Query Match      95.7%; Score 90; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 LPPLSLVFIFGFVGNM 18
DB      33 LPPLSLVFIFGFVGNM 50

RESULT 15
ID      CKR5 CERPY      STANDARD;      PRT;      352 AA.
AC      Q9TV42;
DT      15-MAR-2004 (Rel. 43, Created)
DT      15-MAR-2004 (Rel. 43, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN      CKR5 OR CMKR5.
OS      Cercopithecus pygerythrus (Vervet monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=60710;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=100;
RX      MEDLINE=99335215; PubMed=10408730;
RA      Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
RA      Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT      "Mutations in CKR5-coding sequences are not associated with SIV
RT      carrier status in African nonhuman primates.";
RT      AIDS Res. Hum. Retroviruses 15:931-939 (1999).
CC      -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC      MIP-1-beta and RANTES and subsequently transduces a signal by
CC      increasing the intracellular calcium ions level. May play a role
CC      in the control of granulocytic lineage proliferation or
CC      differentiation.
CC      -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; AF035222; AAD44015.1; -
DR      InterPro: IPR000276; GPCR_Rhodpsn.
DR      Pfam; PF00001; 7tm_1; 1.
DR      PRINTS; P000237; GPCRHHODPSN.
DR      PROSITE; PS00237; G PROTEIN RECP F1.1; 1.
DR      PROSITE; PS0262; G PROTEIN RECP F1.2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT      DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT      TRANSSEM 31 58 1 (POTENTIAL).
FT      DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT      TRANSSEM 69 89 2 (POTENTIAL).
FT      DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT      TRANSSEM 103 124 3 (POTENTIAL).
FT      DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT      TRANSSEM 142 166 4 (POTENTIAL).
FT      DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3D90 CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
Db 33 LPPLYSLVIFGFVGNIL 50

RESULT 16
CKR5_CERTO STANDARD; PRT; 352 AA.
AC O62743; O62744; O62745; O62746;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SiVem isolates use the CKR5 coreceptor from sooty mangabeys
naturally infected in west Africa: a comparison of coreceptor usage
of primary SiVem, HIV-2, and SiVmac."
RL Virology 246:113-124(1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
CC
CC EMBL; AF051902; AAC39830.1; -
CC EMBL; AF051903; AAC39831.1; -
CC EMBL; AF051904; AAC39832.1; -
CC EMBL; AF051905; AAC39833.1; -
CC InterPro: IPR000276; GPCR_Rhodopn.
CC Pfam: PF00001; 7tm.1.1.
CC PRINTS; PR00237; GPCRHDOPSN.
CC PROSITE; PS00237; G PROTEIN RECEPT FL1; 1.
CC PROSITE; PS00262; G PROTEIN RECEPT FL2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 087).
FT VARIANT 25 25 V -> G (IN ISOLATE 087).
FT VARIANT 100 100 M -> K (IN ISOLATE 089).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A1962D47B49CA CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
Db 33 LPPLYSLVIFGFVGNIL 50

RESULT 17
CKR5_MACMU STANDARD; PRT; 352 AA.
AC P79436; O02746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CKR5.
OS Macaca mulatta (Rhesus macaque),
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
glycoproteins of a pathogenic simian immunodeficiency virus,
SiVmac239."
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
CKR5 as a coreceptor for entry."
RL J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;

```

Db 33 LPPLYSLVTFGFGVGNIL 50
|||||
RESULT 18
CKR5_PAPHA
ID CKR5_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Papio hamadryas (Hamadryas baboon), and
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OC NCBI_TaxID=9557, 9555;
RN [1]
RS SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RP MEDLINE=97268687; PubMed=9108095;
RX Edinger A.L., Anedeke A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RT Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains";
RT Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RS SEQUENCE FROM N.A.
RC SPECIES=P.hamadryas;
RP MEDLINE=93210133; PubMed=10195758;
RX Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;
RA "Species-specific changes in the CCR5 gene from African and Asian
RT nonhuman primates";
RT AIDS Res. Hum. Retroviruses 15:479-483(1999).
RN [3]
RS SEQUENCE FROM N.A.
RC SPECIES=P.anubis;
RP Benton P.A., Tmanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RL -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF005658; AAB62552.1; -
CC EMBL; AF105287; AAD20556.1; -
CC EMBL; AF105288; AAD20557.1; -
CC EMBL; AF105289; AAD20558.1; -
CC EMBL; AF105290; AAD20559.1; -
CC EMBL; AF023452; AAC63830.1; -
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00242; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC FT

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FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE8B2 CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
| | | | | | | | | | | | | | | | | |
DB 33 LPPLYSLVIFGFGVGNIL 50

RESULT 19
ID CKRS PYGBI STANDARD; PRT; 352 AA.
AC O97880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154 (1999).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075445; AAD19857.1; -
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSIN.
CC PROSITE; PS00237; G PROTEIN RECEPT F1.1; 1.
CC PROSITE; PS0262; G PROTEIN RECEPT F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.1e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
| | | | | | | | | | | | | | | | | |
DB 33 LPPLYSLVIFGFGVGNIL 50

RESULT 20
ID CKRS PYGBE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154 (1999).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075448; AAD19860.1; -
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm1.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSIN.
CC PROSITE; PS00237; G PROTEIN RECEPT F1.1; 1.
CC PROSITE; PS0262; G PROTEIN RECEPT F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW

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FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40532 MW; FB4F9D98D3B3B861 CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 2.le-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
 |||||
 DB 33 LPPLYSLVIFGFGVGNIL 50

RESULT 21

ID_CKRS_TRAFR STANDARD; PRT; 352 AA.
 AC O97878;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Trachypithecus.
 OX NCBI_TaxID=54180;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF075442; AAD19854.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PS00237; GPCRHOODPSN
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 2.le-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
 |||||
 DB 33 LPPLYSLVIFGFGVGNIL 50

RESULT 22

ID_CKRS_TRAPH STANDARD; PRT; 352 AA.
 AC O97879;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
 GN CKR5 OR CMKBR5.
 OS Trachypithecus phayrei (Phayre's leaf monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Trachypithecus.
 OX NCBI_TaxID=61618;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99416438; PubMed=10486970;
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
 RL Mol. Biol. Evol. 16:1145-1154(1999).
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1-beta and RANTES and subsequently transduces a signal by
 CC increasing the intracellular calcium ions level. May play a role
 CC in the control of granulocytic lineage proliferation or
 CC differentiation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; AF075443; AAD19855.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PS00237; GPCRHOODPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS50262; G-PROTEIN RECEPTOR FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 31 58 1 (POTENTIAL).
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 69 89 2 (POTENTIAL).
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 124 3 (POTENTIAL).
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 142 166 4 (POTENTIAL).
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 199 218 5 (POTENTIAL).
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 236 260 6 (POTENTIAL).
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 278 301 7 (POTENTIAL).
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 101 178 BY SIMILARITY.
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).
 SQ SEQUENCE 352 AA; 40509 MW; 4366FT148D3A5938F CRC64;

Query Match 95.7%; Score 90; DB 1; Length 352;
 Best Local Similarity 94.4%; Pred. No. 2.1e-06;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGFGVGNML 18
 |||||
 DB 33 LPPLSLVIFGFGVGNIL 50

RESULT 23

CKR1 HUMAN
 ID CKR1 HUMAN STANDARD; PRT; 355 AA.
 AC P32246;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
 DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
 DE (RANTES-R) (HML45) (LD78 receptor).
 GN CKR1 OR CMKRL1 OR CMKRL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93161416; PubMed=7679328;
 RA Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;
 RT "Molecular cloning, functional expression, and signaling
 RT characteristics of a C-C chemokine receptor.";
 RL Cell 72:415-425(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93240122; PubMed=7683036;
 RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,
 RA Murphy P.M.;
 RT "Structure and functional expression of the human macrophage
 RT inflammatory protein 1 alpha/RANTES receptor.";
 RL J. Exp. Med. 177:1421-1427(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Monocytes;
 RC MEDLINE=94092629; PubMed=7505609;
 RA Nomura H., Nielsen B.W., Matsushima K.;
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
 RT leukocyte chemotactic peptide receptors.";
 RL Int. Immunol. 5:1239-1249(1993).
 CC -1; FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
 CC MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-

CC beta or MCP-1 and subsequently transduces a signal by increasing
 CC the intracellular calcium ions level. Responsible for affecting
 CC stem cell proliferation.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed in different hematopoietic
 CC cells.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL; L09230; AAA58408.1; -;
 CC EMBL; L10918; AAA36543.1; -;
 CC EMBL; D10925; BAA01723.1; -;
 CC PIR; A45177; A45177.
 CC GeHew; HGNC:1602; CCR1.
 CC MIM; 601159; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004950; F:chemokine receptor activity; TAS.
 CC GO; GO:0007155; P:cell adhesion; TAS.
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0006935; P:chemotaxis; TAS.
 CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.
 CC GO; GO:0006955; P:immune response; TAS.
 CC GO; GO:0006954; P:inflammatory response; TAS.
 CC GO; GO:0007125; P:invasive growth; TAS.
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7tm.1.1.
 CC PRINTS; PR00237; GPCRHOOPS.
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL 2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 60 1 (POTENTIAL).
 FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 65 91 2 (POTENTIAL).
 FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 108 129 3 (POTENTIAL).
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 147 171 4 (POTENTIAL).
 FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 198 223 5 (POTENTIAL).
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 240 264 6 (POTENTIAL).
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 282 305 7 (POTENTIAL).
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 106 183 BY SIMILARITY.
 FT CONFLICT 337 337 E -> D (IN REF. 3).
 SQ SEQUENCE 355 AA; 41172 MW; B2C10FFED275985 CRC64;

Query Match 81.9%; Score 77; DB 1; Length 355;
 Best Local Similarity 77.8%; Pred. No. 0.00019;
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGFGVGNML 18
 |||||
 DB 37 LPPLSLVIFGFGVGNIL 54

RESULT 24

CKR1 MACMU
 ID CKR1 MACMU STANDARD; PRT; 355 AA.
 AC P56482;
 DT 15-JUL-1998 (Rel. 36, Created)


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DR MGD; MGI:104618; Ccr1.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0030395; P:immune cell chemotaxis; IDA.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0030099; P:myeloid blood cell differentiation; IMP.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 60 1 (POTENTIAL).
FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 91 2 (POTENTIAL).
FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 325 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 55 55 M -> V (IN REF. 2 AND 3).
FT CONFLICT 149 149 L -> F (IN REF. 3).
FT CONFLICT 278 278 H -> Q (IN REF. 3).
SQ SEQUENCE 355 AA; 40901 MW; FCB9FFF70B6F38B1 CRC64;

Query Match 81.9%; Score 77; DB 1; Length 355;
Best Local Similarity 83.3%; Pred. No. 0.00019;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGFVGNML 18
Db 37 LPPLYSLVIFGFVGNML 54

RESULT 26
CKR3_MOUSE
ID CKR3_MOUSE STANDARD; PRT; 359 AA.
AC P51678.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3)
DE (CKR3) (CKR3) (Macrophage inflammatory protein-1 alpha receptor-like
DE 2) [MIP-1 alpha RL2].
GN CKR3 OR CMKBR3 OR CMKBR1L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
RT receptors."
RL J. Immunol. 155:5299-5305 (1995).
RN [2].
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a

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RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501 (1995).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
CC amounts in Leukocytes.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U29677; AAA86118.1; -.
CC EMBL; U28406; AAA89155.1; -.
CC MGD; MGI:104618; Ccr3.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0006935; P:chemotaxis; IDA.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 64 1 (POTENTIAL).
FT DOMAIN 65 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 95 2 (POTENTIAL).
FT DOMAIN 96 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 227 5 (POTENTIAL).
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 268 6 (POTENTIAL).
FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 286 309 7 (POTENTIAL).
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT CONFLICT 270 270 R -> S (IN REF. 2).
SQ SEQUENCE 359 AA; 41825 MW; AC11ED6E283CEAF CRC64;

Query Match 81.9%; Score 77; DB 1; Length 359;
Best Local Similarity 77.8%; Pred. No. 0.00019;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGFVGNML 18
Db 41 LPPLYSLVIFGFVGNML 58

RESULT 27
CKR3_RAT
ID CKR3_RAT STANDARD; PRT; 359 AA.
AC O54814; O55169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
DE (CCR3).
GN CKR3 OR CMKBR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1].

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RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Spleen;
RX MEDLINE=98118173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RL allergic encephalomyelitis.";
RN J. Neuroimmunol. 86:11-12(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
CC microglia.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF003954; AAC03337.1; -.
DR EMBL; Y13400; CAA73830.1; -.
DR InterPro; IPR000276; GPCR_Rhodpn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOSN.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 POTENTIAL.
FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 95 POTENTIAL.
FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 113 133 POTENTIAL.
FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 POTENTIAL.
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 227 POTENTIAL.
FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 244 264 POTENTIAL.
FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 289 309 POTENTIAL.
FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 164 164 F -> L (IN REF. 2).
SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;
Query Match 80.9%; Score 76; DB 1; Length 359;
Best Local Similarity 77.8%; Pred. NO. 0.00027;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LPPLSLVFIKFGVGNML 18
Db 41 LPPLSLVFIKGLGNM 58
RESULT 28
CKR4_HUMAN
ID CKR4_HUMAN STANDARD; PRT; 360 AA.
AC P51679; Q9ULY6; Q9ULY7;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 4 (C-C CKR-4) (CC-CKR-4) (CCR-4) (CCR4) (KS-5).

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GN CCR4 OR CMKBR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=95370289; PubMed=7642634;
RA Power C.A., Meyer A., Nemeth K., Bacon K.B., Hoogewerf A.J.,
RA Proudfoot A.E.L., Wells T.N.C.;
RT "Molecular cloning and functional expression of a novel CC chemokine
RL receptor cDNA from a human basophilic cell line.";
RN J. Biol. Chem. 270:19495-19500(1995).
[2]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-130 AND SER-178.
RX MEDLINE=21040311; PubMed=11196669;
RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RN Genes Immun. 1:97-104(1999).
[3]
RP SEQUENCE FROM N.A.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RL mediated by the G-protein coupled receptor TARC is a highly specific
RL Submitter (JUN-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP FUNCTION.
RX MEDLINE=97313486; PubMed=9169480;
RA Imai T., Baba M., Nishimura M., Kakizaki M., Takagi S., Yoshie O.;
RT "The T cell-directed CC chemokine TARC is a highly specific
RL biological ligand for CC chemokine receptor 4.";
RN J. Biol. Chem. 272:15036-15042(1997).
[5]
RP FUNCTION.
RX MEDLINE=98104168; PubMed=9430724;
RA Imai T., Chantry D., Raport C.J., Wood C.L., Nishimura M., Godiska R.,
RA Yoshie O., Gray P.W.;
RT "Macrophage-derived chemokine is a functional ligand for the CC
RL chemokine receptor 4.";
RN J. Biol. Chem. 273:1764-1768(1998).
[6]
RP FUNCTION.
RX MEDLINE=99394604; PubMed=10466728;
RA Campbell J.J., Haraldsen G., Pan J., Rottman J., Qin S., Ponath P.,
RA Andrew D.P., Warke R., Ruffing N., Kassam N., Wu L., Butcher E.C.;
RT "The chemokine receptor CCR4 in vascular recognition by cutaneous but
RL not intestinal memory T cells.";
RN Nature 400:776-780(1999).
[7]
RP FUNCTION, TISSUE SPECIFICITY, AND PHOSPHORYLATION.
RX MEDLINE=20219238; PubMed=10754297;
RA Ingjerdengen M., Damaj B., Maghazachi A.A.;
RT "Human NK cells express CC chemokine receptors 4 and 8 and respond to
RL chemokine, and I-309.";
RN J. Immunol. 164:4048-4054(2000).
-!- FUNCTION: High affinity receptor for the C-C type chemokines
CC TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is
CC mediated by G(i) proteins which activate a phosphatidylinositol-
CC calcium second messenger system. Can function as a chemoattractant
CC homing receptor on circulating memory lymphocytes and as a
CC coreceptor for some primary HIV-2 isolates. In the CNS, could
CC mediate hippocampal-neuron survival.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed in the thymus, in
CC peripheral blood leukocytes, including T cells, mostly cd4+ cells,
CC and basophils, and in platelets; at lower levels, in the spleen
CC and in monocytes. Detected also in macrophages, IL-2-activated
CC natural killer cells and skin-homing memory T cells, mostly the
CC ones expressing the cutaneous lymphocyte antigen (CLA). Expressed
CC in brain microvascular and coronary artery endothelial cells.

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CC -!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; X85740; CAA59743.1; --
CC EMBL; AB023888; BAA86965.1; --
CC EMBL; AB023889; BAA86966.1; --
CC EMBL; AB023890; BAA86967.1; --
CC EMBL; AB023891; BAA86968.1; --
CC EMBL; AB023892; BAA86969.1; --
CC EMBL; AY322539; AAP84352.1; --
CC PIR; A57160; A57160.
CC GENE; HGNC:1605; CCR4.
CC MIM; 604936; --
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004950; F:chemokine receptor activity; TAS.
CC GO; GO:0006935; P:chemotaxis; TAS.
CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
CC GO; GO:0006955; P:immune response; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Polymorphism.
CC DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 67 1 (POTENTIAL).
CC DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 78 98 2 (POTENTIAL).
CC DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 112 133 3 (POTENTIAL).
CC DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 151 175 4 (POTENTIAL).
CC DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 207 226 5 (POTENTIAL).
CC DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 243 267 6 (POTENTIAL).
CC DOMAIN 268 284 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 285 308 7 (POTENTIAL).
CC DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 183 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC DISULFID 110 187 BY SIMILARITY.
CC VARIANT 130 130 L -> V.
CC VARIANT 178 178 /FTID=VAR_010669.
CC SEQUENCE 360 AA; 41402 MW; 51EB12AD1FAFBF CRC64;
CC
CC Query Match 79.8%; Score 75; DB 1; Length 360;
CC Best Local Similarity 81.2%; Pred. No. 0.00039;
CC Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CC
CC QY 1 LPPLYSIVFLFGVGN 16
CC DB 42 LPPLYSIVFLFGVGN 57
CC
CC RESULT 29
CC CKR4 MOUSE
CC ID CKR4 MOUSE STANDARD; PRT; 360 AA.
CC AC P51680;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 4 (C-C CKR-4) (CCR-4) (CCR4).
GN CCR4 OR CMKBR4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX MEDLINE=96136324; PubMed=8573157;
RA Hoogwerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "Molecular cloning of murine CC CKR-4 and high affinity binding of
RL chemokines to murine and human CC CKR-4.";
RL Biochem. Biophys. Res. Commun. 218:337-343(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Cytotoxic T-cell;
RX MEDLINE=97335974; PubMed=9192769;
RA Yoon B.-S., Kim S.-H., Lyu M.S., Kozak C.A., Taub D.D., Kwon B.S.;
RT "Molecular cloning and characterization of a cDNA, CHEMRL, encoding a
RL chemokine receptor with a homology to the human C-C chemokine
RL receptor, CCR-4.";
RL Blood 89:4448-4460(1997).
[3]
RP FUNCTION.
RX MEDLINE=20273981; PubMed=10811868;
RA Buser R., Conquet F., Proudfoot A.E.I., Wells T.N.C., Power C.A.;
RT "A key role for CC chemokine receptor 4 in lipopolysaccharide-induced
RT endotoxic shock.";
RL J. Exp. Med. 191:1755-1764(2000).
CC -!- FUNCTION: High affinity receptor for the C-C type chemokines
CC TAC/SCYA17 and MDC/SCYA22. The activity of this receptor is
CC mediated by G(i) proteins which activate a phosphatidylinositol-
CC calcium second messenger system. Could play a role in
CC lipopolysaccharide (LPS)-induced endotoxic shock. In the CNS,
CC could mediate hippocampal-neuron survival.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the thymus, macrophages and T-
CC and B-cells.
CC -!- DEVELOPMENTAL STAGE: Low expression at 7.5 dpc and 12.5 dpc in the
CC yolk sac.
CC -!- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES
CC PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY
CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2 (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; X90862; CAA62372.1; --
CC EMBL; U15208; AAA92582.1; --
CC PIR; JC4587; JC4587.
CC MGD; MGI:107824; Ccr4.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IMP.
CC GO; GO:0006935; P:chemotaxis; IMP.
CC GO; GO:0006954; P:inflammatory response; IMP.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation.
CC DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 40 67 1 (POTENTIAL).
CC TRANSMEM 40 67 1 (POTENTIAL).

```

FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 78 98 2 (POTENTIAL).
FT DOMAIN 99 111 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 112 133 3 (POTENTIAL).
FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 151 175 4 (POTENTIAL).
FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 207 226 5 (POTENTIAL).
FT DOMAIN 227 242 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 243 267 6 (POTENTIAL).
FT DOMAIN 268 284 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 285 308 7 (POTENTIAL).
FT DOMAIN 309 360 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 343 346 POLY-SER.
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 110 187 BY SIMILARITY.
FT CONFLICT 4 4 T -> I (IN REF. 2).
FT CONFLICT 145 145 S -> T (IN REF. 2).
FT CONFLICT 181 181 E -> Q (IN REF. 2).
FT CONFLICT 205 205 E -> D (IN REF. 2).
FT CONFLICT 221 221 W -> C (IN REF. 2).
FT CONFLICT 241 241 V -> L (IN REF. 2).
FT CONFLICT 246 246 G -> A (IN REF. 2).
FT CONFLICT 293 293 G -> A (IN REF. 2).
FT CONFLICT 311 311 F -> S (IN REF. 2).
SQ SEQUENCE 360 AA; 41462 MW; 97BD8C96D259AE3 CRC64;

Query Match 70.2%; Score 66; DB 1; Length 360;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGVGN 16
DB 42 LPPLYSLVIFGLGVN 57

RESULT 30
CKR3 MACMU STANDARD; PRT; 355 AA.
AC P564B3;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)
DE (CCR3).
GN CCR3 OR CMKBR3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118446; PubMed=9454694;
RA Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;
RT "The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
RT for HIV-2, but not for HIV-1."
RL Virology 240:213-220(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

```

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF017283; AAB70527.1; -.
DR EMBL; Y13776; CAAT4107.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 180 180 K -> E (IN REF. 2).
FT CONFLICT 202 202 K -> R (IN REF. 2).
SQ SEQUENCE 355 AA; 40805 MW; E27F1E694970D9F CRC64;

Query Match 69.1%; Score 65; DB 1; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.012;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGVGNML 18
DB 37 VPPLYSLVFMVGLGNV 54
:|||||:|:|:|
:|||||:|:|:|

Search completed: March 4, 2004, 18:00:02
Job time : 6.07755 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 17:53:42 ; Search time 29.0204 Seconds
(without alignments)
195.701 Million cell updates/sec

Title: US-10-084-813-11

Perfect score:

Sequence: 1 LPPLYSLVFI FGFVGNML 18

Scoring table: BLOSUM62

scoring table: EUC0002
Gapop 10.0 . Gapext 0.5

Searched: 1017041 segs. 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Minimum DB seq	length: 0
Maximum DB seq	length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL 25:*

- ```

sp_archea.*
sp_bacteria.*
sp_fungi.*
sp_human.*
sp_invertebrate.*
sp_mammal.*
sp_mhc.*
sp_organelle.*
sp_phage.*
sp_plant.*
sp_rodent.*
sp_virus.*
sp_vertebrate.*
sp_unclassified.*
sp_ivrus.*
sp_bacteriap.*
sp_archeap.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Query | Score |        |     | DB | ID     | Description |
|------------|-------|-------|--------|-----|----|--------|-------------|
|            |       | Match | Length |     |    |        |             |
| 1          |       | 94    | 100.0  | 215 | 4  | O75303 | homo sapien |
| 2          |       | 94    | 100.0  | 339 | 4  | O9UN26 | homo sapien |
| 3          |       | 94    | 100.0  | 339 | 4  | O9UN23 | homo sapien |
| 4          |       | 94    | 100.0  | 339 | 4  | O9UBJ7 | homo sapien |
| 5          |       | 94    | 100.0  | 339 | 4  | O9UN27 | homo sapien |
| 6          |       | 94    | 100.0  | 339 | 4  | O9UBT9 | homo sapien |
| 7          |       | 94    | 100.0  | 339 | 4  | O9UN28 | homo sapien |
| 8          |       | 94    | 100.0  | 339 | 6  | O9TQW0 | hylobates c |
| 9          |       | 94    | 100.0  | 339 | 6  | O9TUX1 | hylobates c |
| 10         |       | 94    | 100.0  | 339 | 6  | O9UTW8 | gorilla gor |
| 11         |       | 94    | 100.0  | 339 | 6  | O9UTW9 | hylobates c |
| 12         |       | 94    | 100.0  | 339 | 6  | O9TQW4 | pan troglod |
| 13         |       | 94    | 100.0  | 339 | 6  | O9UTW6 | pan troglod |
| 14         |       | 94    | 100.0  | 339 | 6  | O9UTW7 | pan troglod |
| 15         |       | 94    | 100.0  | 339 | 6  | O9UTW3 | pongo pygma |
| 16         |       | 94    | 100.0  | 339 | 6  | O9TQW2 | pongo pygma |

90 90 95.7 339 6 Q9TUR8  
 91 90 95.7 339 6 Q9TUV2  
 92 90 95.7 339 6 Q9TUV5  
 93 90 95.7 339 6 Q9TUV0  
 94 90 95.7 339 6 Q9TUR1  
 95 90 95.7 339 6 Q9TUS9  
 96 90 95.7 340 6 Q9TUV2  
 97 90 95.7 344 6 Q9TOR8  
 98 90 95.7 352 6 Q9TSK1  
 99 90 95.7 352 6 Q9TUV4  
 100 90 95.7 352 6 Q9TUNC4

## ALIGNMENTS

RESULT 1  
 O75303  
 ID Q75303 PRELIMINARY; PRT; 215 AA.  
 AC O75303;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE CC-chemokine receptor.  
 GN CCR-5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tse L., Ehrenberg P.K., Chang G., Michael N.L.;  
 RT "Genomic Organization and Functional Characterization of the Complete  
 Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-  
 Receptor for HIV-1.";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF009362; AAC23944.1; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON TER 1  
 FT NON TER 339  
 SQ SEQUENCE 215 AA; 23946 MW; 3C9146C76BA416F7 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 215;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGVGNML 18  
 |||||  
 DB 33 LPPLSLVIFGVGNML 50

RESULT 2  
 Q9UN26  
 ID Q9UN26 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN26;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161916; AAD47673.1; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON TER 1  
 FT NON TER 339  
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGVGNML 18  
 |||||  
 DB 26 LPPLSLVIFGVGNML 43

RESULT 3  
 Q9UN23  
 ID Q9UN23 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN23;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161920; AAD47677.1; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON TER 1  
 FT NON TER 339  
 SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVIFGVGNML 18  
 |||||  
 DB 26 LPPLSLVIFGVGNML 43

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RESULT 4
Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korb B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161912; AAD47674.1; -.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFF1E2F27A CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVFIQFVGNML 18
DB 26 LPPLSLVFIQFVGNML 43

RESULT 5
Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korb B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

```

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVFIQFVGNML 18
DB 26 LPPLSLVFIQFVGNML 43

RESULT 6
Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korb B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C39FAA7 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLSLVFIQFVGNML 18
DB 26 LPPLSLVFIQFVGNML 43

RESULT 7
Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.

```

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819P92D6DB1A6 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
DB 26 LPPLYSLVIFGFVGNML 43

RESULT 8
Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819P92D6DB1A6 CRC64;

Query Match 100.0%; Score 94; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
DB 26 LPPLYSLVIFGFVGNML 43

RESULT 9
Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39075 MW; 09257F8B34C4AE CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
DB 26 LPPLYSLVIFGFVGNML 43

RESULT 10
Q9TUX8 PRELIMINARY; PRT; 339 AA.
AC Q9TUX8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
DB 26 LPPLYSLVIFGFVGNML 43

RESULT 11
Q9TUM9
ID Q9TUM9 PRELIMINARY; PRT; 339 AA.
AC Q9TUM9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
OS CCR5.
GN Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39024 MW; EC4C848DEEF107E CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
DB 26 LPPLYSLVIFGFVGNML 43

RESULT 12
Q9TQW4
ID Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

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DE C-C chemokine receptor 5 (Fragment).
GN CCR5
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39129 MW; 4A8F8BB601D46A4 CRC64;

Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18
DB 26 LPPLYSLVIFGFVGNML 43

RESULT 13
Q9TUM6
ID Q9TUM6 PRELIMINARY; PRT; 339 AA.
AC Q9TUM6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161900; AAD47657.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339

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SQ SEQUENCE 339 AA; 39103 MW; 4038C132D024C5A4 CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVIFGFVGNML 43

RESULT 14
Q9TUW7
ID Q9TUW7 PRELIMINARY; PRT; 339 AA.
AC Q9TUW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161907; AAD47655.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVIFGFVGNML 43

RESULT 15
Q9TUW3
ID Q9TUW3 PRELIMINARY; PRT; 339 AA.
AC Q9TUW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161907; AAD47655.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39157 MW; 4A9EBAD183E8E72D CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVIFGFVGNML 43

RESULT 16
Q9TUW2
ID Q9TUW2 PRELIMINARY; PRT; 339 AA.
AC Q9TUW2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161907; AAD47655.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39117 MW; 4C4E35825BD54E9C CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVIFGFVGNML 43

RESULT 17
Q9TOR2
ID Q9TOR2 PRELIMINARY; PRT; 339 AA.
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RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161908; AAD47665.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39103 MW; 4350C4625FB0657C CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVIFGFVGNML 43

RESULT 16
Q9TOR2
ID Q9TOR2 PRELIMINARY; PRT; 339 AA.
AC Q9TOR2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161907; AAD47664.1; -.
DR EMBL; AF161906; AAD47663.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39117 MW; 4C4E35825BD54E9C CRC64;
Query Match 100.0%; Score 94; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGFVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVIFGFVGNML 43

RESULT 17
Q9TOR2
ID Q9TOR2 PRELIMINARY; PRT; 339 AA.
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AC Q9TOR2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5 (Fragment).  
GN CCR5  
OS Gorilla gorilla gorilla (Lowland gorilla).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
OX NCBI\_TaxID=9595;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.,  
RT "Sequences of the CCR5 genes from diverse simian and prosimian  
RT species.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF161897; RAD47654.1; -  
DR EMBL; AF161891; RAD47648.1; -  
DR EMBL; AF161892; RAD47649.1; -  
DR EMBL; AF161893; RAD47650.1; -  
DR EMBL; AF161895; RAD47652.1; -  
DR EMBL; AF161896; RAD47653.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR PRINTS; PR00237; GPCRHOOPS.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
FT NON TER 1  
FT NON TER 339  
SQ SEQUENCE 339 AA; 39105 MW; F5400A7AB6FF7AB9 CRC64;  
  
Query Match 100.0%; Score 94; DB 6; Length 339;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LPPLYSLVIFGFVGNML 18  
Db 26 LPPLYSLVIFGFVGNML 43  
  
RESULT 18  
Q9TWS  
ID Q9TWS PRELIMINARY; PRT; 339 AA.  
AC Q9TWS;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5 (Fragment).  
GN CCR5  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.,  
RT "Sequences of the CCR5 genes from diverse simian and prosimian  
RT species.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF161902; RAD47659.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
  
Query Match 100.0%; Score 94; DB 6; Length 339;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LPPLYSLVIFGFVGNML 18  
Db 26 LPPLYSLVIFGFVGNML 43  
  
RESULT 18  
Q9TWS  
ID Q9TWS PRELIMINARY; PRT; 339 AA.  
AC Q9TWS;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5 (Fragment).  
GN CCR5  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.,  
RT "Sequences of the CCR5 genes from diverse simian and prosimian  
RT species.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF161902; RAD47659.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRHOOPS.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
FT NON TER 1  
FT NON TER 339  
SQ SEQUENCE 339 AA; 39141 MW; DC6B1D627907646C CRC64;  
  
Query Match 100.0%; Score 94; DB 6; Length 339;  
Best Local Similarity 100.0%; Pred. No. 1.2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LPPLYSLVIFGFVGNML 18  
Db 26 LPPLYSLVIFGFVGNML 43  
  
RESULT 19  
Q95NC5  
ID Q95NC5 PRELIMINARY; PRT; 352 AA.  
AC Q95NC5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE C-C chemokine receptor 5.  
GN CCR5.  
OS Hylobates syndactylus (Siamang) (Sympalangus syndactylus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
OX NCBI\_TaxID=9590;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhang Y., Ryder O.A., Zhang Y.,  
RT "Sequence comparison of the CCR5 gene in primates and primate  
RT phylogeny.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF177884; AAK43367.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;  
  
Query Match 100.0%; Score 94; DB 6; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LPPLYSLVIFGFVGNML 18  
Db 33 LPPLYSLVIFGFVGNML 50  
  
RESULT 20  
O18771  
ID O18771 PRELIMINARY; PRT; 352 AA.  
AC O18771;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE CCR5 receptor (Fragment).  
GN CCR5.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CHCCRS-141a;

RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";  
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).  
 DR EMBL: AF011539; AAB65739.1; -;  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER  
 SQ SEQUENCE 352 AA; 40466 MW; 3FFPACTABAEID4FB CRC64;  
 Query Match 100.0%; Score 94; DB 6; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LPPLYSLVVFIFGVGNML 18  
 DB 33 LPPLYSLVVFIFGVGNML 50  
 RESULT 21  
 Q95NCO PRELIMINARY; PRT; 352 AA.  
 AC Q95NCO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5.  
 GN CCR5.  
 OS Hylobates moloch (silvery gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=81572;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Ryder O.A., Zhang Y.;  
 RT "Sequence comparison of the CCR5 gene in primates and primate  
 RT phylogeny.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF177899; AAK43382.1; -;  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;  
 Query Match 100.0%; Score 94; DB 6; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LPPLYSLVVFIFGVGNML 18  
 DB 33 LPPLYSLVVFIFGVGNML 50  
 RESULT 22  
 Q9MZA3 PRELIMINARY; PRT; 352 AA.  
 ID Q9MZA3  
 AC Q9MZA3;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE CC chemokine receptor 5.  
 GN CCR5.  
 OS Hylobates agilis unko.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=9583;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20317091; PubMed=10747879;  
 RA Mummidi S., Bamshad M., Ahuja S.S., Gonzalez E., Feuillet P.M.,  
 RA Begum K., Galvis M.C., Kostecki V., Valente A.J., Murthy K.K.,  
 RA Haro L., Dolan M.J., Allan J.S., Ahuja S.K.;  
 RT "Evolution of human and non-human primate CC chemokine receptor 5 gene  
 RT and mRNA. Potential roles for haplotype and mRNA diversity,  
 RT differential haplotype-specific transcriptional activity, and altered  
 RT transcription factor binding to polymorphic nucleotides in the  
 RT pathogenesis of HIV-1 and simian immunodeficiency virus.";  
 RL J. Biol. Chem. 275:18946-18961(2000).  
 DR EMBL: AF252551; AAF87981.1; -;  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 352 AA; 40293 MW; BAF8279ABBAB5309 CRC64;  
 Query Match 100.0%; Score 94; DB 6; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LPPLYSLVVFIFGVGNML 18  
 DB 33 LPPLYSLVVFIFGVGNML 50  
 RESULT 23  
 Q9XS99 PRELIMINARY; PRT; 352 AA.  
 ID Q9XS99  
 AC Q9XS99;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE CC chemokine receptor 5.  
 GN CCR5.  
 OS Gorilla gorilla (gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.  
 OX NCBI\_TaxID=9593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GorillaCCR;  
 RX MEDLINE=99210133; PubMed=10195758;  
 RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T., Lal R.B.;  
 RT "Species-specific changes in the CCR5 gene from African and Asian  
 RT nonhuman primates.";  
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).  
 DR EMBL: AF105291; AAD20560.1; -;  
 DR GO: GO:0016021; C:integral to membrane; IEA.  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.

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KW Receptor.
SQ SEQUENCE 352 AA; 40529 MW; 1BE68C68FE2E7AD0 CRC64;

Query Match 100.0%; Score 94; DB 6; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
| | | | | | | | | | | | | | | | | |
Db 33 LPPLYSLVIFGFGVGNML 50

RESULT 24
Q9UN24 PRELIMINARY; PRT; 339 AA.
AC Q9UN24;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161919; AAD47676.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; R:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 97.9%; Score 92; DB 4; Length 339;
Best Local Similarity 94.4%; Pred. No. 2.5e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
| | | | | | | | | | | | | | | | | |
Db 26 LPPLYSLVIFGFGVGNML 43

RESULT 25
Q8H2T9 PRELIMINARY; PRT; 352 AA.
AC Q8H2T9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine receptor CCR5.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RA Labonte J.A., Babcock G.J., Patel T., Sodroski J.;
RT "Blockade of HIV-1 infection of New World Monkey Cells Occurs
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RT Primarily at the Stage of Virus Entry.";
RL J. Exp. Med. 196;431-445(2002).
DR EMBL; AF452615; AAN14531.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 352 AA; 40542 MW; 9FC896FB7F074647 CRC64;

Query Match 97.9%; Score 92; DB 6; Length 352;
Best Local Similarity 94.4%; Pred. No. 2.6e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18
| | | | | | | | | | | | | | | | | |
Db 33 LPPLYSLVIFGFGVGNML 50

RESULT 26
Q9TUV7 PRELIMINARY; PRT; 316 AA.
AC Q9TUV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161930; AAD47687.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 316
SQ SEQUENCE 316 AA; 4DAD95C3848F04EA CRC64;

Query Match 95.7%; Score 90; DB 6; Length 316;
Best Local Similarity 88.9%; Pred. No. 4.9e-06;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 LPPLYSLVFIFGVGNML 18  
 |||||:|||||  
 Db 3 LPPLYSNVLFGFVGNML 20

RESULT 27  
 Q9TUQ7 PRELIMINARY; PRT; 334 AA.  
 AC Q9TUQ7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Brythocebus patas (Red guenon) (Hussar).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Brythrocebus.  
 OX NCBI\_TaxID=9538;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species."  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF162049; AAD47804.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 334 334  
 SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 95.7%; Score 90; DB 6; Length 334;  
 Best Local Similarity 94.4%; Pred. No. 5.1e-06;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18  
 |||||:|||||  
 Db 21 LPPLYSLVFIFGVGNIL 38

RESULT 28  
 Q9TUV6 PRELIMINARY; PRT; 339 AA.  
 AC Q9TUV6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Saguinus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.  
 OX NCBI\_TaxID=100754;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species."  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF161932; AAD47689.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005507; F:copper ion binding; IEA.

DR GO; GO:0005489; F:electron transporter activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR000923; BlueCu 1.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00196; COPPER\_BLUE; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 38993 MW; 0559F4F0FEC70F5F CRC64;

Query Match 95.7%; Score 90; DB 6; Length 339;  
 Best Local Similarity 88.9%; Pred. No. 5.2e-06;  
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18  
 |||||:|||||  
 Db 26 LPPLYSNVLFGFVGNML 43

RESULT 29  
 Q9TUU9 PRELIMINARY; PRT; 339 AA.  
 ID Q9TUU9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Cercopithecus diana (Diana monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=36224;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species."  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF161948; AAD47704.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 95.7%; Score 90; DB 6; Length 339;  
 Best Local Similarity 94.4%; Pred. No. 5.2e-06;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18  
 |||||:|||||  
 Db 26 LPPLYSLVFIFGVGNIL 43

RESULT 30  
 Q9TUT4

ID O9TUT4 PRELIMINARY; PERT; 339 AA.  
AC O9TUT4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5 (Fragment).  
GN CCR5.  
OS Macaca nemestrina (pig-tailed macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI TaxID=9545;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
RA Shabara R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinsky S.;  
RT "Sequences of the CCR5 genes from diverse simian and prosimian  
RT species.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF161979; RAD47734.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodop.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_RHODOPS.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
FT NON TER 1  
FT NON TER 339  
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;  
  
Query Match 95.7%; Score 90; DB 6; Length 339;  
Best Local Similarity 94.4%; Pred. NO. 5.2e-06;  
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 LPPLSLVFIQFVGNML 18  
Db 26 LPPLSLVFIQFVGNIL 43  
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|||||:|:|

Search completed: March 4, 2004, 18:02:54  
Job time : 31.0204 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:55:22 ; Search time 11.5714 Seconds  
(without alignments)  
80.307 Million cell updates/sec

Title: US-10-084-813-11  
Perfect score: 94  
Sequence: 1 LPPLYSIVFIFGVGNML 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 94    | 100.0       | 83     | 4  | US-09-131-827A-13 |
| 2          | 94    | 100.0       | 87     | 3  | US-09-087-232A-18 |
| 3          | 94    | 100.0       | 100    | 3  | US-09-087-232A-15 |
| 4          | 94    | 100.0       | 184    | 4  | US-08-833-752-4   |
| 5          | 94    | 100.0       | 215    | 3  | US-09-087-232A-17 |
| 6          | 94    | 100.0       | 215    | 4  | US-08-833-752-6   |
| 7          | 94    | 100.0       | 329    | 4  | US-09-502-783A-9  |
| 8          | 94    | 100.0       | 344    | 3  | US-08-466-343D-9  |
| 9          | 94    | 100.0       | 347    | 1  | US-08-461-244-3   |
| 10         | 94    | 100.0       | 352    | 3  | US-08-466-343D-2  |
| 11         | 94    | 100.0       | 352    | 3  | US-09-087-232A-13 |
| 12         | 94    | 100.0       | 352    | 3  | US-08-861-105-14  |
| 13         | 94    | 100.0       | 352    | 3  | US-08-575-967A-2  |
| 14         | 94    | 100.0       | 352    | 3  | US-09-045-583-52  |
| 15         | 94    | 100.0       | 352    | 4  | US-09-517-605-5   |
| 16         | 94    | 100.0       | 352    | 4  | US-09-534-185-52  |
| 17         | 94    | 100.0       | 352    | 4  | US-08-833-752-5   |
| 18         | 94    | 100.0       | 352    | 4  | US-09-796-202-1   |
| 19         | 94    | 100.0       | 352    | 4  | US-09-502-783A-2  |
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| 22         | 94    | 100.0       | 360    | 3  | US-09-045-583-50  |
| 23         | 94    | 100.0       | 360    | 3  | US-09-045-583-51  |
| 24         | 94    | 100.0       | 360    | 4  | US-09-534-185-50  |
| 25         | 94    | 100.0       | 360    | 4  | US-09-534-185-51  |
| 26         | 94    | 100.0       | 360    | 4  | US-08-833-752-7   |
| 27         | 94    | 100.0       | 360    | 4  | US-09-131-827A-2  |

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| 28  | 94 | 100.0 | 360 | 4 | US-09-131-827A-20  | Sequence 20, Appl |
| 29  | 94 | 100.0 | 360 | 5 | PCT-US95-00476-4   | Sequence 4, Appl  |
| 30  | 94 | 100.0 | 374 | 1 | US-08-450-393A-2   | Sequence 2, Appl  |
| 31  | 94 | 100.0 | 374 | 3 | US-08-446-669-2    | Sequence 2, Appl  |
| 32  | 94 | 100.0 | 374 | 5 | PCT-US95-00476-2   | Sequence 2, Appl  |
| 33  | 88 | 93.6  | 354 | 4 | US-08-724-984A-2   | Sequence 2, Appl  |
| 34  | 77 | 81.9  | 355 | 1 | US-08-012-988A-2   | Sequence 2, Appl  |
| 35  | 77 | 81.9  | 355 | 1 | US-08-450-393A-5   | Sequence 5, Appl  |
| 36  | 77 | 81.9  | 355 | 3 | US-08-446-669-5    | Sequence 5, Appl  |
| 37  | 77 | 81.9  | 355 | 3 | US-09-045-583-53   | Sequence 53, Appl |
| 38  | 77 | 81.9  | 355 | 4 | US-09-239-938-1    | Sequence 1, Appl  |
| 39  | 77 | 81.9  | 355 | 4 | US-09-534-185-53   | Sequence 53, Appl |
| 40  | 77 | 81.9  | 355 | 4 | US-08-833-752-9    | Sequence 9, Appl  |
| 41  | 77 | 81.9  | 355 | 4 | US-09-886-319A-13  | Sequence 13, Appl |
| 42  | 77 | 81.9  | 355 | 4 | US-09-886-319A-14  | Sequence 14, Appl |
| 43  | 77 | 81.9  | 355 | 5 | PCT-US95-00476-5   | Sequence 5, Appl  |
| 44  | 75 | 79.8  | 360 | 3 | US-08-875-573-20   | Sequence 20, Appl |
| 45  | 75 | 79.8  | 360 | 3 | US-09-232-878-2    | Sequence 2, Appl  |
| 46  | 75 | 79.8  | 360 | 3 | US-09-045-583-55   | Sequence 55, Appl |
| 47  | 75 | 79.8  | 360 | 4 | US-09-534-185-55   | Sequence 55, Appl |
| 48  | 70 | 74.5  | 360 | 4 | US-08-939-107-34   | Sequence 34, Appl |
| 49  | 70 | 74.5  | 355 | 4 | US-08-720-555-2    | Sequence 2, Appl  |
| 50  | 68 | 72.3  | 360 | 4 | US-08-833-752-10   | Sequence 10, Appl |
| 51  | 65 | 69.1  | 355 | 4 | US-08-833-752-8    | Sequence 8, Appl  |
| 52  | 63 | 67.0  | 355 | 3 | US-08-575-967A-4   | Sequence 4, Appl  |
| 53  | 63 | 67.0  | 355 | 3 | US-08-847-296B-1   | Sequence 1, Appl  |
| 54  | 63 | 67.0  | 355 | 3 | US-09-045-583-54   | Sequence 54, Appl |
| 55  | 63 | 67.0  | 355 | 4 | US-09-534-185-54   | Sequence 54, Appl |
| 56  | 63 | 67.0  | 355 | 4 | US-08-720-555-4    | Sequence 4, Appl  |
| 57  | 63 | 67.0  | 355 | 4 | US-08-720-555-6    | Sequence 6, Appl  |
| 58  | 63 | 67.0  | 356 | 4 | US-08-567-882-7    | Sequence 7, Appl  |
| 59  | 63 | 67.0  | 357 | 4 | US-09-266-464-2    | Sequence 2, Appl  |
| 60  | 63 | 67.0  | 357 | 4 | US-09-170-496D-24  | Sequence 24, Appl |
| 61  | 63 | 67.0  | 357 | 4 | US-09-170-496D-176 | Sequence 176, App |
| 62  | 61 | 64.9  | 378 | 3 | US-09-045-583-5    | Sequence 5, Appl  |
| 63  | 61 | 64.9  | 378 | 4 | US-09-534-185-5    | Sequence 5, Appl  |
| 64  | 60 | 63.8  | 107 | 4 | US-09-621-976-5333 | Sequence 5333, Ap |
| 65  | 60 | 63.8  | 348 | 3 | US-08-852-824-17   | Sequence 17, Appl |
| 66  | 60 | 63.8  | 352 | 1 | US-08-450-393A-6   | Sequence 6, Appl  |
| 67  | 60 | 63.8  | 352 | 3 | US-08-446-669-6    | Sequence 6, Appl  |
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| 70  | 60 | 63.8  | 361 | 3 | US-08-352-678-4    | Sequence 4, Appl  |
| 71  | 60 | 63.8  | 361 | 4 | US-09-536-954-4    | Sequence 4, Appl  |
| 72  | 60 | 63.8  | 361 | 4 | US-09-170-496D-78  | Sequence 78, Appl |
| 73  | 60 | 63.8  | 361 | 4 | US-09-170-496D-206 | Sequence 206, App |
| 74  | 60 | 63.8  | 361 | 5 | PCT-US93-0936-4    | Sequence 4, Appl  |
| 75  | 59 | 62.8  | 373 | 3 | US-08-559-524A-4   | Sequence 4, Appl  |
| 76  | 59 | 62.8  | 373 | 3 | US-08-749-707-4    | Sequence 4, Appl  |
| 77  | 59 | 62.8  | 373 | 4 | US-09-947-922-4    | Sequence 4, Appl  |
| 78  | 58 | 61.7  | 384 | 3 | US-09-045-583-2    | Sequence 2, Appl  |
| 79  | 58 | 61.7  | 384 | 4 | US-09-534-185-2    | Sequence 2, Appl  |
| 80  | 57 | 60.6  | 337 | 1 | US-08-153-848-46   | Sequence 46, Appl |
| 81  | 57 | 60.6  | 337 | 3 | US-09-239-843A-46  | Sequence 46, Appl |
| 82  | 57 | 60.6  | 337 | 4 | US-09-088-337B-46  | Sequence 46, Appl |
| 83  | 57 | 60.6  | 337 | 5 | PCT-US93-11153-46  | Sequence 46, Appl |
| 84  | 57 | 60.6  | 352 | 1 | US-08-203-056-3    | Sequence 3, Appl  |
| 85  | 57 | 60.6  | 352 | 1 | US-08-076-093A-4   | Sequence 4, Appl  |
| 86  | 57 | 60.6  | 352 | 1 | US-08-701-265-4    | Sequence 4, Appl  |
| 87  | 57 | 60.6  | 352 | 2 | US-08-284-586-4    | Sequence 4, Appl  |
| 88  | 57 | 60.6  | 352 | 2 | US-08-805-478-4    | Sequence 4, Appl  |
| 89  | 57 | 60.6  | 352 | 2 | US-08-802-627A-4   | Sequence 4, Appl  |
| 90  | 57 | 60.6  | 352 | 2 | US-08-801-238-4    | Sequence 4, Appl  |
| 91  | 57 | 60.6  | 352 | 2 | US-08-801-228-4    | Sequence 4, Appl  |
| 92  | 57 | 60.6  | 352 | 3 | US-09-104-296-4    | Sequence 4, Appl  |
| 93  | 57 | 60.6  | 352 | 4 | US-09-517-605-4    | Sequence 4, Appl  |
| 94  | 57 | 60.6  | 362 | 3 | US-08-513-974B-374 | Sequence 374, App |
| 95  | 57 | 60.6  | 368 | 3 | US-08-709-838-2    | Sequence 2, Appl  |
| 96  | 57 | 60.6  | 368 | 3 | US-08-829-839-2    | Sequence 2, Appl  |
| 97  | 57 | 60.6  | 368 | 4 | US-09-170-496D-20  | Sequence 20, Appl |
| 98  | 57 | 60.6  | 368 | 4 | US-09-170-496D-174 | Sequence 174, App |
| 99  | 57 | 60.6  | 368 | 4 | US-09-624-594-2    | Sequence 2, Appl  |
| 100 | 56 | 59.6  | 325 | 1 | US-08-118-270-51   | Sequence 51, Appl |

## ALIGNMENTS

## RESULT 1

US-09-131-827A-13  
; Sequence 13, Application US/09131827A  
; Patent No. 6600030  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Michael  
; APPLICANT: O'Brien, Stephen J.  
; APPLICANT: Smith, Michael  
; APPLICANT: Carrington, Mary  
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A  
; TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE  
; FILE REFERENCE: 14014.0333  
; CURRENT APPLICATION NUMBER: US/09/131,827A  
; CURRENT FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/055,659  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 83  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-131-827A-13

Query Match 100.0%; Score 94; DB 4; Length 83;  
Best Local Similarity 100.0%; Pred. No. 7.9e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18  
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Db 45 LPPLYSLVIFGFVGNML 62

## RESULT 2

US-09-087-232A-18  
; Sequence 18, Application US/09087232A  
; Patent No. 6153431  
; GENERAL INFORMATION:  
; APPLICANT: Quillent et al.  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR  
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/087,232A  
; FILING DATE: 28 MAY 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/048,057  
; FILING DATE: 30 MAY 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOLE, LISA B.  
; REGISTRATION NUMBER: 35,225  
; REFERENCE/DOCKET NUMBER: AP 31115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 408-2628  
; TELEFAX: (212) 765-2519  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 100 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-087-232A-18

Query Match 100.0%; Score 94; DB 3; Length 100;

Best Local Similarity 100.0%; Pred. No. 9.6e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18  
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Db 33 LPPLYSLVIFGFVGNML 50

## RESULT 4

US-08-833-752-4  
; Sequence 4, Application US/08833752  
; Patent No. 6448375

; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 87 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-087-232A-18

Query Match 100.0%; Score 94; DB 3; Length 87;  
Best Local Similarity 100.0%; Pred. No. 8.3e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18  
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Db 33 LPPLYSLVIFGFVGNML 50

## RESULT 3

US-09-087-232A-15  
; Sequence 15, Application US/09087232A  
; Patent No. 6153431  
; GENERAL INFORMATION:  
; APPLICANT: Quillent et al.  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR  
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/087,232A  
; FILING DATE: 28 MAY 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/048,057  
; FILING DATE: 30 MAY 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOLE, LISA B.  
; REGISTRATION NUMBER: 35,225  
; REFERENCE/DOCKET NUMBER: AP 31115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 408-2628  
; TELEFAX: (212) 765-2519  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 100 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-087-232A-15

Query Match 100.0%; Score 94; DB 3; Length 100;

Best Local Similarity 100.0%; Pred. No. 9.6e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFVGNML 18  
|||  
Db 33 LPPLYSLVIFGFVGNML 50



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/
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ APPLICANT: PARMENTIER, MARC
/ APPLICANT: VASSART, GILBERT
/ APPLICANT: LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/833,752
/ FILING DATE: 9-APR-1997
/ CLASSIFICATION: 536
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER:
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 184 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
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/ US-08-833-752-4
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/ Query Match 100.0%; Score 94; DB 4; Length 184;
/ Best Local Similarity 100.0%; Pred. No. 1.8e-07;
/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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/ QY 1 LPPLYSLVFIFGVGNML 18
/ Db 33 LPPLYSLVFIFGVGNML 50
/
/ RESULT 5
/ US-09-087-232A-17
/ Sequence 17, Application US/09087232A
/ Patent No. 6153431
/
/ GENERAL INFORMATION:
/ APPLICANT: Quillent et al.
/ TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
/ TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
/ STREET: 30 Rockefeller Plaza
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10112
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/087,232A
/ FILING DATE: 28 MAY 1998
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/048,057
/ FILING DATE: 30 MAY 1997
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/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KOLE, LISA B.
/ REGISTRATION NUMBER: 35,225
/ REFERENCE/DOCKET NUMBER: AP 31115
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 408-2628
/ TELEFAX: (212) 765-2519
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-09-087-232A-17
/
/ Query Match 100.0%; Score 94; DB 3; Length 215;
/ Best Local Similarity 100.0%; Pred. No. 2.1e-07;
/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 LPPLYSLVFIFGVGNML 18
/ Db 33 LPPLYSLVFIFGVGNML 50
/
/ RESULT 6
/ US-08-833-752-6
/ Sequence 6, Application US/08833752
/ Patent No. 6448375
/
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ APPLICANT: PARMENTIER, MARC
/ APPLICANT: VASSART, GILBERT
/ APPLICANT: LIBERT, FREDERICK
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/ TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/833,752
/ FILING DATE: 9-APR-1997
/ CLASSIFICATION: 536
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER:
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-833-752-6
/
/ Query Match 100.0%; Score 94; DB 4; Length 215;
/ Best Local Similarity 100.0%; Pred. No. 2.1e-07;
/ Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 LPPLYSLVFIFGVGNML 18
/ Db 33 LPPLYSLVFIFGVGNML 50
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RESULT 7
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; Sequence 9, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-502-783A-9

Query Match 100.0%; Score 94; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
DB 28 LPPLYSLVFIQFGVGNML 45

RESULT 8
US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; REGISTRATION NUMBER: 36,134
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-9

Query Match 100.0%; Score 94; DB 3; Length 344;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
DB 28 LPPLYSLVFIQFGVGNML 45

RESULT 9
US-08-461-244-3
; Sequence 3, Application US/08461244
; Patent No. 5776729
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Yi, Li
; APPLICANT: Ruben, Steven M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,244
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-445
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-244-3

Query Match 100.0%; Score 94; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
DB 32 LPPLYSLVFIQFGVGNML 49

RESULT 10
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-343D-2

Query Match 100.0%; Score 94; DB 1; Length 347;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
DB 32 LPPLYSLVFIQFGVGNML 49
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;; CITY: WASHINGTON  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/466,343D  
;; FILING DATE: 06-JUN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: STEFFE, ERIC K.  
;; REGISTRATION NUMBER: 36,688  
;; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 371-2600  
;; TELEFAX: (202) 371-2540  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 352 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-466-343D-2

Query Match 100.0%; Score 94; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGFVGNML 18  
Db 33 LPPLYSLVFIFGFVGNML 50

RESULT 11  
US-09-087-232A-13  
; Sequence 13, Application US/09087232A  
; Patent No. 6153431  
; GENERAL INFORMATION:  
; APPLICANT: Quillent et al.  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR  
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/087,232A  
; FILING DATE: 28 MAY 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/048,057  
; FILING DATE: 30 MAY 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOLE, LISA B.  
; REGISTRATION NUMBER: 35,225  
; REFERENCE/DOCKET NUMBER: AP 31115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 408-2628  
; TELEFAX: (212) 765-2519  
; INFORMATION FOR SEQ ID NO: 13:

;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 352 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-09-087-232A-13

Query Match 100.0%; Score 94; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVFIFGFVGNML 18  
Db 33 LPPLYSLVFIFGFVGNML 50

RESULT 12  
US-08-861-105-14  
; Sequence 14, Application US/08861105  
; Patent No. 6258527  
; GENERAL INFORMATION:  
; APPLICANT: LITTMAN, DAN R.  
; APPLICANT: DENG, HONGKUI  
; APPLICANT: ELLMEIER, WILFRIED  
; APPLICANT: LANDAU, NATHANIEL R.  
; APPLICANT: LIU, RONG  
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH  
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,105  
; FILING DATE:  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/666,020  
; FILING DATE: 19-JUN-1996  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,319  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-08-861-105-14

Query Match 100.0%; Score 94; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18  
| | | | | | | | | | | | | | | | | |  
Db 33 LPPLYSLVIFGVGNML 50

RESULT 13  
US-08-575-967A-2  
; Sequence 2, Application US/08575967A  
; Patent No. 6265184  
; GENERAL INFORMATION:  
; APPLICANT: Gray et al.  
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/575,967A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6265184and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32918  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-485-1900  
; TELEFAX: 206-485-1662  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: /= \*88C amino acid sequence\*"

US-08-575-967A-2  
Query Match 100.0%; Score 94; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18  
| | | | | | | | | | | | | | | | | |  
Db 33 LPPLYSLVIFGVGNML 50

RESULT 14  
US-09-045-583-52  
; Sequence 52, Application US/09045583  
; Patent No. 6287805  
; GENERAL INFORMATION:  
; APPLICANT: Graham, Gerard J. et al.  
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts

COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal

US-09-045-583-52  
Query Match 100.0%; Score 94; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18  
| | | | | | | | | | | | | | | | | |  
Db 33 LPPLYSLVIFGVGNML 50

RESULT 15  
US-09-517-605-5  
; Sequence 5, Application US/09517605  
; Patent No. 6391567  
; GENERAL INFORMATION:  
; APPLICANT: Littman, Dan R.  
; APPLICANT: Kwon, Douglas S.  
; APPLICANT: van Kooyk, Yvette  
; APPLICANT: Geijtenbeek, Theo  
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO  
; FILE REFERENCE: 1049-1-017  
; CURRENT APPLICATION NUMBER: US/09/517,605  
; CURRENT FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-517-605-5

Query Match 100.0%; Score 94; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LPPLYSLVIFGVGNML 18  
| | | | | | | | | | | | | | | | | |  
Db 33 LPPLYSLVIFGVGNML 50

RESULT 16  
US-09-534-185-52  
; Sequence 52, Application US/09534185

Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Hepathelical Receptor Superfamily and Uses  
Thereof  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-09-534-185-52  
Query Match 100.0%; Score 94; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LPPLYSLVFIQFVGNNL 18  
Db 33 LPPLYSLVFIQFVGNNL 50  
RESULT 17  
US-08-833-752-5  
Sequence 5, Application US/08833752  
Patent No. 6448375  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
APPLICANT: PARMENTIER, MARC  
APPLICANT: VASSART, GILBERT  
APPLICANT: LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,752  
FILING DATE: 9-APR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E.  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-833-752-5  
Query Match 100.0%; Score 94; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LPPLYSLVFIQFVGNNL 18  
Db 33 LPPLYSLVFIQFVGNNL 50  
RESULT 18  
US-09-502-783A-2  
Sequence 2, Application US/09502783A  
Patent No. 6511826  
GENERAL INFORMATION:  
APPLICANT: Li, Yi  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)  
TITLE OF INVENTION: HDGNNR10  
FILE REFERENCE: 1488.1150006  
CURRENT APPLICATION NUMBER: US/09/502,783A  
CURRENT FILING DATE: 2001-08-23  
PRIOR APPLICATION NUMBER: 08/466,343  
PRIOR FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 2  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-502-783A-2  
Query Match 100.0%; Score 94; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LPPLYSLVFIQFVGNNL 18  
Db 33 LPPLYSLVFIQFVGNNL 50  
RESULT 19  
US-09-796-202-1  
Sequence 1, Application US/09796202  
Patent No. 6548636  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPW/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 1

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; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 94; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYLSLVIFGFGVGNML 18
Db 33 LPPYLSLVIFGFGVGNML 50

RESULT 20
US-08-450-393A-4
; Sequence 4, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: May 25, 1995
; APPLICATION NUMBER: US/08/450,393A
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-450-393A-4

Query Match 100.0%; Score 94; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYLSLVIFGFGVGNML 18
Db 45 LPPYLSLVIFGFGVGNML 62

RESULT 21
US-08-446-669-4
; Sequence 4, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
```

```
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,669
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-237/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-669-4

Query Match 100.0%; Score 94; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYLSLVIFGFGVGNML 18
Db 45 LPPYLSLVIFGFGVGNML 62

RESULT 22
US-09-045-583-50
; Sequence 50, Application US/09045583
; Patent No. 6287805
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
```

REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-045-583-51

Query Match 100.0%; Score 94; DB 3; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVPIFGVGNML 18  
DB 45 LPPLYSLVPIFGVGNML 62

## RESULT 23

US-09-045-583-51  
Sequence 51, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-045-583-51

Query Match 100.0%; Score 94; DB 3; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVPIFGVGNML 18  
DB 45 LPPLYSLVPIFGVGNML 62

## RESULT 24

US-09-534-185-50  
Sequence 50, Application US/09534185  
Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Heptahelical Receptor Superfamily and Uses  
Therefor

NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:

US-09-534-185-50  
Query Match 100.0%; Score 94; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVPIFGVGNML 18  
DB 45 LPPLYSLVPIFGVGNML 62

## RESULT 25

US-09-534-185-51  
Sequence 51, Application US/09534185  
Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Heptahelical Receptor Superfamily and Uses  
Therefor

NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-534-185-51

Query Match 100.0%; Score 94; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18  
|||||  
Db 45 LPPLYSLVIFGFGVGNML 62

RESULT 26  
US-08-833-752-7  
Sequence 7, Application US/08833752  
Patent No. 6448375  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
APPLICANT: PARMENTIER, MARC  
APPLICANT: VASSART, GILBERT  
APPLICANT: LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,752  
FILING DATE: 9-APR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E.  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6448375e  
US-08-833-752-7

Query Match 100.0%; Score 94; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18  
|||||  
Db 45 LPPLYSLVIFGFGVGNML 62

RESULT 27  
US-09-131-827A-2  
Sequence 2, Application US/09131827A  
Patent No. 6600030  
GENERAL INFORMATION:  
APPLICANT: Dean, Michael  
APPLICANT: O'Brien, Stephen J.  
APPLICANT: Smith, Michael  
APPLICANT: Carrington, Mary  
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A  
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE  
FILE REFERENCE: 14014.0333  
CURRENT APPLICATION NUMBER: US/09/131,827A  
CURRENT FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/055,659  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-131-827A-2

Query Match 100.0%; Score 94; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18  
|||||  
Db 45 LPPLYSLVIFGFGVGNML 62

RESULT 28  
US-09-131-827A-20  
Sequence 20, Application US/09131827A  
Patent No. 6600030  
GENERAL INFORMATION:  
APPLICANT: Dean, Michael  
APPLICANT: O'Brien, Stephen J.  
APPLICANT: Smith, Michael  
APPLICANT: Carrington, Mary  
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A  
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE  
FILE REFERENCE: 14014.0333  
CURRENT APPLICATION NUMBER: US/09/131,827A  
CURRENT FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/055,659  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-131-827A-20

Query Match 100.0%; Score 94; DB 4; Length 360;



Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18  
Db 45 LPPLYSLVIFGFGVGNML 62

## RESULT 29

PCT-US95-00476-4

; Sequence 4, Application PC/TUS9500476  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Robbins, Berliner & Carson  
; STREET: 201 N. Figueroa Street, 5th Floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA

; ZIP: 90012-2628  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00476  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berliner, Robert  
; REGISTRATION NUMBER: 20,121  
; REFERENCE/DOCKET NUMBER: 5555-291  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310-977-1001  
; TELEFAX: 310-977-1003  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-00476-4

Query Match 100.0%; Score 94; DB 5; Length 360;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18  
Db 45 LPPLYSLVIFGFGVGNML 62

## RESULT 30

US-08-450-393A-2

; Sequence 2, Application US/08450393A  
; Patent No. 5707815  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; APPLICANT: Coughlin, Shaun  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 Palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA

; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,393A  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cserr, Luann  
; REGISTRATION NUMBER: 31,822  
; REFERENCE/DOCKET NUMBER: UCAL-237/02US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5165  
; TELEFAX: 415-8857-0663  
; TELEX: 380816Coolevpa  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 374 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-450-393A-2

Query Match 100.0%; Score 94; DB 1; Length 374;  
Best Local Similarity 100.0%; Pred. NO. 3.8e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVIFGFGVGNML 18  
Db 45 LPPLYSLVIFGFGVGNML 62

Search completed: March 4, 2004, 18:05:12  
Job time : 12.5714 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: March 4, 2004, 18:03:03 ; Search time 24.0612 Seconds  
(without alignments)  
157.962 Million cell updates/sec

Title: US-10-084-813-11  
Perfect score: 94  
Sequence: 1 LPPLYSLVIFGFVGNML 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues  
Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| 1          | 94    | 100.0       | 18     | 14 | US-10-084-813-11  |
| 2          | 94    | 100.0       | 18     | 14 | US-10-084-813-39  |
| 3          | 94    | 100.0       | 83     | 9  | US-09-131-827A-13 |
| 4          | 94    | 100.0       | 184    | 9  | US-09-938-719-4   |
| 5          | 94    | 100.0       | 184    | 9  | US-09-938-719-4   |
| 6          | 94    | 100.0       | 184    | 9  | US-09-938-719-4   |
| 7          | 94    | 100.0       | 184    | 9  | US-09-938-719-4   |
| 8          | 94    | 100.0       | 215    | 9  | US-09-938-719-6   |
| 9          | 94    | 100.0       | 215    | 9  | US-09-938-719-6   |
| 10         | 94    | 100.0       | 329    | 9  | US-09-938-719-6   |
| 11         | 94    | 100.0       | 329    | 9  | US-09-938-719-6   |
| 12         | 94    | 100.0       | 329    | 9  | US-09-938-719-6   |
| 13         | 94    | 100.0       | 329    | 9  | US-09-938-719-6   |
| 14         | 94    | 100.0       | 329    | 9  | US-09-938-719-6   |
| 15         | 94    | 100.0       | 344    | 9  | US-09-938-719-6   |

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| 15 | 94 | 100.0 | 344 | 9  | US-09-779-880A-9   | Sequence 9, Appli  |
| 17 | 94 | 100.0 | 344 | 14 | US-10-232-686-9    | Sequence 9, Appli  |
| 18 | 94 | 100.0 | 344 | 14 | US-10-067-800-9    | Sequence 9, Appli  |
| 19 | 94 | 100.0 | 344 | 14 | US-10-135-839-9    | Sequence 9, Appli  |
| 20 | 94 | 100.0 | 347 | 9  | US-09-104-792-3    | Sequence 3, Appli  |
| 21 | 94 | 100.0 | 347 | 14 | US-10-176-078-3    | Sequence 3, Appli  |
| 22 | 94 | 100.0 | 352 | 9  | US-09-725-285-2    | Sequence 2, Appli  |
| 23 | 94 | 100.0 | 352 | 9  | US-09-759-841-2    | Sequence 2, Appli  |
| 24 | 94 | 100.0 | 352 | 9  | US-09-779-879A-2   | Sequence 2, Appli  |
| 25 | 94 | 100.0 | 352 | 9  | US-09-779-879A-22  | Sequence 22, Appli |
| 26 | 94 | 100.0 | 352 | 9  | US-09-779-880A-2   | Sequence 2, Appli  |
| 27 | 94 | 100.0 | 352 | 9  | US-09-779-880A-22  | Sequence 22, Appli |
| 28 | 94 | 100.0 | 352 | 9  | US-09-813-653-15   | Sequence 15, Appli |
| 29 | 94 | 100.0 | 352 | 9  | US-09-813-653-17   | Sequence 17, Appli |
| 30 | 94 | 100.0 | 352 | 9  | US-09-796-802-1    | Sequence 1, Appli  |
| 31 | 94 | 100.0 | 352 | 9  | US-09-195-662A-2   | Sequence 2, Appli  |
| 32 | 94 | 100.0 | 352 | 9  | US-09-339-912A-2   | Sequence 2, Appli  |
| 33 | 94 | 100.0 | 352 | 9  | US-09-938-719-5    | Sequence 5, Appli  |
| 34 | 94 | 100.0 | 352 | 9  | US-09-939-226-5    | Sequence 5, Appli  |
| 35 | 94 | 100.0 | 352 | 9  | US-09-938-703-5    | Sequence 5, Appli  |
| 36 | 94 | 100.0 | 352 | 9  | US-09-502-783A-2   | Sequence 2, Appli  |
| 37 | 94 | 100.0 | 352 | 10 | US-09-734-221A-14  | Sequence 14, Appli |
| 38 | 94 | 100.0 | 352 | 11 | US-09-826-509-477  | Sequence 477, App  |
| 39 | 94 | 100.0 | 352 | 13 | US-10-106-623-2    | Sequence 2, Appli  |
| 40 | 94 | 100.0 | 352 | 14 | US-10-232-686-2    | Sequence 2, Appli  |
| 41 | 94 | 100.0 | 352 | 14 | US-10-086-814-1    | Sequence 1, Appli  |
| 42 | 94 | 100.0 | 352 | 14 | US-10-067-800-2    | Sequence 2, Appli  |
| 43 | 94 | 100.0 | 352 | 14 | US-10-067-800-22   | Sequence 22, Appli |
| 44 | 94 | 100.0 | 352 | 14 | US-10-290-058A-6   | Sequence 6, Appli  |
| 45 | 94 | 100.0 | 352 | 14 | US-10-225-567A-352 | Sequence 352, App  |
| 46 | 94 | 100.0 | 352 | 14 | US-10-323-314-1    | Sequence 1, Appli  |
| 47 | 94 | 100.0 | 352 | 14 | US-10-072-301-1    | Sequence 1, Appli  |
| 48 | 94 | 100.0 | 352 | 14 | US-10-164-649-52   | Sequence 52, Appli |
| 49 | 94 | 100.0 | 352 | 14 | US-10-071-866-1    | Sequence 1, Appli  |
| 50 | 94 | 100.0 | 352 | 14 | US-10-135-839-2    | Sequence 2, Appli  |
| 51 | 94 | 100.0 | 352 | 14 | US-10-135-839-22   | Sequence 22, Appli |
| 52 | 94 | 100.0 | 352 | 14 | US-10-239-423-67   | Sequence 67, Appli |
| 53 | 94 | 100.0 | 352 | 14 | US-10-439-845-2    | Sequence 2, Appli  |
| 54 | 94 | 100.0 | 352 | 14 | US-10-439-845-4    | Sequence 4, Appli  |
| 55 | 94 | 100.0 | 352 | 15 | US-10-360-828-1    | Sequence 1, Appli  |
| 56 | 94 | 100.0 | 360 | 9  | US-09-131-827A-2   | Sequence 2, Appli  |
| 57 | 94 | 100.0 | 360 | 9  | US-09-131-827A-20  | Sequence 20, Appli |
| 58 | 94 | 100.0 | 360 | 9  | US-09-938-719-7    | Sequence 7, Appli  |
| 59 | 94 | 100.0 | 360 | 9  | US-09-939-226-7    | Sequence 7, Appli  |
| 60 | 94 | 100.0 | 360 | 9  | US-09-938-703-7    | Sequence 7, Appli  |
| 61 | 94 | 100.0 | 360 | 11 | US-09-826-509-473  | Sequence 473, App  |
| 62 | 94 | 100.0 | 360 | 14 | US-10-225-567A-460 | Sequence 460, App  |
| 63 | 94 | 100.0 | 360 | 14 | US-10-164-649-50   | Sequence 50, Appli |
| 64 | 94 | 100.0 | 360 | 14 | US-10-164-649-51   | Sequence 51, Appli |
| 65 | 94 | 100.0 | 360 | 14 | US-10-239-423-64   | Sequence 64, Appli |
| 66 | 94 | 100.0 | 360 | 14 | US-10-439-845-8    | Sequence 8, Appli  |
| 67 | 94 | 100.0 | 374 | 14 | US-10-239-423-63   | Sequence 63, Appli |
| 68 | 90 | 95.7  | 352 | 13 | US-10-106-623-20   | Sequence 20, Appli |
| 69 | 77 | 81.9  | 279 | 15 | US-10-174-364-58   | Sequence 58, Appli |
| 70 | 77 | 81.9  | 355 | 9  | US-09-961-068-1    | Sequence 1, Appli  |
| 71 | 77 | 81.9  | 355 | 9  | US-09-960-547-1    | Sequence 1, Appli  |
| 72 | 77 | 81.9  | 355 | 9  | US-09-938-719-9    | Sequence 9, Appli  |
| 73 | 77 | 81.9  | 355 | 9  | US-09-939-226-9    | Sequence 9, Appli  |
| 74 | 77 | 81.9  | 355 | 9  | US-09-938-703-9    | Sequence 9, Appli  |
| 75 | 77 | 81.9  | 355 | 14 | US-10-225-567A-62  | Sequence 62, Appli |
| 76 | 77 | 81.9  | 355 | 14 | US-10-245-850-2    | Sequence 2, Appli  |
| 77 | 77 | 81.9  | 355 | 14 | US-10-164-649-53   | Sequence 53, Appli |
| 78 | 77 | 81.9  | 355 | 14 | US-10-376-564-13   | Sequence 13, Appli |
| 79 | 77 | 81.9  | 355 | 14 | US-10-376-564-14   | Sequence 14, Appli |
| 80 | 77 | 81.9  | 355 | 14 | US-10-239-423-62   | Sequence 62, Appli |
| 81 | 77 | 81.9  | 355 | 14 | US-10-439-845-9    | Sequence 9, Appli  |
| 82 | 77 | 81.9  | 355 | 15 | US-10-452-015-2    | Sequence 2, Appli  |
| 83 | 77 | 81.9  | 375 | 14 | US-10-219-834-78   | Sequence 78, Appli |
| 84 | 75 | 79.8  | 360 | 9  | US-09-837-446-2    | Sequence 2, Appli  |
| 85 | 75 | 79.8  | 360 | 9  | US-09-796-744-17   | Sequence 17, Appli |
| 86 | 75 | 79.8  | 360 | 9  | US-09-764-413-20   | Sequence 20, Appli |
| 87 | 75 | 79.8  | 360 | 13 | US-10-120-394-20   | Sequence 20, Appli |
| 88 | 75 | 79.8  | 360 | 14 | US-10-225-567A-66  | Sequence 66, Appli |

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; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-39

Query Match 100.0%; Score 94; DB 14; Length 18;
Best Local Similarity 100.0%; Pred. No. 9,4e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18
 |||||
Db 1 LPPLYSLVFIQFGVGNML 18
 |||||

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### RESULT 3

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/ GENERAL INFORMATION:
/ APPLICANT: Dean, Michael
/ APPLICANT: O'Brien, Stephen J.
/ APPLICANT: Smith, Michael
/ APPLICANT: Carrington, Mary
/ TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
/ TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
/ FILE REFERENCE: 14014.0333
/ CURRENT APPLICATION NUMBER: US/09/131,827A
/ CURRENT FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: 60/055,659
/ PRIOR FILING DATE: 1997-08-14
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 83
/ TYPE: PRN
/ ORGANISM: Homo sapiens
/ US-09-131-827A-13

Query Match 100.0%; Score 94; DB 9; Length 83;
Best local similarity 100.0%; Pred. No. 4.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ov 1 LPPYSLVFTFGFVGNNML 18

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Db 45 LPPLYSLVIFGFGVGNML 62

US-09-938-719-4  
; Sequence 4, Application US/09938719  
; Patent No. US20020106742A1

PARMENTIER, MARC  
 VASSART, GILBERT  
 LIBERT, FREDERICK  
 TITLE OF INVENTION: ACTIVE AND INACTIVE CO-CHEMOKINES RECEPTOR  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Knobbe, Martens, Olson & Bear  
 STREET: 620 Newport Center Drive 16th Floor  
 CITY: Newport Beach  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 92660  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/938,719  
 FILING DATE: 24-AUG-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 27-JULY-2000  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-938-719-4

Query Match 100.0%; Score 94; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18  
DB 33 LPPLYSLVFIQFGVGNML 50

RESULT 5  
US-09-939-226-4  
Sequence 4, Application US/09939226  
Patent No. US20020110805A1  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,226  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 2000-07-27  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-939-226-4

Query Match 100.0%; Score 94; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18  
DB 33 LPPLYSLVFIQFGVGNML 50

RESULT 6  
US-09-938-703-4  
Sequence 4, Application US/09938703  
Patent No. US20020110870A1  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/938,703  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 2000-07-27  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-938-703-4

Query Match 100.0%; Score 94; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18  
DB 33 LPPLYSLVFIQFGVGNML 50

RESULT 7  
US-09-938-719-6  
Sequence 6, Application US/09938719  
Patent No. US20020106742A1  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,226  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 2000-07-27  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 184 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-939-226-4

Query Match 100.0%; Score 94; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIQFGVGNML 18  
DB 33 LPPLYSLVFIQFGVGNML 50

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/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/938,719
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/626,939
/ FILING DATE: 27-JULY-2000
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6

Query Match 100.0%; Score 94; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18
Db 33 LPPLYSLVFIFGFVGNML 50

RESULT 8
US-09-939-226-6
/ Sequence 6, Application US/09939226
/ Patent No. US20020110805A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ PARMENTIER, MARC
/ VASSART, GILBERT
/ LIBERT, FREDERICK
/
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/939,226
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/626,939
/ FILING DATE: 2000-07-27
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-719-6

Query Match 100.0%; Score 94; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18
Db 33 LPPLYSLVFIFGFVGNML 50

RESULT 8
US-09-939-226-6
/ Sequence 6, Application US/09939226
/ Patent No. US20020110805A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ PARMENTIER, MARC
/ VASSART, GILBERT
/ LIBERT, FREDERICK
/
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/939,226
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/626,939
/ FILING DATE: 2000-07-27
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
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/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-226-6

Query Match 100.0%; Score 94; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18
Db 33 LPPLYSLVFIFGFVGNML 50

RESULT 9
US-09-938-703-6
/ Sequence 6, Application US/09938703
/ Patent No. US20020110870A1
/ GENERAL INFORMATION:
/ APPLICANT: SAMSON, MICHEL
/ PARMENTIER, MARC
/ VASSART, GILBERT
/ LIBERT, FREDERICK
/
/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
/
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/938,703
/ FILING DATE: 24-Aug-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/626,939
/ FILING DATE: 2000-07-27
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel E
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 215 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-938-703-6

Query Match 100.0%; Score 94; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18
Db 33 LPPLYSLVFIFGFVGNML 50

RESULT 10
US-09-725-285-9
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; Sequence 9, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-339-912A-9

Query Match 100.0%; Score 94; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
 |||||
DB 28 LPPLYSLVVFIFGVGNML 45

RESULT 11
US-09-195-662A-9
; Sequence 9, Application US/09195662A
; Patent No. US20020076745A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)
; FILE REFERENCE: 1488.1150002
; CURRENT APPLICATION NUMBER: US/09/195,662A
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-195-662A-9

Query Match 100.0%; Score 94; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
 |||||
DB 28 LPPLYSLVVFIFGVGNML 45

RESULT 12
US-09-339-912A-9
; Sequence 9, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
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; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-339-912A-9

Query Match 100.0%; Score 94; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
 |||||
DB 28 LPPLYSLVVFIFGVGNML 45

RESULT 13
US-09-502-783A-9
; Sequence 9, Application US/09502783A
; Patent No. US20020132269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-502-783A-9

Query Match 100.0%; Score 94; DB 9; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVVFIFGVGNML 18
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DB 28 LPPLYSLVVFIFGVGNML 45

RESULT 14
US-10-095-876A-2
; Sequence 2, Application US/10095876A
; Publication No. US20030148294A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Bandman, Olga
; APPLICANT: Coleman, Roger; Wilde, Craig G.
; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
; FILE REFERENCE: PF-0060-1 CON
; CURRENT APPLICATION NUMBER: US/10/095,876A
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 08/638,081
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

Query Match 100.0%; Score 94; DB 14; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYSLVFIQFVGNML 18
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Db 24 LPPYSLVFIQFVGNML 41

RESULT 15
US-09-779-879A-9
; Sequence 9, Application US/09779879A
; Patent No. US20020048786A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000A
; CURRENT APPLICATION NUMBER: US/09/779,879A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-879A-9

Query Match 100.0%; Score 94; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYSLVFIQFVGNML 18
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Db 28 LPPYSLVFIQFVGNML 45

RESULT 16
US-09-779-880A-9
; Sequence 9, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-9

Query Match 100.0%; Score 94; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYSLVFIQFVGNML 18
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Db 28 LPPYSLVFIQFVGNML 45

RESULT 17
US-10-232-686-9
; Sequence 9, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-232-686-9

Query Match 100.0%; Score 94; DB 14; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYSLVFIQFVGNML 18
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Db 28 LPPYSLVFIQFVGNML 45

RESULT 18
US-10-067-800-9
; Sequence 9, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.115000I
; CURRENT APPLICATION NUMBER: US/10/067,800
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-9
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; SEQ ID NO 9  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-800-9

Query Match 100.0%; Score 94; DB 14; Length 344;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18  
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Db 28 LPPLYSLVFIFGVGNML 45

RESULT 19  
US-10-135-839-9  
; Sequence 9, Application US/10135839  
; Publication No. US20030166024A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNR10  
; FILE REFERENCE: 1488.115000A  
; CURRENT APPLICATION NUMBER: US/10/135,839  
; PRIOR FILING DATE: 2002-05-01  
; PRIOR APPLICATION NUMBER: US/09/779,879A  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 344  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-135-839-9

Query Match 100.0%; Score 94; DB 14; Length 344;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 28 LPPLYSLVFIFGVGNML 45

RESULT 20  
US-09-104-792-3  
; Sequence 3, Application US/09104792  
; Patent No. US20020019026A1  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R.  
; APPLICANT: Yi, Li  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
; ADDRESSEE: STUART & OLSTEIN  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/104,792  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,244  
; FILING DATE: 05-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferraro, Gregory D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-445  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 347 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-104-792-3

Query Match 100.0%; Score 94; DB 9; Length 347;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGVGNML 18  
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Db 32 LPPLYSLVFIFGVGNML 49

RESULT 21  
US-10-176-078-3  
; Sequence 3, Application US/10176078  
; Publication No. US20030165901A1  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R.  
; Yi, Li  
; Ruben, Steven M.  
; Rosen, Craig A.  
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
; ADDRESSEE: STUART & OLSTEIN  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/176,078  
; FILING DATE: 21-Jun-2002  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferraro, Gregory D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-445  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 347 amino acids  
; TYPE: amino acid



;  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-176-078-3

Query Match 100.0%; Score 94; DB 14; Length 347;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYSLVFIFFGVGNML 18  
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Db 32 LPPYSLVFIFFGVGNML 49

RESULT 22  
US-09-725-285-2  
; Sequence 2, Application US/09725285  
; Patent No. US20010000241A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10  
; FILE REFERENCE: 1488.1150003  
; CURRENT APPLICATION NUMBER: US/09/725,285  
; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 09/339,912  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 09/195,662  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/466,343  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Artificial Sequence: Genomic  
; FEATURE:  
; OTHER INFORMATION: Deduced Amino Acid Sequence  
US-09-725-285-2

Query Match 100.0%; Score 94; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYSLVFIFFGVGNML 18  
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Db 33 LPPYSLVFIFFGVGNML 50

RESULT 23  
US-09-759-841-2  
; Sequence 2, Application US/09759841  
; Patent No. US20010039026A1  
; GENERAL INFORMATION:  
; APPLICANT: Rickett, Graham A  
; APPLICANT: Dobbs, Susan  
; APPLICANT: Perros, Manousos  
; TITLE OF INVENTION: Assay Method  
; FILE REFERENCE: PC10348APME  
; CURRENT APPLICATION NUMBER: US/09/759,841  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: GB 0000661.9  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000663.5  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000659.3  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2

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; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-759-841-2

Query Match 100.0%; Score 94; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYSLVFIFFGVGNML 18  
| | | | | | | | | | | | | | | | | |  
Db 33 LPPYSLVFIFFGVGNML 50

RESULT 24  
US-09-779-879A-2  
; Sequence 2, Application US/09779879A  
; Patent No. US20020048786A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10  
; FILE REFERENCE: 1488.115000A  
; CURRENT APPLICATION NUMBER: US/09/779,879A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-879A-2

Query Match 100.0%; Score 94; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPYSLVFIFFGVGNML 18  
| | | | | | | | | | | | | | | | | |  
Db 33 LPPYSLVFIFFGVGNML 50

RESULT 25  
US-09-779-879A-22  
; Sequence 22, Application US/09779879A  
; Patent No. US20020048786A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10  
; FILE REFERENCE: 1488.115000A  
; CURRENT APPLICATION NUMBER: US/09/779,879A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 352



US-09-813-653-17

Query Match 100.0%; Score 94; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 33 LPPLYSLVFIFGFVGNML 50

RESULT 30

US-09-796-202-1  
; Sequence 1, Application US/09796202  
; Patent NO. US2002006813A1  
; GENERAL INFORMATION:  
; APPLICANT: Dragic, Tatjana  
; APPLICANT: Olson, William  
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
; FILE REFERENCE: 2048/61010/JPW/SHS  
; CURRENT APPLICATION NUMBER: US/09/796,202  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: human  
US-09-796-202-1

Query Match 100.0%; Score 94; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2e-06;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LPPLYSLVFIFGFVGNML 18  
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Db 33 LPPLYSLVFIFGFVGNML 50

Search completed: March 4, 2004, 18:22:51  
Job time : 25.0612 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 52.3061 Seconds  
(without alignments)  
118.840 Million cell updates/sec

Title: US-10-084-813-12  
Perfect score: 126  
Sequence: 1 QWDFGNTMQLLTGLYFIFGFFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003as.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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| 6          | 126   | 100.0       | 268    | 7  | ADC10144    |
| 7          | 126   | 100.0       | 332    | 2  | AAW26766    |
| 8          | 126   | 100.0       | 352    | 2  | AAW27407    |
| 9          | 126   | 100.0       | 352    | 2  | AAW27123    |
| 10         | 126   | 100.0       | 352    | 2  | AAW27125    |
| 11         | 126   | 100.0       | 352    | 2  | AAW07602    |
| 12         | 126   | 100.0       | 352    | 2  | AAW23835    |
| 13         | 126   | 100.0       | 352    | 2  | AAW88232    |
| 14         | 126   | 100.0       | 352    | 3  | AAW80128    |
| 15         | 126   | 100.0       | 352    | 4  | AAW79089    |
| 16         | 126   | 100.0       | 352    | 4  | AAW07046    |
| 17         | 126   | 100.0       | 352    | 4  | AAW07048    |
| 18         | 126   | 100.0       | 352    | 4  | AAW80111    |
| 19         | 126   | 100.0       | 352    | 4  | AAW04321    |
| 20         | 126   | 100.0       | 352    | 4  | AAW07037    |
| 21         | 126   | 100.0       | 352    | 4  | AAW07039    |
| 22         | 126   | 100.0       | 352    | 4  | AAW46858    |
| 23         | 126   | 100.0       | 352    | 4  | AAW56342    |
| 24         | 126   | 100.0       | 352    | 4  | AAW83354    |
| 25         | 126   | 100.0       | 352    | 4  | AAW82948    |

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|----|-----|-------|-----|---|-----------|
| 26 | 126 | 100.0 | 352 | 5 | AAU97150  |
| 27 | 126 | 100.0 | 352 | 5 | AAU97152  |
| 28 | 126 | 100.0 | 352 | 5 | AAW52829  |
| 29 | 126 | 100.0 | 352 | 5 | AAW52828  |
| 30 | 126 | 100.0 | 352 | 5 | ABG70597  |
| 31 | 126 | 100.0 | 352 | 5 | ABG92883  |
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| 33 | 126 | 100.0 | 352 | 5 | AAE25808  |
| 34 | 126 | 100.0 | 352 | 5 | AAE25811  |
| 35 | 126 | 100.0 | 352 | 5 | ABE81054  |
| 36 | 126 | 100.0 | 352 | 5 | ABE808343 |
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| 38 | 126 | 100.0 | 352 | 6 | ABR58602  |
| 39 | 126 | 100.0 | 352 | 6 | AAO29514  |
| 40 | 126 | 100.0 | 352 | 6 | AAU61654  |
| 41 | 126 | 100.0 | 352 | 6 | ABP97728  |
| 42 | 126 | 100.0 | 352 | 6 | ABP81933  |
| 43 | 126 | 100.0 | 352 | 7 | ADC03341  |
| 44 | 126 | 100.0 | 352 | 7 | ADC03359  |
| 45 | 126 | 100.0 | 371 | 2 | AAW23834  |
| 46 | 126 | 100.0 | 439 | 2 | AAV41280  |
| 47 | 104 | 82.5  | 439 | 2 | AAE88931  |
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| 49 | 87  | 69.0  | 344 | 5 | ABG92881  |
| 50 | 87  | 69.0  | 344 | 6 | ABU61655  |
| 51 | 87  | 69.0  | 360 | 2 | AAW79166  |
| 52 | 87  | 69.0  | 360 | 2 | AAW35833  |
| 53 | 87  | 69.0  | 360 | 4 | AAW80108  |
| 54 | 87  | 69.0  | 360 | 4 | AAU07613  |
| 55 | 87  | 69.0  | 360 | 4 | AAU07614  |
| 56 | 87  | 69.0  | 360 | 4 | ABE56340  |
| 57 | 87  | 69.0  | 360 | 6 | ABP97725  |
| 58 | 87  | 69.0  | 360 | 6 | ABP81987  |
| 59 | 87  | 69.0  | 374 | 2 | AAW79165  |
| 60 | 87  | 69.0  | 374 | 4 | AAW80107  |
| 61 | 87  | 69.0  | 374 | 6 | AAU09083  |
| 62 | 87  | 69.0  | 374 | 7 | ADD44861  |
| 63 | 87  | 69.0  | 374 | 7 | ADD44865  |
| 64 | 84  | 66.7  | 354 | 7 | ADD44859  |
| 65 | 84  | 66.7  | 354 | 7 | ADD44863  |
| 66 | 83  | 65.9  | 18  | 4 | ABE88930  |
| 67 | 83  | 65.9  | 269 | 2 | AAW26429  |
| 68 | 83  | 65.9  | 269 | 4 | AAW68250  |
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| 70 | 82  | 65.1  | 355 | 2 | AAW49807  |
| 71 | 82  | 65.1  | 355 | 2 | AAW56689  |
| 72 | 82  | 65.1  | 355 | 2 | AAW97868  |
| 73 | 82  | 65.1  | 355 | 2 | AAW80115  |
| 74 | 82  | 65.1  | 355 | 4 | ABE56343  |
| 75 | 82  | 65.1  | 355 | 5 | AAU80223  |
| 76 | 82  | 65.1  | 355 | 5 | AAU80222  |
| 77 | 82  | 65.1  | 355 | 5 | AAU77932  |
| 78 | 82  | 65.1  | 355 | 5 | ABP97731  |
| 79 | 82  | 65.1  | 355 | 6 | ABP81794  |
| 80 | 82  | 65.1  | 358 | 5 | AAU77933  |
| 81 | 80  | 63.5  | 354 | 2 | AAW54037  |
| 82 | 76  | 60.3  | 18  | 4 | ABE88933  |
| 83 | 76  | 60.3  | 355 | 2 | AAW29179  |
| 84 | 76  | 60.3  | 355 | 7 | ADD45360  |
| 85 | 74  | 58.7  | 68  | 5 | AAO22921  |
| 86 | 74  | 58.7  | 329 | 4 | AAW46859  |
| 87 | 74  | 58.7  | 329 | 5 | ABE81055  |
| 88 | 74  | 58.7  | 356 | 5 | AAO22920  |
| 89 | 71  | 56.3  | 295 | 4 | AAW80106  |
| 90 | 71  | 56.3  | 355 | 2 | AAE52749  |
| 91 | 71  | 56.3  | 355 | 2 | AAW25751  |
| 92 | 71  | 56.3  | 355 | 2 | AAW26588  |
| 93 | 71  | 56.3  | 355 | 3 | AAE20571  |
| 94 | 71  | 56.3  | 355 | 6 | ABU09082  |
| 95 | 71  | 56.3  | 355 | 6 | ABP97724  |
| 96 | 71  | 56.3  | 355 | 6 | ABP81790  |
| 97 | 71  | 56.3  | 355 | 6 | ABJ03698  |
| 98 | 67  | 53.2  | 355 | 2 | AAW03376  |

99 67 53.2 355 2 AAW03377 CC-chemok  
100 67 53.2 355 2 AAW03378 CC-chemok

## ALIGNMENTS

## RESULT 1

AA888994  
ID AA888994 standard; peptide; 22 AA.

XX  
AC AA888994;

XX DT 23-MAY-2001 (first entry)

XX DE HIV gp120 protein binding peptide #87.

XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
XX KW replication; CCR5; CXCR4; CD4; STRL33.

XX OS Homo sapiens.

XX PN WO200116182-A2.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US023505.

XX PR 27-AUG-1999; 99US-0151270P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Saxinger C;

XX DR WPI; 2001-244398/25.

XX PT Novel polypeptides useful for treating HIV infection, have homology to  
PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
PT and binds to HIV gp120 under physiological conditions.

XX PS Claim 21; Page 38; 114pp; English.

XX CC The present invention describes a number of peptides which are able to  
CC bind to HIV glycoprotein 120 (gp120). These are similar to the human  
CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
CC useful in the treatment of HIV, as they prevent replication of the virus.  
CC The present sequence is an example of a peptide of the invention

XX SQ Sequence 22 AA;

Query Match 100.0%; Score 126; DB 4; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.2e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22

Db 1 QWDFGNTMCQLLTGLYFIFGFFS 22

## RESULT 2

AAW27406

ID AAW27406 standard; protein; 184 AA.

XX AC AAW27406;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor-5; CCR5;

XX KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;

XX KW predisposition; resistance; diagnosis; treatment; prevention;

XX KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;

KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;  
KW atherosclerosis; autoimmune disorder.

OS Homo sapiens.

XX WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

XX PR 01-MAR-1996; 96EP-00870021.

XX PR 06-AUG-1996; 96EP-00870102.

XX PA (EURO-) EUROSREEN SA.

XX FI Samson M, Parmentier M, Vassart G, Libert F;

XX WPI; 1997-479829/44.

XX DR N-PSDB; AAT90116.

XX PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful  
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune  
PT disease and viral infection.

XX PS Claim 1; Fig 1a; 94pp; English.

XX CC The present sequence is an inactive human CC (Cys-Cys) chemokine receptor  
CC '5 (CCRs), which is not a receptor of human immunodeficiency virus type 1  
CC or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat  
CC and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,  
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,  
CC viral infections, especially HIV-1 or HIV-2 infection, cancer,  
CC atherosclerosis and autoimmune disorders. Subjects that express the  
CC inactive receptor have a predisposition, or resistance to HIV-1 and/or  
CC HIV-2

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 126; DB 2; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.2e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22

Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

## RESULT 3

AAW27408

ID AAW27408 standard; protein; 215 AA.

XX AC AAW27408;

XX DT 14-APR-1998 (first entry)

XX DE Inactive human CCR5.

XX KW Inactive; human Cys-Cys chemokine receptor 5; CCR5;  
XX KW human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2;  
XX KW predisposition; resistance; diagnosis; treatment; prevention;  
XX KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;  
XX KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;  
XX KW atherosclerosis; autoimmune disorder.

OS Homo sapiens.

XX WO9732019-A2.

XX PD 04-SEP-1997.

XX PF 28-FEB-1997; 97WO-BE000023.

Fri Mar 5 14:59:12 2004

```

PR 01-MAR-1996; 96EP-00870021.
PR 06-AUG-1996; 96EP-00870102.
XX
XX (EURO-) EUROSCREEN SA.
XX
XX Samson M, Parmentier M, Vassart G, Libert F;
PI
XX WPI; 1997-479829/44.
XX N-PSDB; AAT90118.
XX
XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful
PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune
PT disease and viral infection.
XX
XX Claim 7; Fig id-e; 94pp; English.
XX
XX The present sequence is an inactive human CC (Cys-Cys) chemokine receptor
CC 5 (CCR5), which lacks the last 3 transmembrane regions and the regions
CC involved in G protein-coupling. CCR5 or its cDNA can be used to diagnose,
CC treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis,
CC glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis,
CC viral infections, especially human immunodeficiency virus type 1 or type
CC 2 (HIV-1 or HIV-2) infection, cancer, atherosclerosis and autoimmune
CC disorders. Subjects that express the inactive receptor have a
CC predisposition, or resistance to HIV-1 and/or HIV-2
XX
XX Sequence 215 AA;
SQ
Query Match 100.0%; Score 126; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 QWDFGNTMCQLLTGLYFIQFFS 22
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114
RESULT 4
AAW88238
ID AAW88238 standard; protein; 215 AA.
XX
XX AAW88238;
XX
XX 15-MAR-1999 (first entry)
XX
XX HIV-1 co-receptor CCR5 variant CCR5-delta32.
XX
XX HIV-1; CCR5; CCR5-delta32; co-receptor; infection; diagnosis; AIDS;
KW gene therapy; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 32..56
XX /note="transmembrane domain 1"
XX Domain 67..87
XX /note="transmembrane domain 2"
XX Domain 103..124
XX /note="transmembrane domain 3"
XX Domain 142..167
XX /note="transmembrane domain 4"
XX
XX W09854317-A1.
XX
XX 03-DEC-1998.
XX
XX 29-MAY-1998; 98WO-EP003437.
XX
XX 30-MAY-1997; 97US-0048057P.
XX
XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.
XX
XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;
PI
XX
XX WPI; 1999-059835/05.
XX N-PSDB; AAV84159.
XX
XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing
PT resistance of CCR5-expressing cells to HIV-1 infection.
XX
XX Disclosure; Page 38-39; 55pp; English.
XX
XX This is the amino acid sequence of a CCR5 variant protein, designated
CC CCR5-delta32, that includes the first 4 transmembrane domains of wild-
CC type CCR5 (see AAW88232), but lacks transmembrane domains 5-7. CCR5
CC serves as a co-receptor for infection by macrophage-tropic (M-tropic)
CC strains of HIV-1. Individuals homozygous for the CCR5-delta32 mutation
CC are resistant to HIV-1 infection, but heterozygous individuals are
CC susceptible. The invention additionally relates to the identification of
CC variant CCR5s303 (see AAW88231), which lacks transmembrane domains 3-7 of
CC CCR5. The detection of CCR5 variants may be used to identify individuals
CC at lower risk of infection relative to the general population who, if
CC infected, may exhibit slower progression to AIDS. Probes and primers (see
CC AAV84127-36) are provided for use in diagnostic methods for detecting the
CC presence of such variants. A method is provided for inhibiting HIV-1
CC infection of a cell expressing the CCR5 receptor. This involves
CC introducing a nucleic acid encoding a CCR5 variant into the cell, thereby
CC reducing the number of functional CCR5 molecules present on the cell
CC surface
XX
XX Sequence 215 AA;
SQ
Query Match 100.0%; Score 126; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 QWDFGNTMCQLLTGLYFIQFFS 22
Db 93 QWDFGNTMCQLLTGLYFIQFFS 114
RESULT 5
ADC10142
ID ADC10142 standard; protein; 268 AA.
XX
XX ADC10142;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human NOVX polypeptide SEQ ID NO: 162.
XX
XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;
KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;
KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;
KW inflammatory disorder; chromosome mapping; tissue typing;
KW predictive medicine.
XX
XX Homo sapiens.
XX
XX W02003000842-A2.
XX
XX 03-JAN-2003.
XX
XX 04-JUN-2002; 2002WO-US017443.
XX
XX 04-JUN-2001; 2001US-0295607P.
XX
XX 04-JUN-2001; 2001US-0295661P.
XX
XX 06-JUN-2001; 2001US-0296404P.
XX
XX 06-JUN-2001; 2001US-0296418P.
XX
XX 07-JUN-2001; 2001US-0296575P.
XX
XX 11-JUN-2001; 2001US-0297414P.
XX
XX 12-JUN-2001; 2001US-0295573P.
XX
XX 12-JUN-2001; 2001US-0297567P.
XX
XX 14-JUN-2001; 2001US-0298285P.
XX
XX 15-JUN-2001; 2001US-0298528P.
XX
XX 18-JUN-2001; 2001US-0299133P.

```

New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-

RESULTS  
ADCl0144  
ID ADCl0144 standard; protein; 268 AA.

PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
 PT or CNS diseases.

PS Claim 1; SEQ ID NO 164; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the  
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
 CC polypeptide comprising one or more conservative substitutions. The NOVX  
 CC polypeptide is useful for treating or preventing a pathology associated  
 CC with the polypeptide e.g. disorders associated with aberrant expression  
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
 CC endocrine, CNS and inflammatory disorders. They can also be used in  
 CC various detection and screening assays, chromosome mapping, tissue typing  
 CC and predictive medicine. This sequence corresponds to one of the  
 CC polypeptides of the invention.

XX Sequence 268 AA;

Query Match 100.0%; Score 126; DB 7; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNMTCQLLTGLYFIFGFFS 22  
 |||||  
 Db 93 QWDFGNMTCQLLTGLYFIFGFFS 114

RESULT 7

AAW26766  
 ID AAW26766 standard; protein; 332 AA.

AC AAW26766;

XX 21-MAY-1998 (first entry)

XX Human chemokine receptor MMLR-CCR.

XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;  
 KW monocyte; macrophage; chemotaxis; haematopoiesis; infection;  
 KW inflammation; proliferative disease; cardiovascular disease; tumour;  
 KW rheumatoid arthritis; alveolitis; atherosclerosis;  
 KW chronic granulomatous disease; asthma; myasthenia gravis; diabetes;  
 KW inflammatory bowel disease; toxic shock syndrome; septic shock;  
 KW Chediak-Higashi syndrome; therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers  
 XX Peptide 107..128

FT /note= "conserved peptide"

FT Misc-difference 121  
 FT /note= "a claimed polypeptide has isoleucine at residue  
 121"

XX WO9741225-A2.

XX 06-NOV-1997.

XX 25-APR-1997; 97WO-US006993.

XX 26-APR-1996; 96US-00638081.

XX (INCY) INCYTE PHARM INC.

XX Au-Young J, Bandman O, Coleman R, Wilde CG;

XX WPI; 1997-549729/50.

XX N-PSDB; AAT99542.

XX Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful  
 PT to study, diagnose and treat, e.g. infection, inflammation, solid tumour  
 PT and proliferative and cardiovascular disease.

PS Claim 8; Page 37-38; 59pp; English.

XX This protein comprises human MMLR-CCR, a novel C-C chemokine receptor  
 CC associated with monocyte/macrophage infiltration and chemotaxis and  
 CC haematopoiesis. The amino acid sequence was deduced from a cDNA clone  
 CC (see AAT99542) obtained from a cDNA library made from mononuclear cells  
 CC collected on day 2 of a mixed lymphocyte culture, i.e. cells associated  
 CC with inflammation and immunomodulation. Another novel chemokine receptor,  
 CC MPHG-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7  
 CC transmembrane spanning segments connected by a series of intracellular  
 CC and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study, is  
 CC diagnose and treat disease states in which normal leukocyte function via  
 CC perturbed by normal leukopoiesis or inappropriate activation, is  
 CC chemokine agonists or antagonists, such as infection, inflammation,  
 CC proliferative disease, tumorigenesis, autoimmune disease, abnormal cell  
 CC proliferation, solid tumours, cardiovascular disease, rheumatoid  
 CC arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,  
 CC asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic  
 CC shock syndrome, septic shock and Chediak-Higashi syndrome

XX Sequence 332 AA;

Query Match 100.0%; Score 126; DB 2; Length 332;

Best Local Similarity 100.0%; Pred. No. 2.4e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNMTCQLLTGLYFIFGFFS 22

|||||

Db 84 QWDFGNMTCQLLTGLYFIFGFFS 105

RESULT 8

AAW27407

ID AAW27407 standard; protein; 352 AA.

XX AAW27407;

XX 14-APR-1998 (first entry)

XX Human CCR5.

XX Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;  
 KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;  
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;  
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;  
 KW atherosclerosis; autoimmune disorder.

XX Homo sapiens.

XX WO9732019-A2.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-BE000023.

XX 01-MAR-1996; 96EP-00870021.

XX 06-AUG-1996; 96EP-00870102.

XX (EURO-) EUROSREEN SA.

XX Samson M, Parmentier M, Vassart G, Libert F;

XX WPI; 1997-479829/44.

XX N-PSDB; AAT90117.

XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful  
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune  
 PT disease and viral infection.

XX Claim 4; Fig 1b-c; 94pp; English.

XX The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),  
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but



CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,  
 CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)  
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency  
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to  
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid  
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and  
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,  
 CC atherosclerosis and autoimmune disorders  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22  
 |||||  
 Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 9  
 AAW27123  
 ID AAW27123 standard; protein; 352 AA.  
 XX  
 AC AAW27123;  
 XX  
 DT 14-DEC-1997 (first entry)  
 XX  
 DE Human chemokine receptor 88C.  
 XX  
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;  
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;  
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;  
 KW modulator; antibody; human.  
 XX  
 OS Homo sapiens.

| Key    | Location/Qualifiers          |
|--------|------------------------------|
| Domain | 1..32                        |
| Domain | /label= Extracellular_domain |
| Domain | 56..67                       |
| Domain | /label= Intracellular_domain |
| Domain | 89..112                      |
| Domain | /label= Extracellular_domain |
| Domain | 125..145                     |
| Domain | /label= Intracellular_domain |
| Domain | 166..191                     |
| Domain | /label= Extracellular_domain |
| Domain | 213..235                     |
| Domain | /label= Intracellular_domain |
| Domain | 259..280                     |
| Domain | /label= Extracellular_domain |
| Domain | 301..352                     |
| Domain | /label= Intracellular_domain |

WO9722698-A2.  
 26-JUN-1997.  
 20-DEC-1996; 96WO-US020759.  
 20-DEC-1995; 95US-00575967.  
 07-JUN-1996; 96US-00661393.  
 XX (ICOS-) ICOS CORP.  
 Gray PW, Schweickart VL, Raport CU;  
 WPI; 1997-341689/31.  
 N-PSDB; AAT85161.  
 New nucleic acid encoding chemokine receptors 88-2B and 88C - used to  
 modulate leukocyte trafficking, e.g. for treatment of inflammation,

PT tumours, viral infections, auto-immune diseases, etc.  
 XX  
 PS Claim 16; Page 47-48; 65pp; English.  
 XX  
 CC This polypeptide sequence comprises novel human chemokine receptor 88C, a  
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its  
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a  
 CC macrophage library. It shows 62% identity to CCR1. Chemokine receptor  
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors  
 CC and their polypeptide fragments can be produced in transformed host  
 CC cells. The receptors, peptides comprising one or more of the  
 CC extracellular or intracellular domains, and anti-receptor antibodies can  
 CC be used to modulate receptor activities, particularly ligand and G  
 CC protein binding, and are potentially useful in the treatment  
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral  
 CC infection, AIDS, inflammatory conditions, pathological immune response,  
 CC abnormal haematopoietic processes etc  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22  
 |||||  
 Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 10  
 AAW27125  
 ID AAW27125 standard; protein; 352 AA.  
 XX  
 AC AAW27125;  
 XX  
 DT 14-DEC-1997 (first entry)  
 XX  
 DE Macaque chemokine receptor 88C.  
 XX  
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;  
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;  
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;  
 KW modulator; antibody.

Macaca sp.  
 WO9722698-A2.  
 26-JUN-1997.  
 20-DEC-1996; 96WO-US020759.  
 20-DEC-1995; 95US-00575967.  
 07-JUN-1996; 96US-00661393.  
 XX (ICOS-) ICOS CORP.  
 Gray PW, Schweickart VL, Raport CU;  
 WPI; 1997-341689/31.  
 N-PSDB; AAT85163.  
 New nucleic acid encoding chemokine receptors 88-2B and 88C - used to  
 modulate leukocyte trafficking, e.g. for treatment of inflammation,  
 tumours, viral infections, auto-immune diseases, etc.

Claim 36; Page 57-58; 65pp; English.  
 This polypeptide sequence comprises macaque chemokine receptor 88C, a G  
 protein coupled receptor that is involved in leukocyte trafficking. Its  
 amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR  
 amplification. It shows 97% identity to human 88C (AAW27123). 88C  
 receptors and their polypeptide fragments can be produced in transformed

CC host cells. The receptors, peptides comprising one or more of the  
 CC extracellular or intracellular domains, and anti-receptor antibodies can  
 CC be used to modulate receptor activities, particularly ligand and G  
 CC protein binding, and are potentially useful in the treatment  
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral  
 CC infection, AIDS, inflammatory conditions, pathological immune response,  
 CC abnormal haematopoietic processes etc. A hybridoma that produces an  
 CC antibody that specifically binds to macaque 88C is claimed  
 XX  
 XX SQ Sequence 352 AA;  
 Query Match 100.0%; Score 126; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTWCQLLTGLYFIGFFS 22  
 DB 93 QWDFGNTWCQLLTGLYFIGFFS 114  
 RESULT 11  
 AAW07602  
 ID AAW07602 standard; protein; 352 AA.  
 AC AAW07602;  
 XX  
 XX 26-FEB-1997 (first entry)  
 DT Human G-protein chemokine receptor HDGNR10.  
 DE  
 XX  
 XX G-protein chemokine receptor; HDGNR10; signal transduction;  
 KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;  
 KW therapy.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX W09639437-A1.  
 PN  
 XX  
 XX 12-DEC-1996.  
 PD  
 XX  
 XX 06-JUN-1995; 95WO-US007173.  
 PF  
 XX  
 XX 06-JUN-1995; 95WO-US007173.  
 PR  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX  
 XX Li Y, Ruben SM;  
 PI  
 XX  
 XX WPI; 1997-043072/04.  
 DR  
 XX  
 XX N-PSDB; AAT44042.  
 DR  
 XX  
 XX Human G-protein chemokine receptor, HDGNR10 - useful to identify  
 PT (antagonists, for treatment of haematopoiesis, leukaemia, chronic and  
 PT acute inflammation, rheumatoid arthritis, etc.  
 PT  
 XX  
 XX Claim 1; Page 44-46; 61pp; English.  
 PS  
 XX  
 XX Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7  
 CC -transmembrane protein involved in signal transduction. Its amino acid  
 CC sequence was deduced from a cDNA clone (AAT44042) isolated from a human  
 CC monocyte library. Isolation of the cDNA allows prodn. of recombinant  
 CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant  
 CC receptor can be used to identify agonists or antagonists of the receptor;  
 CC such cpds. can be used to treat conditions related to the under- and over  
 CC -expression of G-protein chemokine receptors  
 CC  
 XX  
 XX SQ Sequence 352 AA;  
 Query Match 100.0%; Score 126; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTWCQLLTGLYFIGFFS 22

DB 93 QWDFGNTWCQLLTGLYFIGFFS 114  
 RESULT 12  
 AAW23835  
 ID AAW23835 standard; protein; 352 AA.  
 AC AAW23835;  
 XX  
 XX 08-JUN-1998 (first entry)  
 DT Human CC chemokine receptor 5 (CCR5).  
 DE  
 XX  
 XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;  
 KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.  
 KW  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Location/Qualifiers  
 FH Key  
 FT Domain  
 FT 29..55  
 FT /label= I  
 FT /note= "transmembrane domain"  
 FT 104..126  
 FT /label= III  
 FT /note= "transmembrane domain"  
 FT 109..120  
 FT /note= "extracellular loop-1 (Claim 19)"  
 FT 143..171  
 FT /label= IV  
 FT /note= "transmembrane domain"  
 FT 187..210  
 FT /note= "extracellular loop-2 (Claim 19)"  
 FT 194..219  
 FT /label= V  
 FT /note= "transmembrane domain"  
 FT 238..258  
 FT /label= VI  
 FT /note= "transmembrane domain"  
 FT 261..276  
 FT /note= "extracellular loop-3 (Claim 19)"  
 FT 277..300  
 FT /label= VII  
 FT /note= "transmembrane domain"  
 FT  
 XX  
 XX W09745543-A2.  
 PN  
 XX  
 XX 04-DEC-1997.  
 PD  
 XX  
 XX 28-MAY-1997; 97WO-US009586.  
 PF  
 XX  
 XX 28-MAY-1996; 96US-0018508P.  
 PR  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX  
 XX Combadiere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;  
 PI Broder CC, Kennedy PE;  
 PI  
 XX  
 XX WPI; 1998-032650/03.  
 DR N-PSDB; AAT76920.  
 DR  
 XX  
 XX CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion  
 PT between HIV and a target cell.  
 PT  
 XX  
 XX Claim 68; Fig 1C; 70pp; English.  
 PS  
 XX  
 XX This protein sequence comprises of a novel human macrophage-selective CC  
 CC chemokine receptor that has been designated CCR5. The sequence was  
 CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant  
 CC (see W238340 of CCR5 was also identified. The susceptibility of human  
 CC macrophages to HIV infection depends on cell surface expression of CD4  
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-  
 CC protein coupled cell surface molecules. It plays an essential role in the

CC membrane fusion step of infection by some HIV isolates. The establishment  
 CC of stable, non-human cell lines and transgenic mammals having cells that  
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV  
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding  
 CC agents capable of blocking membrane fusion between HIV and target cells  
 CC represent potential anti-HIV therapeutics for macrophage tropic strains  
 CC of HIV

XX Sequence 352 AA;

SQ Query Match 100.0%; Score 126; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFS 22  
 DB 93 QWDFGNTMCLLTGLYFIFGFS 114

RESULT 13  
 AAW88232  
 ID AAW88232 standard; protein; 352 AA.

XX AC AAW88232;

XX DT 15-MAR-1999 (first entry)

XX DE HIV-1 co-receptor CCR5.

XX KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;  
 XX gene therapy; human.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

FT Domain 32..56 /note= "transmembrane domain 1"

FT Domain 67..87 /note= "transmembrane domain 2"

FT Domain 101 /note= "transmembrane domain 3"

FT FT Misc-difference 101 /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA  
 (stop) in CCR5m303"

FT Domain 103..124

FT Domain 142..167 /note= "transmembrane domain 4"

FT Domain 200..223 /note= "transmembrane domain 5"

FT Domain 236..260 /note= "transmembrane domain 6"

FT Domain 275..301 /note= "transmembrane domain 7"

FT Domain 302..323 /note= "transmembrane domain 8"

FT Domain 324..345 /note= "transmembrane domain 9"

FT Domain 346..367 /note= "transmembrane domain 10"

FT Domain 368..389 /note= "transmembrane domain 11"

FT Domain 390..411 /note= "transmembrane domain 12"

FT Domain 412..433 /note= "transmembrane domain 13"

FT Domain 434..455 /note= "transmembrane domain 14"

FT Domain 456..477 /note= "transmembrane domain 15"

FT Domain 478..499 /note= "transmembrane domain 16"

FT Domain 500..521 /note= "transmembrane domain 17"

FT Domain 522..543 /note= "transmembrane domain 18"

FT Domain 544..565 /note= "transmembrane domain 19"

FT Domain 566..587 /note= "transmembrane domain 20"

FT Domain 590..611 /note= "transmembrane domain 21"

FT Domain 612..633 /note= "transmembrane domain 22"

FT Domain 634..655 /note= "transmembrane domain 23"

FT Domain 656..677 /note= "transmembrane domain 24"

FT Domain 678..699 /note= "transmembrane domain 25"

FT Domain 699..720 /note= "transmembrane domain 26"

FT Domain 721..742 /note= "transmembrane domain 27"

FT Domain 743..764 /note= "transmembrane domain 28"

FT Domain 765..786 /note= "transmembrane domain 29"

FT Domain 787..808 /note= "transmembrane domain 30"

FT Domain 809..830 /note= "transmembrane domain 31"

FT Domain 831..852 /note= "transmembrane domain 32"

FT Domain 853..874 /note= "transmembrane domain 33"

FT Domain 875..896 /note= "transmembrane domain 34"

FT Domain 897..918 /note= "transmembrane domain 35"

FT Domain 919..940 /note= "transmembrane domain 36"

CC This is the amino acid sequence of wild-type human CCR5, which serves as  
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of  
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see  
 CC AAW88231), designated CCR5m303, comprising the first two transmembrane  
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The  
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a  
 CC positive correlation with resistance to infection with M-tropic HIV-1  
 CC strains, and may indicate slower progression of the disease. The  
 CC detection of CCR5 variants may be used to identify individuals at lower  
 CC risk of infection relative to the general population who, if infected,  
 CC may exhibit slower progression to AIDS. Probes and primers (see AAW84127-  
 CC 36) are provided for use in diagnostic methods for detecting the presence  
 CC of such variants. A method is provided for inhibiting HIV-1 infection of  
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic  
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number  
 CC of functional CCR5 molecules present on the cell surface

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFS 22

DB 93 QWDFGNTMCLLTGLYFIFGFS 114

RESULT 14

AAW80128

ID AAY80128 standard; protein; 352 AA.

XX AC AAY80128;

XX DT 19-MAY-2000 (first entry)

XX DE Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.

XX KW Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;  
 XX diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;  
 XX tumour; infection; leukaemia; psoriasis; allergy;  
 XX T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;  
 XX inflammation; allergic reaction; silicosis; sarcoidosis;  
 XX rheumatoid arthritis; hyper-eosinophilia syndrome.

XX OS Homo sapiens.

XX PN US6025154-A.

XX PD 15-FEB-2000.

XX PF 06-JUN-1995; 95US-00466343.

XX PR 06-JUN-1995; 95US-00466343.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Li Y, Ruben SM;

XX DR WPI; 2000-181807/16.

XX DR N-PSDB; AAZ91481.

XX PT Isolated nucleic acid encoding human G-protein chemokine receptor useful  
 XX for diagnostic assays, scientific research and screening for compounds  
 XX which bind to and activate or inhibit activation of the receptor  
 XX polypeptides.

XX PS Claim 1; Fig 1; 22pp; English.

XX CC The present sequence represents a human G-protein chemokine receptor  
 XX designated HDGNR10. HDGNR10 polynucleotides are useful in methods of  
 XX screening for compounds which bind to and either: (1) activate the  
 XX HDGNR10 polypeptides causing stimulation of haematopoiesis, wound

CC healing, coagulation, and angiogenesis; treatment of solid tumours,  
 CC chronic infections, leukemia, T-cell mediated autoimmune diseases,  
 CC parasitic infections, psoriasis, and to stimulate growth factor activity;  
 CC or (2) inhibit activation of the HDGFR10 polypeptides which is useful for  
 CC preventing and/or treating allergy, atherogenesis, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin  
 CC E-mediated allergic reactions, prostaglandin-independent fever, bone  
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and  
 CC hyper-eosinophilia syndrome. The polynucleotides are also useful for  
 CC diagnostic assays for detecting diseases related to mutations in the  
 CC nucleic acid sequences encoding the polypeptides and for detecting an  
 CC altered level of the soluble form of the receptor polypeptides. The  
 CC polynucleotides are also useful for in vitro purposes related to  
 CC scientific research, synthesis of DNA and manufacture of DNA vectors  
 XX  
 XX Sequence 352 AA;  
 SQ

Query Match 100.0%; Score 126; DB 3; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
 DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 15  
 AAG79089  
 ID AAG79089 standard; protein; 352 AA.  
 XX  
 XX AAG79089;  
 AC  
 DT 10-DEC-2001 (first entry)  
 DE Amino acid sequence of human CCR5 protein.  
 XX  
 KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;  
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200164752-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US006322.  
 XX  
 PR 02-MAR-2000; 2000US-00517605.  
 XX  
 PA (UYNV ) UNIV NEW YORK STATE.  
 PA (UYNV-) UNIV NIJMEGEN.  
 XX  
 PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;  
 XX  
 DR WPI; 2001-602565/68.  
 XX  
 PT An antibody for the treatment or prevention of HIV-infection comprises a  
 PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of  
 PT DC-SIGN due to concomitant conformational change.  
 XX  
 PS Disclosure; Page 118-119; 131pp; English.  
 XX  
 CC The specification describes an antibody which is specific for an  
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or  
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant  
 CC conformational change. DC-SIGN is a receptor that is specifically  
 CC expressed on dendritic cells and facilitates infection of T lymphocytes  
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC  
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)  
 CC with high affinity. The antibody of the invention inhibits the trans  
 CC enhancement of HIV entry into a T cell or macrophage facilitated by  
 CC dendritic cells. The antibody is useful to treat or prevent HIV  
 CC infection. The present sequence represents a human CCR5 protein, which is

CC a translocation promoting agent that interacts with CD4. This receptor  
 CC functions in HIV-1 entry into cells  
 XX  
 XX Sequence 352 AA;  
 SQ

Query Match 100.0%; Score 126; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
 DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 16  
 AAE07046  
 ID AAE07046 standard; protein; 352 AA.  
 XX  
 XX AAE07046;  
 AC  
 DT 16-OCT-2001 (first entry)  
 DE Human G-protein chemokine receptor (CCR5) HDGFR10 protein #1.  
 XX  
 KW Human; G-protein chemokine receptor; CCR5; HDGFR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;  
 KW cytosatic; immunosuppressive; neutrotropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.  
 XX  
 OS Homo sapiens.  
 XX

Key Location/Qualifiers  
 Domain 1..36  
 /label= Extracellular\_domain  
 Domain 37..305  
 /label= Transmembrane\_domain  
 Domain 37..58  
 /label= Transmembrane\_domain  
 /note= "Segment 1"  
 Domain 59..67  
 /label= Intracellular\_loop\_1  
 Domain 68..88  
 /label= Transmembrane\_domain  
 /note= "Segment 2"  
 Domain 89..102  
 /label= Extracellular\_loop\_1  
 Domain 103..124  
 /label= Transmembrane\_domain  
 /note= "Segment 3"  
 Domain 125..141  
 /label= Intracellular\_loop\_2  
 Domain 142..166  
 /label= Transmembrane\_domain  
 /note= "Segment 4"  
 Domain 167..195  
 /label= Extracellular\_loop\_2  
 Domain 196..223  
 /label= Transmembrane\_domain  
 /note= "Segment 5"  
 Domain 224..235  
 /label= Intracellular\_loop\_3  
 Domain 236..260  
 /label= Transmembrane\_domain  
 /note= "Segment 6"  
 Domain 261..274  
 /label= Extracellular\_loop\_3  
 Domain 287..305  
 /label= Transmembrane\_domain  
 FT

```

FT /note= "Segment 7"
FT 306, 352
FT /label= Intracellular_domain
XX
PN WO200158916-A2.
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004153.
XX
PR 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
PI WPI; 2001-488966/53.
DR N-PSDB; AAD13282.
XX
PT Isolated nucleic acid encoding a human G-protein chemokine receptor
PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
PT neurodegenerative disorders.
XX
PS Claim 102; Fig 1; 518pp; English.
XX
CC The invention relates to human G-protein chemokine receptor (CCR5)
CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
CC useful for treating, preventing or ameliorating a disease or disorder
CC associated with inflammation, defective or aberrant chemotaxis of immune
CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
CC sarcoma) or defective or aberrant T-cell antigen presenting cell
CC interaction. The disease or disorder may also be an infectious disease
CC (e.g. a viral infection such as an early stage HIV infection, a
CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
CC disease or disorder may be associated with aberrant CCR5 expression, lack
CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
CC protein, antibodies, agonists and antagonists are also useful in the
CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
CC present sequence is human CCR5 HDGNR10 protein
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLTGLYFTGFPS 22
DB 93 QWDFGNTMCQLTGLYFTGFPS 114

RESULT 17
AAE07048
ID AAE07048 standard; protein; 352 AA.
AC
XX AAE07048;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.
XX

```

```

KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;
KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerrary;
KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;
KW cardiovascular disorder; myocardial ischaemia.
XX
OS Homo sapiens.
XX
WO200158916-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004153.
XX
PR 09-FEB-2000; 2000US-0181258P.
PR 09-MAR-2000; 2000US-0187999P.
PR 22-SEP-2000; 2000US-0234336P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Roschke V, Li Y, Ruben SM;
XX
PI WPI; 2001-488966/53.
DR N-PSDB; AAD13299.
XX
PT Isolated nucleic acid encoding a human G-protein chemokine receptor
PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune
PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and
PT neurodegenerative disorders.
XX
PS Example 40; Page 504-505; 518pp; English.
XX
CC The invention relates to human G-protein chemokine receptor (CCR5)
CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are
CC useful for treating, preventing or ameliorating a disease or disorder
CC associated with inflammation, defective or aberrant chemotaxis of immune
CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's
CC sarcoma) or defective or aberrant T-cell antigen presenting cell
CC interaction. The disease or disorder may also be an infectious disease
CC (e.g. a viral infection such as an early stage HIV infection, a
CC cytomegalovirus infection, or a poxvirus infection), an autoimmune
CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The
CC disease or disorder may be associated with aberrant CCR5 expression, lack
CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand
CC function. CCR5 HDGNR10 protein is used as a food additive or preservative
CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful
CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,
CC protein, antibodies, agonists and antagonists are also useful in the
CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal
CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,
CC urogenital); immune disorders (Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)
CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The
CC present sequence is human CCR5 HDGNR10 protein
XX
SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLTGLYFTGFPS 22
DB 93 QWDFGNTMCQLTGLYFTGFPS 114

RESULT 18
AAG80111

```

ID AAG80111 standard; protein; 352 AA.  
 AC AAG80111;  
 XX  
 DT 17-JAN-2002 (first entry)  
 XX  
 DE Human CCR5 protein.  
 XX  
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
 KW chronic bowel inflammation; rheumatoid arthritis; cystostatic;  
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
 KW antirheumatic; antiarthritic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200172830-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 02-APR-2001; 2001WO-EP003708.  
 XX  
 PR 31-MAR-2000; 2000DE-01016013.  
 XX  
 PA (IPFP-) IPF PHARM GMBH.  
 PA (FORS/) FORSMANN U.  
 XX  
 PI Forssmann W, Adermann K, Heitland A, Spodsberg N;  
 XX  
 DR WPI; 2001-626256/72.  
 XX  
 PT Diagnostic agent containing two or more receptor-specific ligands, useful  
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand  
 PT inhibitors.  
 XX  
 PS Disclosure; Page 10; 26pp; German.  
 XX  
 CC This invention describes a novel diagnostic agent (A) comprising at least  
 CC two different ligands (I) for receptors (II) that are implicated in  
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal  
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.  
 CC Also inhibitors of (I) are used therapeutically against tumors (and their  
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel  
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
 CC endocrine, motor or urogenital systems or skin are affected, and bone  
 CC marrow diseases. The products of the invention are chemokine derivatives  
 CC which have cystostatic, antinflammatory, antiasthmatic,  
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.  
 CC Chemokines act on specific tumor and inflammatory cells through a  
 CC constellation of chemokine receptors (CR), which control migration and  
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
 CC fragments used to illustrate the method of the invention  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 126; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTWCQLLGLYFIFGFS 22  
 DB 93 QWDFGNTWCQLLGLYFIFGFS 114  
 RESULT 19  
 ID AAE04321 standard; protein; 352 AA.  
 AC AAE04321;  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.  
 XX  
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnary;  
 KW cytostatic; immunosuppressive; neurotropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 XX

DE Human chemokine receptor (CCR), CC-CCR-5 related protein #2.  
 XX  
 KW Human; transformed mammalian cell; CD4; reporter gene; translocation;  
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;  
 KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;  
 KW CC-CCR-5; envelope glycoprotein; anti-HIV.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6258527-B1.  
 XX  
 PD 10-JUL-2001.  
 XX  
 PF 21-MAY-1997; 97US-00861105.  
 XX  
 PR 20-MAY-1996; 96US-0017157P.  
 PR 19-JUN-1996; 96US-0020043P.  
 PR 19-MAY-1997; 97US-00858660.  
 XX  
 PA (AARO-) AARON DIAMOND AIDS RES CENT.  
 PA (UTNY ) UNIV NEW YORK STATE.  
 XX  
 PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;  
 XX  
 DR WPI; 2001-417127/44.  
 DR N-PSDB; AAD08577.  
 XX  
 PT Transformed mammalian cell (I) that contains a CD4 gene, reporter gene  
 PT and HIV LTR for identification of drugs and antibodies for treatment of  
 PT HIV.  
 XX  
 PS Disclosure; Col 47-50; 37pp; English.  
 XX  
 CC The present invention relates to a transformed mammalian cell that  
 CC contains a gene encoding CD4, a construct encoding a reporter gene under  
 CC the regulation of an human immuno deficiency virus (HIV) long terminal  
 CC repeat (LTR) and that has been transduced with a vector encoding a human  
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the  
 CC cell surface of transformed mammalian cell. The invention is useful for  
 CC identifying drugs or antibodies that interfere with the translocation of  
 CC HIV into transformed mammalian cell or for identifying a human chemokine  
 CC receptor that facilitates the infection of a particular HIV strain into  
 CC the transformed mammalian cell. Compounds identified can be used to treat  
 CC cellular dysfunction and to prevent or combat HIV infection. The present  
 CC sequence is a human chemokine receptor (CCR). CC-CCR-5 related protein.  
 CC CC-CCR-5 is the principal cofactor for entry mediated by the envelope  
 CC glycoproteins of primary macrophage-tropic strains of HIV-1  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 126; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTWCQLLGLYFIFGFS 22  
 DB 93 QWDFGNTWCQLLGLYFIFGFS 114  
 RESULT 20  
 ID AAE07037 standard; protein; 352 AA.  
 XX  
 AC AAE07037;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.  
 XX  
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnary;  
 KW cytostatic; immunosuppressive; neurotropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 XX

XW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.  
 XX

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH 1..36  
 FT Domain /label= Extracellular\_domain  
 FT 37..305  
 FT Domain /label= Transmembrane\_domain  
 FT 37..58  
 FT Domain /label= Transmembrane\_domain  
 FT 59..67  
 FT Domain /note= "Segment 1"  
 FT 68..88  
 FT Domain /label= Intracellular\_loop\_1  
 FT 89..102  
 FT Domain /label= Transmembrane\_domain  
 FT 103..124  
 FT Domain /label= Extracellular\_loop\_1  
 FT 125..141  
 FT Domain /label= Transmembrane\_domain  
 FT 142..166  
 FT Domain /label= Intracellular\_loop\_2  
 FT 167..195  
 FT Domain /label= Transmembrane\_domain  
 FT 196..223  
 FT Domain /label= Extracellular\_loop\_2  
 FT 224..235  
 FT Domain /label= Transmembrane\_domain  
 FT 236..260  
 FT Domain /label= Intracellular\_loop\_3  
 FT 261..274  
 FT Domain /label= Transmembrane\_domain  
 FT 287..305  
 FT Domain /label= Extracellular\_loop\_3  
 FT 306..352  
 FT Domain /label= Transmembrane\_domain  
 FT /label= Intracellular\_domain  
 XX

PN WO200158915-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004152.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488965/53.

XX N-PSDB; AAD13181.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor  
 (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 neurodegenerative disorders.

XX Claim 102; Fig 1; 495pp; English.

CC The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10  
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5  
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a  
 CC disease or disorder associated with inflammation, defective or aberrant  
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii  
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen  
 CC presenting cell interaction. The disease or disorder may also be an  
 CC infectious disease (e.g. a viral infection such as an early stage HIV  
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an  
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative  
 CC disorder. The disease or disorder may be associated with aberrant CCR5  
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or  
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food  
 CC additive or preservative to increase or decrease storage capabilities.  
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene  
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists  
 CC are also useful in the diagnosis, treatment and prevention of cancer  
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,  
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,  
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis); cardiovascular disorders (myocardial ischaemia) and wound  
 CC healing  
 XX

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYTFIGFFS 22

DB 93 QWDFGNTMCQLLTGLYTFIGFFS 114

RESULT 21

AAE07039

ID AAE07039 standard; protein; 352 AA.

XX AC AAE07039;

XX DT 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;

XX human immunodeficiency virus; antimicrobial; vasodilator; vulnery;

XX cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;

XX rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;

XX gastrointestinal tract; lung; liver; immune disorder; Addison's disease;

XX haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;

XX multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;

XX cardiovascular disorder; myocardial ischaemia.

XX OS Homo sapiens.

XX WO200158915-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004152.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488965/53.

XX N-PSDB; AAD13196.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor  
PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
XX neurodegenerative disorders.

XX Example 40; Page 486-487; 495pp; English.

XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10  
CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or  
CC ameliorating a disease or disorder associated with inflammation.  
CC defective or aberrant chemotaxis of immune cells, HIV infection (such as  
CC Pneumocystis carinii pneumonia or Kaposi's sarcoma), HIV infection (such as  
CC aberrant T-cell antigen presenting cell interaction. The disease or  
CC disorder may also be an infectious disease (e.g. a viral infection such  
CC as an early stage HIV infection, a cytomegalovirus infection, or a  
CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or  
CC a neurodegenerative disorder. The disease or disorder may be associated  
CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5  
CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein  
CC is used as a food additive or preservative to increase or decrease  
CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome  
CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,  
CC antibodies, agonists and antagonists are also useful in the diagnosis,  
CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,  
CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune  
CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,  
CC autoimmune rheumatoid arthritis, diabetes mellitus, Crohn's disease, multiple  
CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular  
CC disorders (myocardial ischaemias) and wound healing

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLGLYFIGFFS 22  
DB 93 QWDFGNTWCQLLGLYFIGFFS 114

RESULT 22  
TAB46858  
XX AAB46858 standard; protein; 352 AA.  
XX AAB46858;  
XX 16-AUG-2001 (revised)  
XX 02-AUG-2001 (revised)  
XX 04-MAY-2001 (first entry)  
XX Human HDGNR10 protein.  
XX HDGNR10; human; G-protein chemokine receptor; antiinflammatory;  
XX immunomodulatory; anticoagulant; antiallergic; immunosuppressive;  
XX cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;  
XX vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;  
XX angiogenesis; solid tumour; infection; leukemia; growth factor activity;  
XX T-cell mediated autoimmune disease; psoriasis; allergy; atherosclerosis;  
XX anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;  
XX immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;  
XX prostaglandin-independent fever; bone marrow failure; sarcoidosis;  
XX hyper-eosinophilic syndrome; vulnary.

XX Homo sapiens.  
XX OS  
XX US2001000241-A1.  
XX PN  
XX 12-APR-2001.  
XX PD  
XX 29-NOV-2000; 2000US-00725285.  
XX PF  
XX 29-NOV-2000; 2000US-00725285.  
XX PR

PR 06-JUN-1995; 95US-00466343.  
PR 18-NOV-1998; 98US-00195662.  
PR 25-JUN-1999; 99US-00339912.  
XX (LIYY/) LI Y.  
PA (RUBB/) RUBEN S M.  
XX Li Y, Ruben SM;  
XX WPI: 2001-226317/23.  
XX N-PSDB; AAF26390.  
XX New human G-protein chemokine receptor polypeptides and polynucleotides,  
PT useful for identifying (ant)agonists to the G-protein chemokine receptor.  
XX Claim 1a; Page 15; 22pp; English.  
XX This invention describes a novel receptor polypeptide (I) selected from  
CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the  
CC specification; and (ii) a polypeptide encoded by the cDNA contained in a  
CC plasmid, and fragments, analogs and derivatives of the polypeptide. The  
CC products of the invention have antiinflammatory, immunomodulatory,  
CC anticoagulant, antiallergic, immunosuppressive, vulnary, cytostatic,  
CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic  
CC activity and can be used for gene therapy. The G-protein chemokine  
CC receptors, HDGNR10, (I) are useful for screening for compounds which  
CC activate or inhibit activation of (I). The products of the invention can  
CC also be used for stimulating haematopoiesis, wound healing, coagulation,  
CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-  
CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and  
CC stimulating growth factor activity. HDGNR10 is useful for treating  
CC allergy, atherosclerosis, anaphylaxis, malignancy, chronic and acute  
CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic  
CC reactions, prostaglandin-independent fever, bone marrow failure,  
CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-  
CC eosinophilic syndrome. (N.B. This record was resubmitted to correct  
CC errors in the keyword formatting)

XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLGLYFIGFFS 22  
DB 93 QWDFGNTWCQLLGLYFIGFFS 114

RESULT 23  
ABB56342  
XX ABB56342 standard; protein; 352 AA.  
XX ABB56342;  
XX 18-FEB-2002 (first entry)  
XX Non-endogenous human GPCR protein, SEQ ID NO: 477.  
XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;  
XX constitutively activated GPCR; agonist; disease.  
XX Homo sapiens.  
XX OS  
XX WO20017172-A2.  
XX PN  
XX 18-OCT-2001.  
XX PD  
XX 05-APR-2001; 2001WO-US011098.  
XX PF  
XX 07-APR-2000; 2000US-0195747P.  
XX PR



PA (AREN-) ARENA PHARM INC.  
 XX Lehmann-Bruinsma K, Liaw CW, Lin I;  
 XX WPI: 2001-648759/74.  
 DR N-PSDB; ARI97978.  
 XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in  
 PT disease treatment, comprises contacting candidate compounds with versions  
 of GPCRs.  
 XX Claim 1; Page 277-278; 394pp; English.  
 XX The invention relates to G protein-coupled receptors (GPCRs) for which  
 CC the endogenous ligand has been identified. Non-endogenous constitutively  
 CC activated versions of known GPCRs are used in the invention for the  
 CC direct identification of candidate compounds as receptor agonists,  
 CC inverse agonists or partial agonists. Such agonists are useful as  
 CC therapeutic agents for diseases or disorders associated with GPCRs. The  
 CC present sequence is a non-endogenous version of a known human GPCR  
 XX  
 XX Sequence 352 AA;  
 Query Match 100.0%; Score 126; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. NO. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTMQLLTGLYFIFGFFS 22  
 DB 93 QWDFGNTMQLLTGLYFIFGFFS 114  
 RESULT 24  
 AAB83354  
 ID AAB83354 standard; protein; 352 AA.  
 AC AAB83354;  
 XX 09-OCT-2001 (first entry)  
 DT Human CCR5 protein sequence.  
 DE Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;  
 KW human immunodeficiency virus; anti-inflammatory disease; human.  
 XX Homo sapiens.  
 OS EP1118858-A2.  
 PN 25-JUL-2001.  
 PD 03-JAN-2001; 2001EP-00300020.  
 XX 12-JAN-2000; 2000GB-00000659.  
 PR 12-JAN-2000; 2000GB-00000661.  
 PR 12-JAN-2000; 2000GB-00000663.  
 XX (PFIZ ) PFIZER LTD.  
 PA (PFIZ ) PFIZER INC.  
 XX Dobbs S, Perros M, Rickett GA;  
 XX WPI: 2001-477088/52.  
 DR N-PSDB; AAF87099.  
 XX Determining if an agent can modulate CCR5-gp120 interaction, comprises  
 PT incubating the agent with CCR5 and gp120 and determining if the agent  
 PT modulates the interaction.  
 XX Claim 1; Page 110; 113pp; English.  
 PS This sequence represents the human CCR5 protein sequence. The invention  
 CC relates to a method for determining whether an agent is capable of

CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)  
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and  
 CC determining whether the agent modulates the interaction, where gp120 is  
 CC associated with CD4, and where the interaction is a low affinity binding.  
 CC The method is used to identify an agent capable of modulating the  
 CC interaction of CCR5 with gp120. An agent identified by the method is used  
 CC to prepare a pharmaceutical composition for the treatment of a disease or  
 CC condition associated with CCR5 and gp120 interaction, to treat a subject  
 CC with a disease or condition associated with CCR5 and gp120 interaction,  
 CC and for preparing a pharmaceutical for treating human immunodeficiency  
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method  
 CC is commercially useful, amenable to high throughput screening, and  
 CC detects interaction of gp120 with cells expressing only CCR5.  
 XX Sequence 352 AA;  
 Query Match 100.0%; Score 126; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. NO. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTMQLLTGLYFIFGFFS 22  
 DB 93 QWDFGNTMQLLTGLYFIFGFFS 114  
 RESULT 25  
 AAB82948  
 ID AAB82948 standard; protein; 352 AA.  
 XX AAB82948;  
 AC AAB82948;  
 XX 21-DEC-2001 (first entry)  
 DT Human HIV-1 co-receptor CCR5.  
 DE CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;  
 KW infection; therapy; vaccine; anti-HIV-1.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 FH Binding-site 2..18 /note= "binds to HIV-1 gp120"  
 FT WO200164710-A2.  
 XX 07-SEP-2001.  
 PD 28-FEB-2001; 2001WO-US006699.  
 PF 29-FEB-2000; 2000US-0185667P.  
 PR 19-MAY-2000; 2000US-0205839P.  
 PR 07-FEB-2001; 2001US-0267231P.  
 XX (PROG-) PROGENICS PHARM INC.  
 PA (AARO-) AARON DIAMOND AIDS RES CENT.  
 XX Dragic T, Olson WC;  
 XX WPI: 2001-611273/70.  
 DR N-PSDB; AAR26903.  
 XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-  
 PT receptor) amino terminal domain including negatively charged and two  
 PT sulfated tyrosine residues is useful for treating HIV infection in  
 PT humans.  
 XX Claim 1; Page 30; 163pp; English.  
 PS The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids  
 XX 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding  
 CC site that determines the specificity of the interaction between CCR5 and  
 CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the

CC CCR5 N-terminus is required for gp120 binding and may critically modulate  
 CC the susceptibility of target cells to HIV-1 infection in vivo. The  
 CC invention provides claimed sulfated peptides (see AB82947) that are  
 CC based on the CCR5 N-terminal region and which are effective for  
 CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed  
 CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+  
 CC cells from becoming infected with HIV, of treating a subject whose CD4+  
 CC cells are infected with HIV, and of identifying an agent which inhibits  
 CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried  
 CC out in a subject, especially a human, infected (therapeutic method), not  
 CC infected with HIV (prophylactic method), or in a subject who is not  
 CC infected with, but has been exposed to, HIV  
 XX  
 XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22  
 |||||  
 Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

## RESULT 26

AAU97150  
 ID AAU97150 standard; protein; 352 AA.

AC AAU97150;

DT 13-AUG-2002 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;  
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;  
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;  
 KW hyperproliferative disease; neurological disease; receptor.

XX Homo sapiens.

OS US2002048786-A1.

PN 25-APR-2002.

PD 09-FEB-2001; 2001US-00779879.

PF 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

XX (ROSE/) ROSEN C A.

PA (ROSC/) ROSCHKE V.

PA (LIY/) LI Y.

PA (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

PI WPI; 2002-434754/46.

XX N-PSDB; ABK51853.

DR New nucleic acid encoding an antibody specific for the G-protein  
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.  
 PT inflammation.

XX Claim 61; Fig 1; 180pp; English.

XX The present invention relates to the isolation of a novel human G-protein  
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide  
 CC sequences encoding it. The invention also describes antibodies that bind  
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide  
 CC sequences encoding the antibodies. The antibodies are useful for treating  
 CC or preventing inflammation, defective or aberrant chemotaxis of immune

CC cells and T-cell/antigen-presenting cell interactions, infections and  
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral  
 CC infections (especially early-stage human immune deficiency virus (HIV),  
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions  
 CC associated with aberrant or deficient expression of the CCR5 receptor or  
 CC its ligands. The antibodies are also useful to determine CCR5 expression,  
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other  
 CC hyperproliferative diseases. The polynucleotide sequences encoding human  
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the  
 CC recombinant receptor, and in the treatment of a wide range of diseases  
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.  
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The  
 CC present sequence represents human G-protein chemokine receptor (CCR5)  
 CC HDGNR10 #1  
 XX  
 XX Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22  
 |||||  
 Db 93 QWDFGNTMCQLLTGLYFIFGFFS 114

## RESULT 27

AAU97152

ID AAU97152 standard; protein; 352 AA.

XX AC AAU97152;

DT 13-AUG-2002 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGNR10 #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;  
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;  
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;  
 KW hyperproliferative disease; neurological disease; receptor.

XX Homo sapiens.

OS US2002048786-A1.

PN 25-APR-2002.

PD 09-FEB-2001; 2001US-00779879.

PF 09-FEB-2000; 2000US-0181258P.

PR 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.

XX (ROSE/) ROSEN C A.

PA (ROSC/) ROSCHKE V.

PA (LIY/) LI Y.

PA (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

PI WPI; 2002-434754/46.

XX N-PSDB; ABK51870.

DR New nucleic acid encoding an antibody specific for the G-protein  
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.  
 PT inflammation.

XX Disclosure; Page 165-166; 180pp; English.

XX The present invention relates to the isolation of a novel human G-protein  
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide  
 CC sequences encoding it. The invention also describes antibodies that bind  
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide

CC sequences encoding the antibodies. The antibodies are useful for treating  
 CC or preventing inflammation, defective or aberrant chemotaxis of immune  
 CC cells and T-cell/antigen-presenting cell interactions, infections and  
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral  
 CC infections (especially early-stage human immune deficiency virus (HIV),  
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions  
 CC associated with aberrant or deficient expression of the CCR5 receptor or  
 CC its ligands. The antibodies are also useful to determine CCR5 expression,  
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other  
 CC hyperproliferative diseases. The polynucleotide sequences encoding human  
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the  
 CC recombinant receptor, and in the treatment of a wide range of diseases  
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.  
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The  
 CC present sequence represents human G-protein chemokine receptor (CCR5)  
 CC HDGNR10 #2  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22  
 Db 93 QWDFGNTMCQLLTGLYFIIGFFS 114

RESULT 28  
 AAM52829  
 ID AAM52829 standard; protein; 352 AA.  
 XX  
 AC AAM52829;

DT 22-FEB-2002 (first entry)  
 DE Human CCR5 Gln 55 variant.

KW CCR5; CC chemokine receptor 5; human; HIV infection;  
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
 KW drug screening; identification; variant.

OS Homo sapiens.

FX Key Location/Qualifiers

FT Misc-difference 55

FT /note= "Glu replaces wild-type Leu; encoded by CTG"

FT Misc-difference 58

FT /note= "Encoded by AGC"

FX WO200171346-A2.

PD 27-SEP-2001.

PE 21-MAR-2001; 2001WO-US009155.

XX 21-MAR-2000; 2000US-0190946P.

PR 21-MAR-2000; 2000US-0190996P.

PR 21-MAR-2000; 2000US-0191299P.

PR 20-MAR-2001; 2001US-00813448.

PR 20-MAR-2001; 2001US-00813651.

PR 20-MAR-2001; 2001US-00813653.

XX (CONS-) CONSENSUS PHARM INC.

XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;

XX WPI; 2002-010610/01.

DR N-PSDB; ABA02318.

XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
 PT comprises binding a molecule from library to a molecule having binding  
 PT property corresponding to CCR5 and identifying bound molecule.

XX Example 3; Fig 4B; 50pp; English.

XX The invention relates to a method for identifying a binding compound for  
 CC chemokine receptor 5 (CCR5). The method involves screening a library  
 CC of test molecules (particularly peptides) with immobilised CCR5, and then  
 CC identifying those molecules which bind. The invention also relates to  
 CC CCR5-binding molecules identified using the method of the invention, a  
 CC methods for identifying consensus motifs for CCR5-binding peptides, a  
 CC transfer vector encoding tagged CCR5, a computer-aided methods for  
 CC determining the relative binding affinity of a test molecule to CCR5 and  
 CC a computer aided drug screening assay that utilises the three-dimensional  
 CC structure of CCR5. Compounds identified using the methods of the  
 CC invention are useful for treating or preventing HIV (human  
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency  
 CC syndrome) in a patient. The methods of the invention may also be used to  
 CC identify agonists or antagonists of the interaction of CCR5 with its  
 CC natural ligand, and to determine a binding motif for CCR5. The present  
 CC sequence represents a naturally occurring variant of human CCR5 in which  
 CC there is a glutamine, rather than a leucine, at position 55  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22

Db 93 QWDFGNTMCQLLTGLYFIIGFFS 114

RESULT 29

AAM52828

ID AAM52828 standard; protein; 352 AA.

XX AAM52828;

DT 22-FEB-2002 (first entry)

DE Human CC chemokine receptor 5 (CCR5).

KW CCR5; CC chemokine receptor 5; human; HIV infection;  
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
 KW drug screening; identification.

OS Homo sapiens.

FX WO200171346-A2.

PD 27-SEP-2001.

PE 21-MAR-2001; 2001WO-US009155.

XX 21-MAR-2000; 2000US-0190946P.

PR 21-MAR-2000; 2000US-0190996P.

PR 21-MAR-2000; 2000US-0191299P.

PR 20-MAR-2001; 2001US-00813448.

PR 20-MAR-2001; 2001US-00813651.

PR 20-MAR-2001; 2001US-00813653.

XX (CONS-) CONSENSUS PHARM INC.

XX Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;

XX WPI; 2002-010610/01.

DR N-PSDB; ABA02317.

XX Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
 PT comprises binding a molecule from library to a molecule having binding  
 PT property corresponding to CCR5 and identifying bound molecule.

XX Example 3; Fig 4A; 50pp; English.

XX The invention relates to a method for identifying a binding compound for  
 CC chemokine receptor 5 (CCR5). The method involves screening a library  
 CC of test molecules (particularly peptides) with immobilised CCR5, and then  
 CC identifying those molecules which bind. The invention also relates to  
 CC CCR5-binding molecules identified using the method of the invention, a  
 CC method for identifying consensus motifs for CCR5-binding peptides, a  
 CC transfer vector encoding tagged CCR5, a computer-aided method for  
 CC determining the relative binding affinity of a test molecule to CCR5 and  
 CC a computer aided drug screening assay that utilises the three-dimensional  
 CC structure of CCR5. Compounds identified using the methods of the  
 CC invention are useful for treating or preventing HIV (human  
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency  
 CC syndrome) in a patient. The methods of the invention may also be used to  
 CC identify agonists or antagonists of the interaction of CCR5 with its  
 CC natural ligand, and to determine a binding motif for CCR5. The present  
 CC sequence represents human CCR5  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
 DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

## RESULT 30

ABG70597

ID ABG70597 standard; protein; 352 AA.

AC ABG70597;

DT 03-DEC-2002 (first entry)

DE Human G-protein chemokine receptor, HDGNR10.

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XX The invention relates to a method for identifying a binding compound for  
 CC chemokine receptor 5 (CCR5). The method involves screening a library  
 CC of test molecules (particularly peptides) with immobilised CCR5, and then  
 CC identifying those molecules which bind. The invention also relates to  
 CC CCR5-binding molecules identified using the method of the invention, a  
 CC method for identifying consensus motifs for CCR5-binding peptides, a  
 CC transfer vector encoding tagged CCR5, a computer-aided method for  
 CC determining the relative binding affinity of a test molecule to CCR5 and  
 CC a computer aided drug screening assay that utilises the three-dimensional  
 CC structure of CCR5. Compounds identified using the methods of the  
 CC invention are useful for treating or preventing HIV (human  
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency  
 CC syndrome) in a patient. The methods of the invention may also be used to  
 CC identify agonists or antagonists of the interaction of CCR5 with its  
 CC natural ligand, and to determine a binding motif for CCR5. The present  
 CC sequence represents human CCR5  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
 DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

## RESULT 30

ABG70597

ID ABG70597 standard; protein; 352 AA.

AC ABG70597;

DT 03-DEC-2002 (first entry)

DE Human G-protein chemokine receptor, HDGNR10.

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XX Claim 7; Fig 1; 22pp; English.  
 PS  
 XX The present invention relates to the isolation of human G-protein  
 CC chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide  
 CC sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences  
 CC are useful for diagnosing a disease or a susceptibility to a disease  
 CC related to underexpression of HDGNR10. They are useful for identifying  
 CC modulators for stimulating haematopoiesis, wound healing, coagulation,  
 CC angiogenesis, to treat solid tumours, chronic infections, leukaemia, T-  
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, or  
 CC for stimulating growth factor activity. The sequences are also useful for  
 CC preventing and/or treating allergy, atherogenesis, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin  
 CC E (IgE)-mediated allergic reactions, prostaglandin-independent fever,  
 CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-  
 CC eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be  
 CC used in gene therapy to treat conditions related to underexpression of  
 CC HDGNR10. The present sequence represents human G-protein chemokine  
 CC receptor, HDGNR10  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 126; DB 5; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.6e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22

DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

Search completed: March 4, 2004, 17:59:21

Job time : 53.3061 secs

Novel human G-protein chemokine receptor polypeptide useful for  
 identifying modulators for stimulating hematopoiesis, wound healing,  
 leukemia, for treating allergy, rheumatoid arthritis, shock and as  
 research agents.

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 11.2245 Seconds  
(without alignments)  
188.535 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFNTMCLLTGLYFIGRFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 126   | 100.0       | 352    | 2 A43113 | chemokine (C-C) re |
| 2          | 87    | 69.0        | 360    | 2 JC2443 | chemokine (C-C) re |
| 3          | 87    | 69.0        | 374    | 2 I38450 | chemokine (C-C) re |
| 4          | 82    | 65.1        | 355    | 2 JC5067 | G protein-coupled  |
| 5          | 76    | 60.3        | 355    | 2 I49339 | macrophage inflam  |
| 6          | 74    | 58.7        | 356    | 2 I49340 | MIP-1 alpha recept |
| 7          | 71    | 56.3        | 355    | 2 A45177 | chemokine (C-C) re |
| 8          | 70    | 55.6        | 359    | 2 I49341 | MIP-1 alpha recept |
| 9          | 67    | 53.2        | 355    | 2 G02436 | chemokine (C-C) re |
| 10         | 66    | 52.4        | 360    | 2 A57160 | chemokine (C-C) re |
| 11         | 65    | 51.6        | 344    | 2 JC5942 | chemokine receptor |
| 12         | 65    | 51.6        | 360    | 2 JC4587 | chemokine (C-C) re |
| 13         | 60    | 47.6        | 354    | 2 I58186 | probable G protein |
| 14         | 59    | 46.8        | 369    | 2 JC5068 | G protein-coupled  |
| 15         | 56    | 44.4        | 355    | 2 JC4304 | orphan G protein-c |
| 16         | 55    | 43.7        | 383    | 2 S55594 | G protein-coupled  |
| 17         | 53.5  | 42.5        | 328    | 2 I38973 | G protein-coupled  |
| 18         | 53    | 42.1        | 378    | 2 A57335 | G protein-coupled  |
| 19         | 53    | 42.1        | 422    | 2 JC7080 | melanin-concentrat |
| 20         | 52    | 41.3        | 378    | 2 A45680 | G protein-coupled  |
| 21         | 52    | 41.3        | 378    | 2 B55735 | lymphocyte-specifi |
| 22         | 51    | 40.5        | 352    | 1 S27357 | complement C5a ana |
| 23         | 50    | 39.7        | 350    | 2 JN0621 | G protein-coupled  |
| 24         | 50    | 39.7        | 359    | 2 A48921 | interleukin-8 rece |
| 25         | 50    | 39.7        | 435    | 2 T37324 | probable JNK-activ |
| 26         | 50    | 39.7        | 448    | 2 T16256 | hypothetical prote |
| 27         | 49.5  | 39.3        | 359    | 2 I51372 | angiotensin II rec |
| 28         | 49    | 38.9        | 354    | 2 B55733 | G protein-coupled  |
| 29         | 49    | 38.9        | 367    | 2 JE0349 | interferon-inducib |

mu opioid receptor  
thrombin receptor  
alpha-thrombin rec  
hypothetical prote  
probable TonB-depe  
fusin (LESTRA) - c  
neuropeptide Y/pep  
probable transport  
probable transport  
thrombin receptor  
G protein-coupled  
olfactory channel  
protein B0212.5 [i  
heptahelical P2Y5-  
bradykinin B1 rece  
kappa opioid recep  
opioid receptor ho  
G protein-coupled  
orphan opioid rece  
hypothetical prote  
phosphomannomutase  
hypothetical prote  
hypothetical prote  
angiotensin recept  
probable amino aci  
hypothetical prote  
probable ferredoxi  
phosphomannomutase  
probable RING zinc  
G protein-coupled  
probable sugar upt  
bradykinin B1 rece  
interleukin-8 rece  
angiotensin II rec  
ubiquinol-cytochro  
bradykinin B2 rece  
kappa opioid recep  
kappa opioid recep  
kappa opioid recep  
kappa opioid recep  
hypothetical prote  
proteinase activat  
probable integral  
hypothetical prote  
probable glycosyl  
potassium-transport  
potassium-transport  
ubiquinol-cytochro  
ubiquinol-cytochro  
ubiquinol-cytochro  
ubiquinol-cytochro  
ubiquinol-cytochro  
ubiquinol-cytochro  
ubiquinol-cytochro  
ubiquinol-cytochro  
G protein-coupled  
ubiquinol-cytochro  
ubiquinol-cytochro  
ubiquinol-cytochro  
ubiquinol-cytochro  
ubiquinol-cytochro  
rhodopsin - giant  
probable membrane  
polyamine transport  
hypothetical prote  
G protein-coupled

30 49 38.9 398 2 A57510  
31 49 38.9 425 2 A37912  
32 49 38.9 427 2 S17148  
33 48.5 38.5 186 2 AG1086  
34 48.5 38.5 706 2 A81848  
35 48 38.1 352 2 G00048  
36 48 38.1 352 2 A45747  
37 48 38.1 409 2 F65067  
38 48 38.1 409 2 F91091  
39 48 38.1 409 2 A85937  
40 48 38.1 420 2 I51667  
41 48 38.1 482 2 S65766  
42 48 38.1 937 2 T37241  
43 48 38.1 957 2 D88651  
44 47.5 37.7 370 2 JC5549  
45 47 37.3 334 2 JC4681  
46 47 37.3 367 2 I49022  
47 47 37.3 367 2 JC2421  
48 47 37.3 367 2 I56520  
49 47 37.3 370 2 S43087  
50 47 37.3 505 2 T16583  
51 47 37.3 557 2 A11182  
52 46 36.5 299 2 T26789  
53 46 36.5 380 2 I38435  
54 46 36.5 409 2 AH0868  
55 46 36.5 457 2 T29741  
56 46 36.5 471 2 H83451  
57 46 36.5 578 2 B83788  
58 45 35.7 237 2 G84678  
59 45 35.7 308 2 I50241  
60 45 35.7 319 2 G95978  
61 45 35.7 352 2 S60024  
62 45 35.7 356 2 S42096  
63 45 35.7 359 2 JC1194  
64 45 35.7 360 2 T11067  
65 45 35.7 364 2 JC1488  
66 45 35.7 380 2 JC2434  
67 45 35.7 380 2 A48227  
68 45 35.7 380 2 JC2338  
69 45 35.7 380 2 S36143  
70 45 35.7 380 2 A55259  
71 45 35.7 391 2 T32714  
72 45 35.7 399 2 I48705  
73 45 35.7 436 2 AG0272  
74 45 35.7 525 2 A99557  
75 45 35.7 581 2 T29830  
76 45 35.7 679 2 AD0507  
77 45 35.7 681 2 AG1785  
78 45 35.7 681 2 AH1409  
79 44.5 35.3 133 2 C23725  
80 44.5 35.3 133 2 G23725  
81 44.5 35.3 133 2 A41824  
82 44.5 35.3 133 2 I23725  
83 44.5 35.3 133 2 H23725  
84 44.5 35.3 133 2 B41824  
85 44.5 35.3 133 2 A23725  
86 44.5 35.3 133 2 F23725  
87 44.5 35.3 133 2 B23725  
88 44.5 35.3 333 2 I38974  
89 44.5 35.3 378 2 T12009  
90 44.5 35.3 378 2 T09812  
91 44.5 35.3 380 1 CBRT  
92 44.5 35.3 381 2 T11776  
93 44.5 35.3 382 1 S33573  
94 44.5 35.3 386 2 T11286  
95 44.5 35.3 455 1 OOCG  
96 44.5 35.3 285 2 AI0633  
97 44 34.9 289 2 A83608  
98 44 34.9 328 2 T30999  
99 44 34.9 333 2 I65989  
100 44 34.9 333 2 I65989

chemokine (C-C) receptor 5 - human  
N:Alternate names: C-C CKR-5; CCR5  
C:Species: Homo sapiens (man)  
C>Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000  
C:Citation: A43113; S71808; A58832; G02653; A58833  
A:Accession: A43113; S71808; A58832; G02653; A58833  
R:Sanson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
Biochemistry 35, 3362-3367, 1996  
A>Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
A:Reference number: A43113; MUID:96241590; PMID:8639485  
A:Accession: A43113  
A:Molecule type: mRNA  
A:Residues: 1-352 <SAM>  
A:Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811  
R:Sanson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragost  
M.; Imai, T.; Rana, S.; Ye, Y.; Smyth, R.D.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa  
Nature 382, 722-725, 1996  
A>Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles o  
A:Reference number: S71808; MUID:96345670; PMID:8751444  
A:Accession: S71808  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 182-206;207-230 <SMM2>  
A:Accession: A58834  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-184; [IKDSHIGAGPAAACHGHLGNPKNSASVSK] <SAM3>  
A:Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063  
A>Note: This frameshift mutation results in a non-functional receptor but confers a dege  
nd may have had a selective advantage by conferring resistance to Yersinia plague infect  
J. Combadiere, C.; Anujya, S.K.; Tiffany, H.L.; Murphy, P.M.  
J. Leukoc. Biol. 60, 147-152, 1996  
A>Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec  
A:Reference number: A58832; MUID:96295970; PMID:8699119  
A:Accession: A58832  
A:Molecule type: mRNA  
A:Residues: 1-352 <COM1>  
A:Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409  
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
R:Combadiere, C.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: H01541  
A:Accession: G02653  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-89;1'-91-352 <COM2>  
A:Cross-references: EMBL:U57840  
R:Rapport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
J. Biol. Chem. 271, 17161-17166, 1996  
A>Title: Molecular cloning and functional characterization of a novel human CC chemokine  
A:Reference number: A58833; MUID:96291862; PMID:8663314  
A:Accession: A58833  
A:Molecule type: mRNA  
A:Residues: 1-352 <RAP>  
A:Cross-references: GB:U54994; NID:g1457945; PIDN:AAC50598.1; PID:g1457946  
C:Comment: This is a receptor for chemokines MIP-1alpha (see FIR:A30574), MIP-1beta (see  
C:Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine (C  
C:Genetics:  
A:Gene: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CXCR5; ChemR13  
A:Cross-references: GDB:I230510; OMIM:601373  
A:Map position: 3p21-3p21  
C:Function:  
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTE  
A>Note: probably acts to control granulocyte proliferation and differentiation  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran  
F:32-56/Domain: transmembrane #status predicted &ltTM1>  
F:67-87/Domain: transmembrane #status predicted &ltTM2>  
F:103-124/Domain: transmembrane #status predicted &ltTM3>

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Query Match 100.0%; Score 126; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QWDFGNTMCQLLTGLTYFGFFS 22
 |||||
DB 93 QWDFGNTMCQLLTGLTYFGFFS 114
 |||||

RESULT 2
JC2443
chemokine (C-C) receptor 2, splice form B - human
N/Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1; CCR2; CCR2L; CCR2L1; CCR2L2; CCR2L3; CCR2L4; CCR2L5; CCR2L6; CCR2L7; CCR2L8; CCR2L9; CCR2L10; CCR2L11; CCR2L12; CCR2L13; CCR2L14; CCR2L15; CCR2L16; CCR2L17; CCR2L18; CCR2L19; CCR2L20; CCR2L21; CCR2L22; CCR2L23; CCR2L24; CCR2L25; CCR2L26; CCR2L27; CCR2L28; CCR2L29; CCR2L30; CCR2L31; CCR2L32; CCR2L33; CCR2L34; CCR2L35; CCR2L36; CCR2L37; CCR2L38; CCR2L39; CCR2L40; CCR2L41; CCR2L42; CCR2L43; CCR2L44; CCR2L45; CCR2L46; CCR2L47; CCR2L48; CCR2L49; CCR2L50; CCR2L51; CCR2L52; CCR2L53; CCR2L54; CCR2L55; CCR2L56; CCR2L57; CCR2L58; CCR2L59; CCR2L60; CCR2L61; CCR2L62; CCR2L63; CCR2L64; CCR2L65; CCR2L66; CCR2L67; CCR2L68; CCR2L69; CCR2L70; CCR2L71; CCR2L72; CCR2L73; CCR2L74; CCR2L75; CCR2L76; CCR2L77; CCR2L78; CCR2L79; CCR2L80; CCR2L81; CCR2L82; CCR2L83; CCR2L84; CCR2L85; CCR2L86; CCR2L87; CCR2L88; CCR2L89; CCR2L90; CCR2L91; CCR2L92; CCR2L93; CCR2L94; CCR2L95; CCR2L96; CCR2L97; CCR2L98; CCR2L99; 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CCR2L500
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C;Accession: I38450  
R;Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
A;Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2  
A;Reference number: A53477; MUID:94195821; PMID:8146186  
A;Accession: I38450  
A;Status: preliminary  
A;Molecule type: mRNA  
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A;Cross-references: EMBL:U03882; NID:g472555; PIDN:AAA19119.1; PID:g472556  
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A;Map position: 3p21-3p21  
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C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein  
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F;154-178/Domain: transmembrane #status predicted <TM4>  
F;208-226/Domain: transmembrane #status predicted <TM5>  
F;244-265/Domain: transmembrane #status predicted <TM6>  
F;292-309/Domain: transmembrane #status predicted <TM7>  
F;14/Binding site: carbohydrate (Aen) (covalent) #status predicted  
F;32-277/113-190/Disulfide bonds: #status predicted

Query Match 69.0%; Score 87; DB 2; Length 374;  
Best Local Similarity 66.7%; Pred. No. 1.5e-05;  
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWFGNTMCKLGLYFHYGFF 21  
:|||||:|||||:|||||:  
Db 105 EWFGNACMKLGLYHIGYF 125

RESULT 4  
JC5067  
N;Alternate names: chemokine receptor-L1 - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text\_change 21-Jul-2000  
C;Accession: JC5067; G02776; G02387  
R;Zaballo, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.  
Biochem. Biophys. Res. Commun. 227, 846-853, 1996  
A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like genes  
A;Reference number: JC5067; MUID:97040707; PMID:8886020  
A;Accession: JC5067  
A;Molecule type: DNA  
A;Residues: 1-355 <ZAB>  
A;Cross-references: EMBL:Z79782; NID:g1668735; PIDN:CAB02142.1; PID:g1668736  
R;Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.  
submitted to the EMBL Data Library, June 1996  
A;Accession: G02776  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-355 <NAP>  
A;Cross-references: EMBL:U62556; NID:g1468978; PID:g1468979  
R;Bonner, T.I.  
submitted to the EMBL Data Library, January 1996  
A;Reference number: H01154  
A;Accession: G02387  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-355 <BON>  
A;Cross-references: EMBL:U45983; NID:g1245056; PID:g1245057  
C;Comment: This protein belongs to the family of beta chemokine receptors.  
C;Genetics:  
A;Gene: GDB:CMKBR8; CMKBR2; TER1; CKR-L1  
A;Cross-references: GDB:6053733; OMIM:601834  
A;Map position: 3p21-3p21  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; transmembrane protein

F;36-63/Domain: transmembrane #status predicted <TM1>  
F;73-94/Domain: transmembrane #status predicted <TM2>  
F;108-129/Domain: transmembrane #status predicted <TM3>  
F;147-171/Domain: transmembrane #status predicted <TM4>  
F;200-222/Domain: transmembrane #status predicted <TM5>  
F;239-260/Domain: transmembrane #status predicted <TM6>  
F;281-304/Domain: transmembrane #status predicted <TM7>

Query Match 65.1%; Score 82; DB 2; Length 355;  
Best Local Similarity 54.5%; Pred. No. 7.9e-05;  
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWFGNTMCKLGLYFHYGFFS 22  
:|||||:|||||:|||||:  
Db 98 QWFGTMCCKVSGFYIGFYS 119

RESULT 5  
I49339  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C;Accession: I49339  
R;Gao, J.L.; Murphy, P.M.  
J. Biol. Chem. 270, 17494-17501, 1995  
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine genes  
A;Reference number: I49339; MUID:95340546; PMID:7542241  
A;Accession: I49339  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-355 <RES>  
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548  
C;Superfamily: vertebrate rhodopsin

Query Match 60.3%; Score 76; DB 2; Length 355;  
Best Local Similarity 52.4%; Pred. No. 0.00065;  
Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNTMCKLGLYFHYGFFS 22  
:|||||:|||||:|||||:  
Db 99 WIFGDMCKLGLYFHYGYS 119

RESULT 6  
I49340  
MIP-1 alpha receptor like-1 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C;Accession: I49340  
R;Gao, J.L.; Murphy, P.M.  
J. Biol. Chem. 270, 17494-17501, 1995  
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine genes  
A;Reference number: I49339; MUID:95340546; PMID:7542241  
A;Accession: I49340  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-356 <RES>  
A;Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550  
C;Superfamily: vertebrate rhodopsin

Query Match 58.7%; Score 74; DB 2; Length 356;  
Best Local Similarity 47.6%; Pred. No. 0.0013;  
Matches 10; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 WDFGNTMCKLGLYFHYGFFS 22  
:|||||:|||||:|||||:  
Db 100 WIFGNAMCKVSGFYIGLYS 120

RESULT 7  
A45177  
chemokine (C-C) receptor 1 - human  
N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor

RESULT 9

G02436

chemokine (C-C) receptor 3 - human

NrAlternate names: C-C CKR-3

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 04-Mar-2000

C:Accession: G02436; A:Accession: G02436

R:R:Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A:Reference number: H01272

A:Accession: G02436

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 <POM>

A:Crossa-references: EMBL:U49727; NID:g1477560; PIDN:AA09726.1; PID:g1477561

R:Combiadere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor

A:Reference number: A57237; MUID:95348056; PMID:7622448

A:Accession: A57237

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-106, 'N', 108-275, 'S', 277-280, 'R', 282-355 <COM>

A:Crossa-references: GB:U28694; NID:g1199579; PIDN:AA05469.1; PID:g1199580

A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AA05469.1

C:Genetics:

A:Gene: GDB:CMKBR3

A:Crossa-references: GDB:579624; OMIM:601268

A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

C:35-60/Domain: transmembrane #status predicted <TM1>

F71791/Domain: transmembrane #status predicted <TM2>

FF17108-129/Domain: transmembrane #status predicted <TM3>

FF17147-171/Domain: transmembrane #status predicted <TM4>

F7205-223/Domain: transmembrane #status predicted <TM5>

F7240-261/Domain: transmembrane #status predicted <TM6>

F7288-305/Domain: transmembrane #status predicted <TM7>

F724-273, 106-183/Disulfide bonds: #status predicted

F7345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

QY 2 WDFGNTMQLLTGLYFIFGFS 22

DB 99 WVFCHGCKLLSGFYFTGLYS 119

QY

Best Match 53.2%; Score 67; DB 2; Length 355;

Query Local Similarity 52.4%; Pred. No. 0.015;

Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

RESULT 10

A57160

chemokine (C-C) receptor 4 - human

NrAlternate names: C-C CKR-4

C:Species: Homo sapiens (man)

C:Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000

C:Accession: A57160

R:R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.; V

J. Biol. Chem. 270, 19495-19500, 1995

A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor of

A:Reference number: A57160; MUID:95370289; PMID:7642634

A:Accession: A57160

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-360 <POM>

A:Crossa-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452

A:Note: source clone X5-5

C:Genetics:

A:Gene: GDB:CMKBR4

A:Crossa-references: GDB:677463

A:Map position: 3p21-3p21



C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
 F;40-65/Domain: transmembrane #status predicted <TM1>  
 F;76-97/Domain: transmembrane #status predicted <TM2>  
 F;112-133/Domain: transmembrane #status predicted <TM3>  
 F;151-175/Domain: transmembrane #status predicted <TM4>  
 F;208-226/Domain: transmembrane #status predicted <TM5>  
 F;243-264/Domain: transmembrane #status predicted <TM6>  
 F;291-308/Domain: transmembrane #status predicted <TM7>  
 F;29-276,110-187/Disulfide Bonds: #status predicted  
 F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
 F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F;183,194/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 52.4%; Score 66; DB 2; Length 360;  
 Best Local Similarity 40.9%; Pred. No. 0.022;  
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QWFGNTMQLLTGLYFIFGFS 22  
 ||| :|:|:| :|:|:  
 Db 102 QWVFGGLCKLMSWMLVGFYS 123

RESULT 11  
 JCS942  
 Chemokine receptor - human  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
 C;Accession: JCS942  
 R;Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.  
 Biochem. Biophys. Res. Commun. 243, 264-268, 1998  
 A;Title: Cloning and characterization of a novel human chemokine receptor.  
 A;Reference number: JCS942; MUID:98139902; PMID:9473515  
 A;Accession: JCS942  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-344 <FAN>  
 A;Cross-references: GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071  
 C;Superfamily: vertebrate rhodopsin

Query Match 51.6%; Score 65; DB 2; Length 344;  
 Best Local Similarity 55.6%; Pred. No. 0.03;  
 Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GNTMQLLTGLYFIFGFS 22  
 | :|:| :|:|:  
 Db 99 GDPMKILIGLVFGLYS 116

RESULT 12  
 JCS587  
 Chemokine (C-C) receptor 4 - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000  
 C;Accession: JCS587  
 R;Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996  
 A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to  
 A;Reference number: JCS587; MUID:96136324; PMID:8573157  
 A;Accession: JCS587  
 A;Molecule type: mRNA  
 A;Residues: 1-360 <HOO>  
 A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852  
 A;Experimental source: thymus  
 C;Genetics:  
 A;Gene: cc ckr-4  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: glycoprotein; phosphoprotein; receptor; thymus  
 F;2,183,194/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred  
 F;145/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
 F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 51.6%; Score 65; DB 2; Length 360;  
 Best Local Similarity 40.9%; Pred. No. 0.031;  
 Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QWFGNTMQLLTGLYFIFGFS 22  
 ||| :|:|:| :|:|:  
 Db 102 QWVFGGLCKLMSWMLVGFYS 123

RESULT 13  
 JS8186  
 probable G protein-coupled receptor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 21-Jul-2000  
 C;Accession: JS8186  
 R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.  
 Neurosci. Lett. 169, 85-89, 1994  
 A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and  
 A;Reference number: JS8186; MUID:94323113; PMID:8047298  
 A;Accession: JS8186  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-354 <RES>  
 A;Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor

Query Match 47.6%; Score 60; DB 2; Length 354;  
 Best Local Similarity 62.5%; Pred. No. 0.18;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 NTMQLLTGLYFIFGFS 21  
 ||| :|:|:| :|:|:  
 Db 100 NAMCKLTTFATFFIGFF 115

RESULT 14  
 JCS068  
 G protein-coupled receptor CKR-L3 - human  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 21-Jul-2000  
 C;Accession: JCS068  
 R;Zaballos, A.; Varona, R.; Guierrez, J.; Lind, P.; Marquez, G.  
 Biochem. Biophys. Res. Commun. 227, 846-853, 1996  
 A;Title: Molecular cloning and RNA expression of two new human chemokine receptor-like  
 A;Reference number: JCS067; MUID:97040707; PMID:8886020  
 A;Accession: JCS068  
 A;Molecule type: DNA  
 A;Residues: 1-369 <ZAB>  
 A;Cross-references: EMBL:Z79784; NID:g1668737; PIDN:CA802144.1; PID:g1668738  
 C;Comment: This protein belongs to the family of alpha chemokine receptors.  
 C;Genetics:  
 A;Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4  
 A;Cross-references: GDB:5370639; OMIM:601835  
 A;Map position: 6q27-6q27  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; transmembrane protein  
 F;42-68/Domain: transmembrane #status predicted <TM1>  
 F;79-99/Domain: transmembrane #status predicted <TM2>  
 F;115-136/Domain: transmembrane #status predicted <TM3>  
 F;160-180/Domain: transmembrane #status predicted <TM4>  
 F;212-233/Domain: transmembrane #status predicted <TM5>  
 F;250-271/Domain: transmembrane #status predicted <TM6>  
 F;292-315/Domain: transmembrane #status predicted <TM7>

Query Match 46.8%; Score 59; DB 2; Length 369;  
 Best Local Similarity 52.6%; Pred. No. 0.26;  
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 2 WFGNTMQLLTGLYFIFG 20  
 ||| :|:|:| :|:|:  
 Db 106 WVFSSNATCKLKGIVAINF 124

RESULT 15  
 JC4304  
 G protein-coupled receptor - human  
 A:Alternate names: V28 protein  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 19-May-2000  
 C:Accession: JC4304  
 C:Report, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.  
 Gene 163, 295-299, 1995  
 A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to S  
 A:Reference number: JC4304; MUID:96011651; PMID:7590284  
 A:Accession: JC4304  
 A:Molecule type: mRNA  
 A:Residues: 1-355 <RAP>  
 A:Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581  
 A:Experimental source: peripheral blood mononuclear cell  
 C:Comment: This protein is a cell-surface receptor which recognizes extracellular signal  
 C:Comment: This protein is a key regulator of many immune and homeostatic responses, and  
 C:Genetics:  
 A:Gene: V28  
 A:Map position: 3pter-p21  
 C:Superfamily: G protein-coupled receptor; lymphokine; transmembrane protein  
 F:35-57/Domain: transmembrane #status predicted <TM1>  
 F:66-88/Domain: transmembrane #status predicted <TM2>  
 F:104-125/Domain: transmembrane #status predicted <TM3>  
 F:146-165/Domain: transmembrane #status predicted <TM4>  
 F:197-217/Domain: transmembrane #status predicted <TM5>  
 F:230-254/Domain: transmembrane #status predicted <TM6>  
 F:275-296/Domain: transmembrane #status predicted <TM7>  
 Query Match 44.4%; Score 56; DB 2; Length 355;  
 Best Local Similarity 56.2%; Pred. No. 0.72;  
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 6 NTMCQLLTGLYFGFF 21  
 ||| :||| :  
 99 NAMCKFTTAFFFIGFF 114  
 DBb  
 RESULT 16  
 S55594  
 G protein-coupled receptor E1 - equine herpesvirus 2  
 C:Species: equine herpesvirus 2  
 C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 13-Aug-1999  
 C:Accession: S55594  
 R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
 J. Mol. Biol. 249, 520-528, 1995  
 A:Title: The DNA sequence of equine herpesvirus 2.  
 A:Reference number: S55594; MUID:95302501; PMID:7783207  
 A:Accession: S55594  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: DNA  
 A:Residues: 1-383 <TEL>  
 A:Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor  
 Query Match 43.7%; Score 55; DB 2; Length 383;  
 Best Local Similarity 38.1%; Pred. No. 1.1;  
 Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 WDFGNMQLLTGLYFGFFS 22  
 ||| :||| : : :  
 Db 138 WTEGISLCKLLRGVCYMSLYS 158  
 RESULT 17  
 I38973  
 G protein-coupled receptor 7 - human  
 C:Species: Homo sapiens (man)

RESULT 21

B55735

lymphocyte-specific G protein-coupled receptor EB11 - human

C:Species: Homo sapiens (man)

C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 19-May-2000

C:Accession: B55735, S52443

R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B. Genomics 23, 643-650, 1994

A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor

A:Reference number: A55735; MUID:95154835; PMID:7851893

A:Accession: B55735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-378 <SCH>

A:Cross-references: KB131581; NID:9468319; PIDN:AAA74231.1; PID:g468320

R:Burgstahler, R.; Kempkes, B.; Staube, K.; Liipp, M. submitted to the EMBL Data Library, February 1995

A:Description: The expression of the chemokine receptor BLR2/EB11 is specifically trans

A:Reference number: S52443

A:Accession: S52443

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 21-378 <BUR>

A:Cross-references: EMBL:X84702

C:Genetics:

A:Gene: GDB:CMKBR7; EB11; BLR2

A:Cross-references: GDB:342065; OMIM:600242

A:Map position: 17q12-17q21.2

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match 41.3% Score 52; DB 2; Length 378;

Best Local Similarity 42.9% Pred. No. 3.1;

Matches 9. Conservative 4; Mismatches 8; Indels 0; Gaps 0;

F;200-222/Domain: transmembrane #status predicted <TM5>  
F;242-265/Domain: transmembrane #status predicted <TM6>  
F;284-306/Domain: transmembrane #status predicted <TM7>  
F;6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.7%; Score 50; DB 2; Length 350;  
Best Local Similarity 38.1%; Pred. No. 5.8;  
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 WDFGNTMCCQLLTGLYIFIGFFS 22  
DB 105 WVLGKIMCKVTSALTNYFVS 125

RESULT 24  
A48921  
N;Alternate names: G-protein coupled receptor Gpcrlf  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1999  
C;Accession: A48921; A53677; I49348; I55421; H48909; I53774  
R;Caretto, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993  
A;Title: The murine homologue of the human interleukin-8 receptor type B maps near the  
A;Reference number: A48921; MUID:94117014; PMID:8288247  
A;Accession: A48921  
A;Molecule type: DNA  
A;Residues: 1-359 <CR>  
A;Cross-references: GB:I23637; NID:G435093; PIDN:AAA39305.1; PID:G435094  
R;Suzuki, H.; Prado, G.N.; Wilkenson, N.; Navarro, J.  
J. Biol. Chem. 269, 18263-18266, 1994  
A;Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding  
A;Reference number: A53677; MUID:94308043; PMID:7518496  
A;Accession: A53677  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-359 <SUZ>  
A;Cross-references: GB:I26549  
R;Lee, J.; Sequence extracted from NCBI backbone (NCBIP:149812)  
J. Immunol. 155, 2158-2164, 1995  
A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.  
A;Reference number: 149348; MUID:95363183; PMID:7636264  
A;Accession: I49348  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-359 <RES>  
A;Cross-references: EMBL:U31207; NID:G950174; PIDN:AAC52239.1; PID:G950175  
R;Bozic, C.R.; Gerard, N.P.; von Uexkull-Guldenband, C.; Kolakowski, L.F.  
J. Biol. Chem. 269, 29355-29358, 1994  
A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression  
A;Reference number: I55421; MUID:95050766; PMID:7961909  
A;Accession: I55421  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-359 <RE2>  
A;Cross-references: GB:LI3239; NID:G293665; PIDN:AAA62109.1; PID:G293666  
R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.  
Genomics 18, 175-184, 1993  
A;Title: Identification, chromosomal location, and genome organization of mammalian G-protein coupled receptor  
A;Reference number: A48909; MUID:94116980; PMID:8288218  
A;Accession: H48909  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 145-258 <WTL>  
A;Cross-references: GB:LI20337; NID:G438800; PIDN:AAA16853.1; PID:G438801  
R;Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K.  
Gene 142, 297-300, 1994  
A;Title: Cloning of a cDNA encoding a mouse homologue of the interleukin-8 receptor.  
A;Reference number: I53774; MUID:94252584; PMID:8194768  
A;Accession: I53774  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA

A;Residues: 1-359 <RE3>  
A;Cross-references: GB:DI7630; NID:G493671; PIDN:BAA04536.1; PID:G493672  
C;Genetics:  
A;Gene: il1rb  
A;Introns: #status absent  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
F;49-74/Domain: transmembrane #status predicted <TM1>  
F;84-106/Domain: transmembrane #status predicted <TM2>  
F;120-141/Domain: transmembrane #status predicted <TM3>  
F;163-182/Domain: transmembrane #status predicted <TM4>  
F;213-234/Domain: transmembrane #status predicted <TM5>  
F;251-271/Domain: transmembrane #status predicted <TM6>  
F;308-328/Domain: transmembrane #status predicted <TM7>

Query Match 39.7%; Score 50; DB 2; Length 359;  
Best Local Similarity 33.3%; Pred. No. 6;  
Matches 7; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 WDFGNTMCCQLLTGLYIFIGFFS 22  
DB 111 WTFGSTLCKIFSVKVFYS 131

RESULT 25  
T37324  
probable JNK-activating protein kinase (EC 2.7.1.-) JNK-1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C;Accession: T37324  
R;Kawasaki, M.; Hisamoto, N.; Iino, Y.; Yamamoto, M.; Ninomiya-Tsuji, J.; Matsumoto, K.  
EMBO J. 18, 3604-3615, 1999  
A;Title: A Caenorhabditis elegans JNK signal transduction pathway regulates coordinated  
A;Reference number: Z21688; MUID:99321749; PMID:10393177  
A;Accession: T37324  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-435 <KAW>  
A;Cross-references: EMBL:AB024086; NID:G5668698; PIDN:BAA02641.1; PID:G5668699  
C;Genetics:  
A;Gene: jkk-1  
C;Function:  
A;Description: activation of JNK-1  
A;Pathway: JNK signaling pathway  
A;Note: JNK pathway functions in type-D GABAergic motor neurons and thereby modulates c  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: ATP; phosphotransferase; signal transduction

Query Match 39.7%; Score 50; DB 2; Length 435;  
Best Local Similarity 60.0%; Pred. No. 7.3;  
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 WDFGNTMCCQLLTGLY 16  
DB 307 WSLGIVTVQLVTGLY 321

RESULT 26  
T16256  
hypothetical protein F35C8.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Jan-2000  
C;Accession: T16256  
R;Wu, X.  
submitted to the EMBL Data Library, November 1995  
A;Description: The sequence of C. elegans cosmid F35C8.  
A;Reference number: Z18486  
A;Accession: T16256  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-448 <WUX>  
A;Cross-references: EMBL:U40941; NID:G1072184; PID:G1072189; PIDN:AAA81711.1; CESP:F35C1  
C;Genetics:

A;Reference number: A57333; MUID:95154831; PMID:7851889

A;Accession: B57333

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-354 <MAR>

A;Cross-references: GB:U13667

C;Genetics:

A;Gene: GDB:GPR2

A;Cross-references: GDB:371708; OMIM:600240

A;Map position: 17q21.1-17q21.3

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor

Query Match 38.9%; Score 49; DB 2; Length 354;  
Best Local Similarity 36.8%; Pred. No. 8.4;  
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 WDFGNMCQLLTGLTYFTGF 20  
| : | : | : | : |  
DB 98 WSLGSATCRITISGLYSASF 116

RESULT 29

JEO349

A;Title: interferon-inducible protein 10 (IP-10) receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000

C;Accession: JEO349

R;Tamari, M.; Tomingaga, Y.; Yatsunami, K.; Narumi, S.  
Biochem. Biophys. Res. Commun. 251, 41-48, 1998

A;Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its

A;Reference number: JEO349; MUID:99009219; PMID:9790904

A;Accession: JEO349

A;Molecule type: mRNA

A;Residues: 1-367 <TAM>

A;Cross-references: DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PID:g3798732

C;Comment: This protein is important for lymphocyte trafficking to lymphoid organs.

C;Superfamily: vertebrate rhodopsin

Query Match 38.9%; Score 49; DB 2; Length 367;  
Best Local Similarity 36.4%; Pred. No. 8.7;  
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 QWDFNTMCQLLTGLTYFTGFPS 22  
| : | : | : | : | : |  
DB 115 QWVFGPLCKVAGALFNIFYA 136

RESULT 30

A57510

A;Title: mu opioid receptor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 24-Nov-1999

C;Accession: A57510; I48665; S66513; I49300

R;Kaufman, D.L.; Keith Jr., D.E.; Anton, B.; Tian, J.; Magendzo, K.; Newman, D.; Tran, T.; J. Biol. Chem. 270, 15877-15883, 1995

A;Title: Characterization of the murine mu opioid receptor gene.

A;Reference number: A57510; MUID:95318184; PMID:7797593

A;Accession: A57510

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-398 <KAU>

A;Cross-references: GB:U19380

R;Man, B.H.; Augustin, L.B.; Fehseim, R.F.; Fuchs, J.A.; Loh, H.H.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9081-9085, 1994

A;Title: Genomic structure analysis of promoter sequence of a mouse mu opioid receptor

A;Reference number: I48665; MUID:94377496; PMID:8090773

A;Accession: I48665

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-398 <RES>

A;Cross-references: EMBL:U10561; NID:g555696; PIDN:AAB60673.1; PID:g5556069

R;Rosi, G.C.; Pan, Y.X.; Brown, G.P.; Pasternak, G.W.

Fri Mar 5 14:59:14 2004

FEBS Lett. 369, 192-196, 1995  
A;Title: Antisense mapping the MOR-1 opioid receptor: evidence for alternative splicing  
A;Reference number: I49300; MUID:95377399; PMID:7649256  
A;Accession: S66513  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-398 <ROS>  
A;Cross-references: EMBL:U26915; NID:G1055230; PID:AAA81170.1; PID:G1055231  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995  
C;Genetics:  
A;Gene: MOR-1  
A;Introns: 95/2; 213/1; 386/3  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran

Query Match 38.9%; Score 49; DB 2; Length 398;  
Best Local Similarity 28.6%; Pred. No. 9.5;  
Matches 6; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 2 WDFGNTWCOLLGLYFIGFFS 22  
| | | | : | : | :  
Db 133 WPGNICKIVISIDYNNMFT 153

Search completed: March 4, 2004, 18:03:58  
Job time : 13.2245 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 7.18367 Seconds  
(without alignments)  
159.465 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNTMQLLTGLYFGPFS 22

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 126   | 100.0       | 352    | 1     | CKR5_CERAB  |
| 2          | 126   | 100.0       | 352    | 1     | CKR5_CERP   |
| 3          | 126   | 100.0       | 352    | 1     | CKR5_CERTO  |
| 4          | 126   | 100.0       | 352    | 1     | CKR5_GORGO  |
| 5          | 126   | 100.0       | 352    | 1     | CKR5_HUMAN  |
| 6          | 126   | 100.0       | 352    | 1     | CKR5_HYLL   |
| 7          | 126   | 100.0       | 352    | 1     | CKR5_HYML   |
| 8          | 126   | 100.0       | 352    | 1     | CKR5_HYLSY  |
| 9          | 126   | 100.0       | 352    | 1     | CKR5_MACMU  |
| 10         | 126   | 100.0       | 352    | 1     | CKR5_PANTR  |
| 11         | 126   | 100.0       | 352    | 1     | CKR5_PAPHA  |
| 12         | 126   | 100.0       | 352    | 1     | CKR5_PONPY  |
| 13         | 126   | 100.0       | 352    | 1     | CKR5_PYGBI  |
| 14         | 126   | 100.0       | 352    | 1     | CKR5_PYGNE  |
| 15         | 126   | 100.0       | 352    | 1     | CKR5_TPAFR  |
| 16         | 126   | 100.0       | 352    | 1     | CKR5_TPAFR  |
| 17         | 89    | 70.6        | 353    | 1     | CKR8_MOUSE  |
| 18         | 87    | 69.0        | 374    | 1     | CKR2_HUMAN  |
| 19         | 86    | 68.3        | 373    | 1     | CKR2_RAT    |
| 20         | 84    | 66.7        | 354    | 1     | CKR5_RAT    |
| 21         | 83    | 65.9        | 269    | 1     | VC03_SPKA   |
| 22         | 83    | 65.9        | 370    | 1     | VK02_SPKA   |
| 23         | 83    | 65.9        | 373    | 1     | CKR2_MOUSE  |
| 24         | 82    | 65.1        | 355    | 1     | CKR8_HUMAN  |
| 25         | 82    | 65.1        | 356    | 1     | CKR8_MACMU  |
| 26         | 81    | 64.3        | 360    | 1     | CKR2_MACMU  |
| 27         | 80    | 63.5        | 354    | 1     | CKR5_MOUSE  |
| 28         | 79    | 62.7        | 358    | 1     | CKR3_CAVPO  |
| 29         | 76    | 60.3        | 355    | 1     | CKR1_MOUSE  |
| 30         | 75    | 59.5        | 359    | 1     | CKR3_RAT    |
| 31         | 74    | 58.7        | 356    | 1     | CKR7_MOUSE  |
| 32         | 71    | 56.3        | 355    | 1     | CKR1_HUMAN  |
| 33         | 71    | 56.3        | 355    | 1     | CKR1_MACMU  |

|     |      |      |     |   |             |
|-----|------|------|-----|---|-------------|
| 34  | 70   | 55.6 | 359 | 1 | CKR3_MOUSE  |
| 35  | 67   | 53.2 | 355 | 1 | CKR3_HUMAN  |
| 36  | 66   | 52.4 | 342 | 1 | CKR6_CERAB  |
| 37  | 66   | 52.4 | 360 | 1 | CKR4_HUMAN  |
| 38  | 65   | 51.6 | 342 | 1 | CKR6_HUMAN  |
| 39  | 65   | 51.6 | 342 | 1 | CKR6_MACNE  |
| 40  | 65   | 51.6 | 342 | 1 | CKR6_PANTR  |
| 41  | 65   | 51.6 | 343 | 1 | CKR6_MACFA  |
| 42  | 65   | 51.6 | 343 | 1 | CKR6_MACMU  |
| 43  | 65   | 51.6 | 360 | 1 | CKR4_MOUSE  |
| 44  | 61   | 48.4 | 381 | 1 | VQ3L_CAVPK  |
| 45  | 60   | 47.6 | 354 | 1 | C3X1_MOUSE  |
| 46  | 60   | 47.6 | 354 | 1 | C3X1_RAT    |
| 47  | 59   | 46.8 | 374 | 1 | CKR6_HUMAN  |
| 48  | 59   | 46.8 | 384 | 1 | CKD6_HUMAN  |
| 49  | 58   | 46.0 | 355 | 1 | CKR3_CERAB  |
| 50  | 58   | 46.0 | 355 | 1 | CKR3_MACMU  |
| 51  | 56   | 44.4 | 355 | 1 | C3X1_HUMAN  |
| 52  | 56   | 44.4 | 395 | 1 | GP44_HUMAN  |
| 53  | 55   | 43.7 | 362 | 1 | CKRA_MOUSE  |
| 54  | 55   | 43.7 | 378 | 1 | CKD6_MOUSE  |
| 55  | 55   | 43.7 | 382 | 1 | GP44_MOUSE  |
| 56  | 54   | 42.9 | 357 | 1 | CKR9_HUMAN  |
| 57  | 54   | 42.9 | 382 | 1 | CKD6_RAT    |
| 58  | 53.5 | 42.5 | 328 | 1 | GP7_HUMAN   |
| 59  | 53   | 42.1 | 360 | 1 | MCRI_RAT    |
| 60  | 53   | 42.1 | 378 | 1 | CKR7_MOUSE  |
| 61  | 53   | 42.1 | 388 | 1 | MCRI_MACMU  |
| 62  | 53   | 42.1 | 422 | 1 | MCRI_HUMAN  |
| 63  | 53   | 42.1 | 423 | 1 | MCRI_MOUSE  |
| 64  | 52.5 | 41.7 | 146 | 1 | GP7_MOUSE   |
| 65  | 52   | 41.3 | 368 | 1 | CCR3_HUMAN  |
| 66  | 52   | 41.3 | 369 | 1 | CKR9_MOUSE  |
| 67  | 52   | 41.3 | 370 | 1 | OPRX_CAVPO  |
| 68  | 52   | 41.3 | 378 | 1 | CKR7_HUMAN  |
| 69  | 51   | 40.5 | 352 | 1 | C5AR_CANFA  |
| 70  | 51   | 40.5 | 367 | 1 | CKR6_MOUSE  |
| 71  | 51   | 40.5 | 371 | 1 | NY6R_RABIT  |
| 72  | 51   | 40.5 | 537 | 1 | P2Y8_XENLA  |
| 73  | 50.5 | 40.1 | 522 | 1 | NFF2_HUMAN  |
| 74  | 50   | 39.7 | 350 | 1 | CKRB_BOVIN  |
| 75  | 50   | 39.7 | 350 | 1 | CKRB_HUMAN  |
| 76  | 50   | 39.7 | 359 | 1 | IL8B_MOUSE  |
| 77  | 50   | 39.7 | 371 | 1 | NY6R_MOUSE  |
| 78  | 50   | 39.7 | 389 | 1 | UR2R_HUMAN  |
| 79  | 49.5 | 39.3 | 359 | 1 | AG2R_CHICK  |
| 80  | 49.5 | 39.3 | 359 | 1 | AG2R_MELGA  |
| 81  | 49   | 38.9 | 349 | 1 | IL8A_RAT    |
| 82  | 49   | 38.9 | 362 | 1 | CKRA_HUMAN  |
| 83  | 49   | 38.9 | 367 | 1 | CCR3_MOUSE  |
| 84  | 49   | 38.9 | 398 | 1 | OPRM_MOUSE  |
| 85  | 49   | 38.9 | 425 | 1 | PAR1_HUMAN  |
| 86  | 49   | 38.9 | 425 | 1 | PAR1_PAPHA  |
| 87  | 49   | 38.9 | 428 | 1 | PAR1_CRILLO |
| 88  | 48.5 | 38.5 | 337 | 1 | OPSK_MOUSE  |
| 89  | 48.5 | 38.5 | 383 | 1 | CYB_CALCR   |
| 90  | 48   | 38.1 | 345 | 1 | C5AR_CAVPO  |
| 91  | 48   | 38.1 | 352 | 1 | CCR4_CERTO  |
| 92  | 48   | 38.1 | 352 | 1 | CCR4_HUMAN  |
| 93  | 48   | 38.1 | 352 | 1 | CCR4_MACFA  |
| 94  | 48   | 38.1 | 352 | 1 | CCR4_MACMU  |
| 95  | 48   | 38.1 | 352 | 1 | CCR4_PAPAN  |
| 96  | 48   | 38.1 | 382 | 1 | CCR4_MOUSE  |
| 97  | 48   | 38.1 | 397 | 1 | PAR2_RAT    |
| 98  | 48   | 38.1 | 409 | 1 | YOE6_ECOLI  |
| 99  | 48   | 38.1 | 420 | 1 | PAR1_XENLA  |
| 100 | 48   | 38.1 | 482 | 1 | CJAR_HUMAN  |

ALIGNMENTS

RESULT 1

Fri Mar 5 14:59:14 2004

```

CRK5 CERAE
ID CRK5 CERAE STANDARD; PRT; 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CRK5 OR CMKR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
RX MEDLINE=98001387; PubMed=9343222;
RC TISSUE=Kidney;
RA Kuhlmann S.E., Platt E.J., Korak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
RT implicate specific amino acids in infections by simian and human
RT immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor
RT gene.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U83324; AAC51795.1; -.
CC EMBL; U83325; AAC51796.1; -.
CC EMBL; AB015944; BAA31328.1; -.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPT_F2_1; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;
KW Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15

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FT VARIANT 14 14 N -> Y.
FT VARIANT 352 352 F -> L.
SQ SEQUENCE 352 AA; 40561 MW; 7F52B690C72EC29A CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 1 QMDPGNTMCQLLTGLYFIFGFS 22
Db 93 QMDPGNTMCQLLTGLYFIFGFS 114

RESULT 2
CRK5 CERPY
ID CRK5 CERPY STANDARD; PRT; 352 AA.
AC Q9TV42;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CRK5 OR CMKR5.
OS Cercopithecus pygerythrus (Vervet monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
NCBI_TaxID=60710;
RX MEDLINE=99335215; PubMed=10408730;
RC STRAIN=100;
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,
RT Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;
RT "Mutations in CCR5-coding sequences are not associated with SIV
RT carrier status in African nonhuman primates.";
RT AIDS Res. Hum. Retroviruses 15:931-939(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF035222; AAD44015.1; -.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G-PROTEIN RECEPT_F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPT_F2_1; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW Polymorphism.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).

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FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;  
 Query Match 100.0%; Score 126; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTMCLLTGLYFIFGFS 22  
 DB 93 QWDFGNTMCLLTGLYFIFGFS 114  
 RESULT 3  
 CKR5 CERTO STANDARD; PRT; 352 AA.  
 ID Q62743; Q62744; Q62745; Q62746;  
 AC Q62743; Q62744; Q62745; Q62746;  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN Cercobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OS Cercobus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecidae;  
 OC NCBI\_TaxID=9531;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Isolate 079, 085, 087, and 089;  
 RX MEDLINE=98321155; PubMed=9656999;  
 RA Chen Z., Gettie A., Ho D.D., Marx P.A.;  
 RT "Primary HIV isolates use the CCR5 coreceptor from sooty mangabeys  
 naturally infected in west Africa: a comparison of coreceptor usage  
 of primary HIV-1, HIV-2, and SIVmac.";  
 RL Virology 246:113-124 (1998).  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 increasing the intracellular calcium ions level. May play a role  
 in the control of granulocytic lineage proliferation or  
 differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; AF051902; AAC39830.1; -  
 CC EMBL; AF051903; AAC39831.1; -  
 CC EMBL; AF051904; AAC39832.1; -  
 CC EMBL; AF051905; AAC39833.1; -  
 CC InterPro: IPR000276; GPCR\_Rhodpsn.  
 CC Pfam: PF00001; 7tm.1; 1.  
 CC PRINTS; PR00237; GPCR\_Rhodpsn.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 CC PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).  
 FT VARIANT 2 2 D -> E (IN ISOLATE 087).  
 FT VARIANT 3 3 Y -> D (IN ISOLATE 079).  
 FT VARIANT 25 25 V -> G (IN ISOLATE 087).  
 FT VARIANT 100 100 M -> K (IN ISOLATE 079).  
 FT VARIANT 107 107 L -> V (IN ISOLATE 089).  
 FT VARIANT 134 134 V -> G (IN ISOLATE 079).  
 FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).  
 FT VARIANT 340 340 T -> I (IN ISOLATE 079).  
 SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;  
 Query Match 100.0%; Score 126; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTMCLLTGLYFIFGFS 22  
 DB 93 QWDFGNTMCLLTGLYFIFGFS 114  
 RESULT 4  
 CKR5 GORGO STANDARD; PRT; 352 AA.  
 ID CKR5 GORGO STANDARD; PRT; 352 AA.  
 AC P56439;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN Gorilla gorilla gorilla (Lowland gorilla).  
 OS Gorilla gorilla gorilla (Lowland gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 OC NCBI\_TaxID=9595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Feiler S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 simian immunodeficiency virus strains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 MIP-1-beta and RANTES and subsequently transduces a signal by  
 increasing the intracellular calcium ions level. May play a role  
 in the control of granulocytic lineage proliferation or  
 differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; AF005659; AAB62553.1; -  
 CC InterPro: IPR000276; GPCR\_Rhodpsn.  
 CC Pfam: PF00001; 7tm.1; 1.  
 CC PRINTS; PR00237; GPCR\_Rhodpsn.

DR PROSITE; P500237; G PROTEIN RECEPTOR FL 1; 1.  
DR PROSITE; P500262; G PROTEIN RECEPTOR FL 2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 59 68  
FT TRANSMEM 69 89  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 103 124  
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 142 166  
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 199 218  
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 236 260  
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 278 301  
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 101 178 BY SIMILARITY.  
FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
FT MOD RES 15 15 SULFATION (BY SIMILARITY).  
SQ SEQUENCE 352 AA; 40515 MW; D056FCB9PE5EAC84 CRC64;  
  
Query Match 100.0%; Score 126; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QWDFGNTMQLLTGLYFIFGFS 22  
DB 93 QWDFGNTMQLLTGLYFIFGFS 114  
  
RESULT 5  
CXRS HUMAN STANDARD; PRT; 352 AA.  
ID CXRS HUMAN STANDARD; PRT; 352 AA.  
AC P51681; O14692; O14693; O14696; O14697; O14698; O14699;  
AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;  
AC O14708; O15538; Q9UPA4;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)  
DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).  
DE CCR5 OR CMKR5.  
GN Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
RX MEDLINE-96241590; PubMed=8639485;  
RX Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;  
RT "Molecular cloning and functional expression of a novel human  
RT CC chemokine receptor gene";  
RL Biochemistry 35:3362-3367(1996).  
[2]  
SEQUENCE FROM N.A.  
RX MEDLINE-96291862; PubMed=8663314;  
RX Report C.J., Goeling J., Schweichart V.L., Gray P.W., Charo I.F.;  
RT "Molecular cloning and functional characterization of a novel human  
RT CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha";  
RL J. Biol. Chem. 271:17161-17166(1996).  
[3]  
SEQUENCE FROM N.A.  
RX MEDLINE-96295970; PubMed=8699119;  
RX Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;  
RT "Cloning and functional expression of CC CKR5, a human monocyte CC  
RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and  
RT RANTES";  
RL J. Leukoc. Biol. 60:147-152(1996).  
[4]

RP SEQUENCE FROM N.A.  
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,  
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,  
RA Porcel B.M., Dragan Y., Giacalone J., Fae A., Powell E.,  
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,  
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
[5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-98001387; PubMed=9343222;  
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
RT "polymorphisms in the CCR5 genes of African green monkeys and mice  
RT implicate specific amino acids in infections by simian and human  
RT immunodeficiency viruses";  
RL J. Virol. 71:8642-8656(1997).  
[6]  
RP SEQUENCE FROM N.A., AND POLYMORPHISMS.  
RX MEDLINE-98022612; PubMed=9359654;  
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
RA Ho D.D.;  
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";  
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
[7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-98049523; PubMed=9388201;  
RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;  
RT "The human C-C chemokine receptor 5 (CCR5) gene. Multiple transcripts  
RT with 5'-end heterogeneity, dual promoter usage, and evidence for  
RT polymorphisms within the regulatory regions and noncoding exons";  
RL J. Biol. Chem. 272:30662-30671(1997).  
[8]  
RP SEQUENCE FROM N.A., AND VARIANT ARG-178.  
RA Magierowska M., Barre-Sinoussi F., Isafras H., Theodorou I.,  
RA Debre P.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
[9]  
RP SEQUENCE FROM N.A.  
RX Kopatz S.A., Aronstam R.S., Sharma S.V.;  
RT "cDNA clones of human proteins involved in signal transduction  
RT sequenced by the Guthrie cDNA resource center (www.cdna.org)";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
[10]  
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
RX MEDLINE-96260017; PubMed=8649511;  
RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,  
RA di Marzio P., Broder C., Spector R.E., Hill C.M., Davis C.B.,  
RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;  
RT "Identification of a major co-receptor for primary isolates of  
RT HIV-1";  
RL Nature 381:661-666(1996).  
[11]  
RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
RX MEDLINE-96260018; PubMed=8649512;  
RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,  
RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,  
RA Paxton W.A.;  
RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor  
RT CC-CKR-5";  
RL Nature 381:667-673(1996).  
[12]  
RP SULFATION.  
RX MEDLINE-99189752; PubMed=10089882;  
RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,  
RA Gerard N.P., Gerard C., Sodroski J., Choe H.;  
RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1  
RT entry";  
RL Cell 96:667-676(1999).  
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
CC MIP-1-beta and rantes and subsequently transduces a signal by  
CC increasing the intracellular calcium ions level. May play a role  
CC in the control of granulocytic lineage proliferation or  
CC

differentiation. Acts as co-receptor with CD4 for primary non-syngonium-inducing strains (NSI) (macrophage-tropic) of HIV-1 virus. It promotes Env-mediated fusion of the virus.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- TISSUE SPECIFICITY: Found in promyelocytic cells.

-1- PTM: Sulfation contributes to the efficiency of HIV-1 entry.

-1- PTM: Modified by O-linked glycosylation, but not by N-linked glycosylation.

-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; X91492; CRA62796.1; -  
EMBL; U54994; AAC50598.1; -  
EMBL; U57840; AAB17071.1; -  
EMBL; U95626; AAB57793.1; -  
EMBL; U83326; AAC51797.1; -  
EMBL; AF011500; AAB65700.1; -  
EMBL; AF011501; AAB65701.1; -  
EMBL; AF011502; AAB65702.1; -  
EMBL; AF011503; AAB65703.1; -  
EMBL; AF011505; AAB65705.1; -  
EMBL; AF011506; AAB65706.1; -  
EMBL; AF011507; AAB65707.1; -  
EMBL; AF011508; AAB65708.1; -  
EMBL; AF011509; AAB65709.1; -  
EMBL; AF011510; AAB65710.1; -  
EMBL; AF011511; AAB65711.1; -  
EMBL; AF011512; AAB65712.1; -  
EMBL; AF011513; AAB65713.1; -  
EMBL; AF011514; AAB65714.1; -  
EMBL; AF011515; AAB65715.1; -  
EMBL; AF011516; AAB65716.1; -  
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EMBL; AF011520; AAB65720.1; -  
EMBL; AF011521; AAB65721.1; -  
EMBL; AF011522; AAB65722.1; -  
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EMBL; AF011524; AAB65724.1; -  
EMBL; AF011525; AAB65725.1; -  
EMBL; AF011526; AAB65726.1; -  
EMBL; AF011527; AAB65727.1; -  
EMBL; AF011528; AAB65728.1; -  
EMBL; AF011529; AAB65729.1; -  
EMBL; AF011530; AAB65730.1; -  
EMBL; AF011531; AAB65731.1; -  
EMBL; AF011532; AAB65732.1; -  
EMBL; AF011533; AAB65733.1; -  
EMBL; AF011534; AAB65734.1; -  
EMBL; AF011535; AAB65735.1; -  
EMBL; AF011536; AAB65736.1; -  
EMBL; AF011537; AAB65737.1; -  
EMBL; AF011538; AAB65738.1; -  
EMBL; AF011539; AAB65739.1; -  
EMBL; AY221093; AAB65971.1; -  
GenBank; U000000000; CCR5.

MIM; 601373; - C-Endosome; TAS.

GO; GO:0005768; C-integral to plasma membrane; TAS.

GO; GO:0005887; F-C-C chemokine receptor activity; NAS.

GO; GO:0016493; F-C-C chemokine receptor activity; NAS.

GO; GO:0007267; P-cell-cell signaling; TAS.

GO; GO:0006968; P-cell-cell defense response; TAS.

GO; GO:0006935; P-chemotaxis; TAS.

GO; GO:0007204; P-cytosolic calcium ion concentration elevation; TAS.

DR GO:0007186; P-G-protein coupled receptor protein signalin. . . ; TAS.  
DR GO:0006954; P-inflammatory response; TAS.  
DR GO:0007125; P-invasive growth; TAS.  
DR GO:0007203; P-phosphatidylinositol-4,5-bisphosphate hydro. . . ; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PROSITE; PS00237; G-PROTEIN RECP Fl 1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECP Fl 2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
KW Polymorphism. 1 30 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 31 58 1 (POTENTIAL).  
FT TRANSMEM 59 68 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 69 89 2 (POTENTIAL).  
FT TRANSMEM 90 102 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 103 124 3 (POTENTIAL).  
FT TRANSMEM 125 144 4 (POTENTIAL).  
Query Match 100.0%; Score 126; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1e-11; 0; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QMDFGNTMCLLTGLYFIFGFS 22  
DB 93 QMDFGNTMCLLTGLYFIFGFS 114  
RESULT 6  
ID CCR5\_HYLL STANDARD; PRT; 352 AA.  
AC 097883;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
DE CCR5 OR CXCR5.  
OS Hylobates leucogenys (White-cheeked gibbon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.  
OX NCBI\_TaxID=61853;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99416438; PubMed=10486970;  
RZ Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";  
RL Mol. Biol. Evol. 16:1145-1154(1999).  
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
CC MIP-1-beta and RANTES and subsequently transduces a signal by  
CC increasing the intracellular calcium ions level. May play a role  
CC in the control of granulocytic lineage proliferation or  
CC differentiation.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

Fri Mar 5 14:59:14 2004

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FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 7 (POTENTIAL).
FT TRANSMEM 236 260 8 (POTENTIAL).
FT DOMAIN 261 277 9 (POTENTIAL).
FT TRANSMEM 278 301 10 (POTENTIAL).
FT DOMAIN 302 352 11 (POTENTIAL).
FT DISULFID 101 178 12 (POTENTIAL).
FT MOD RES 3 3 13 (POTENTIAL).
FT MOD RES 10 10 14 (POTENTIAL).
FT MOD RES 14 14 15 (POTENTIAL).
SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DQ 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 7
CKR5_HYLM L STANDARD; PRT; 352 AA.
AC Q95NC0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Hylobates moloch (Silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF177899; AAK43382.1; -.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm1.1;
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1 1; 1.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1 2; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR; Transmembrane; Glycoprotein; Sulfation.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 7 (POTENTIAL).
FT TRANSMEM 236 260 8 (POTENTIAL).
FT DOMAIN 261 277 9 (POTENTIAL).
FT TRANSMEM 278 301 10 (POTENTIAL).
FT DOMAIN 302 352 11 (POTENTIAL).
FT DISULFID 101 178 12 (POTENTIAL).
FT MOD RES 3 3 13 (POTENTIAL).
FT MOD RES 10 10 14 (POTENTIAL).
FT MOD RES 14 14 15 (POTENTIAL).
SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DQ 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 8
CKR5_HYLS Y STANDARD; PRT; 352 AA.
AC Q95NC5;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF177884; AAK43367.1; -.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm1.1;
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1 1; 1.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1 2; 1.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR; Transmembrane; Glycoprotein; Sulfation.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).

```

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 199 218 5 (POTENTIAL).

FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 236 260 6 (POTENTIAL).

FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 278 301 7 (POTENTIAL).

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.

FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).

FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).

FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).

SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF58A CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 1e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIFGFFS 22

Db 93 QWDFGNTMCLLTGLYFIFGFFS 114

RESULT 9

CKR5 MACMU STANDARD; PRT; 352 AA.

AC P79436; O02746;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

GN CKR5 OR CXCR5.

OS Macaca mulatta (Rhesus macaque),

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and

OS Macaca nemestrina (Pig-tailed macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.

OX NCBI\_TaxID=9544; 9541, 9545;

[1] SEQUENCE FROM N.A.

RP SPECIES=M.mulatta;

RX MEDLINE=97184592; PubMed=9032394;

RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,

RA Newman W., Gerard N., Gerard C., Sodroski J.;

RT "Utilization of C-C chemokine receptor 5 by the envelope

RT glycoproteins of a pathogenic simian immunodeficiency virus,

RT SIVmac239.";

RL J. Virol. 71:2522-2527 (1997).

[2] SEQUENCE FROM N.A.

RP SPECIES=M.mulatta;

RX MEDLINE=97213934; PubMed=9060623;

RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;

RA "Genetically divergent strains of simian immunodeficiency virus use

RT CCR5 as a coreceptor for entry.";

RL J. Virol. 71:2705-2714 (1997).

[3] SEQUENCE FROM N.A.

RP SPECIES=M.mulatta;

RX MEDLINE=21354176; PubMed=11461684;

RA Margulies B.J., Hauer D.A., Clements J.E.;

RA "Identification and comparison of eleven rhesus macaque chemokine

RT receptors.";

RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).

[4] SEQUENCE FROM N.A.

RP SPECIES=M.mulatta;

RX MEDLINE=97268687; PubMed=9108095;

RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,

RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,

RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;

RT "Differential utilization of CCR5 by macrophage and T cell tropic

RT simian immunodeficiency virus strains.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).

CC 1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role

CC in the control of granulocytic lineage proliferation or

CC differentiation.

CC 1- SUBCELLULAR LOCATION: Integral membrane protein.

CC 1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC

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CC

EMBL; U77672; AAC511109.1; -

EMBL; U73739; AAC511158.1; -

EMBL; U6762; AAC34132.1; -

EMBL; AF005660; AAB62554.1; -

EMBL; AF005661; AAB62555.1; -

EMBL; AF005662; AAB62556.1; -

DR InterPro; IPR00276; GPCR\_Rhodpsn.

DR Pfam; PF00001; 7tm1.1;

DR PRINTS; PR00237; GPCRHOPOPSN.

DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.

DR PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 31 58 1 (POTENTIAL).

FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).

FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 142 166 4 (POTENTIAL).

FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 199 218 5 (POTENTIAL).

FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 236 260 6 (POTENTIAL).

FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 278 301 7 (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.

FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).

FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).

FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).

FT CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 241 241 M -> I (IN REF. 3).

FT CONFLICT 292 292 I -> M (IN REF. 3).

SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 1e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCLLTGLYFIFGFFS 22

Db 93 QWDFGNTMCLLTGLYFIFGFFS 114

RESULT 10

CKR5 PANTR STANDARD; PRT; 352 AA.

AC P56440; O02778;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

GN CCR5 OR CMKR5.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=97268687; PubMed=9108095;  
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,  
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
RT "Differential utilization of CCR5 by macrophage and T cell tropic  
RT simian immunodeficiency virus strains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX Zimmerman P.A., Ruckler-White A., Alkhatib G.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=98022612; PubMed=9359654;  
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
RA Ho D.D.;  
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";  
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
RN [4]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=97426118; PubMed=9282822;  
RA Zacharova V., Zachar V., Goustin A.S.;  
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural  
RT HIV type 1 host.";  
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).  
RN [5]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=98090115; PubMed=9430250;  
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;  
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";  
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).  
RN [6]  
RN SEQUENCE FROM N.A.  
RA Zhang Y., Ryder O.A., Zhang Y.;  
RT "Sequence comparison of the CCR5 gene in primates and primate  
RT phylogeny.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
CC MIP-1-beta and RANTES and subsequently transduces a signal by  
CC increasing the intracellular calcium ions level. May play a role  
CC in the control of granulocytic lineage proliferation or  
CC differentiation.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF005663; AAB62557.1; -  
CC EMBL; U94329; AAB58446.1; -  
CC EMBL; AF011542; AAB65742.1; -  
CC EMBL; U97666; AAC51670.1; -  
CC EMBL; AF011540; AAB65740.1; -  
CC EMBL; U97979; AAC03717.1; -  
CC EMBL; AF177894; AAK43377.1; -  
CC InterPro: IPR000276; GPCR\_Rhodopsin.  
CC Pfam: PF00001; 7tm\_1; 1.  
CC PRINTS; PR00237; GPCR\_RHODOPSIN.  
CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.  
CC PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
KW

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 69 89 2 (POTENTIAL).  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 103 124 3 (POTENTIAL).  
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 142 166 4 (POTENTIAL).  
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 199 218 5 (POTENTIAL).  
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 236 260 6 (POTENTIAL).  
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 278 301 7 (POTENTIAL).  
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 101 178 BY SIMILARITY.  
FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
FT MOD RES 15 15 SULFATION (BY SIMILARITY).  
FT CAREOXYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 123 123 T -> S (IN REF. 1).  
SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. le-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFS 22  
DB 93 QWDFGNTMCLLTGLYFIFGFS 114

RESULT 11  
CCRS PAPA  
ID CCR5 PAPA STANDARD; PRT; 352 AA.  
AC P56441;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
GN CCR5 OR CMKR5.  
OS Papio hamadryas (Hamadryas baboon), and  
OS Papio anubis (Olive baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Papio.  
OX NCBI\_TaxID=9557, 9555;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC SPECIES=P.hamadryas;  
RX MEDLINE=97268687; PubMed=9108095;  
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphey-Corb M.,  
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
RT "Differential utilization of CCR5 by macrophage and T cell tropic  
RT simian immunodeficiency virus strains.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
RN [2]  
RN SEQUENCE FROM N.A.  
RC SPECIES=P.hamadryas;  
RX MEDLINE=99210133; PubMed=10195758;  
RA Sakseena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;  
RT "Species-specific changes in the CCR5 gene from African and Asian  
RT nonhuman primates.";  
RL AIDS Res. Hum. Retroviruses 15:479-483(1999).  
RN [3]  
RN SEQUENCE FROM N.A.  
RC SPECIES=P.anubis;  
RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
CC MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF005658; AAB62552.1; -  
 DR EMBL; AF105287; AAD20556.1; -  
 DR EMBL; AF105288; AAD20557.1; -  
 DR EMBL; AF105289; AAD20558.1; -  
 DR EMBL; AF105290; AAD20559.1; -  
 DR EMBL; AF023452; AAC63830.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PRO0237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT TRANSMEM 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 7 (POTENTIAL).  
 FT TRANSMEM 278 301 8 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).  
 FT CARBOHYD 268 268 N-LINKED (GLCNAC..). (POTENTIAL).  
 SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE8B2 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1e-11; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22  
 |||||  
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 12  
 CRR5\_PONPY  
 ID\_CRR5\_PONPY STANDARD; PRT; 352 AA.  
 AC O97881;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKBR5.  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.  
 OC NCBI\_TaxID=9600;  
 RN [1]  
 RP SEQUENCE FROM N.A.

MEDLINE-99416438; PubMed-10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";  
 RL Mol. Biol. Evol. 16:1145-1154 (1999).  
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF075446; AAD19858.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PRO0237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT TRANSMEM 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 7 (POTENTIAL).  
 FT TRANSMEM 278 301 8 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1e-11; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22  
 |||||  
 DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 13  
 CRR5\_PYGBI  
 ID\_CRR5\_PYGBI STANDARD; PRT; 352 AA.  
 AC O97880;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKBR5.  
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Pygathrix.  
 OC NCBI\_TaxID=61621;  
 RN [1]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075445; AAD19857.1; -.
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 142 166 4 (POTENTIAL).
CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 199 218 5 (POTENTIAL).
CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 236 260 6 (POTENTIAL).
CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 278 301 7 (POTENTIAL).
CC DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
CC DISULFID 101 178 BY SIMILARITY.
CC MOD RES 3 3 SULFATION (BY SIMILARITY).
CC MOD RES 10 10 SULFATION (BY SIMILARITY).
CC MOD RES 14 14 SULFATION (BY SIMILARITY).
CC MOD RES 15 15 SULFATION (BY SIMILARITY).
CC SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 14
CKR5_PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKRS5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OC NCBI_TaxID=54133;

```

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RN SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075448; AAD19860.1; -.
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 31 58 1 (POTENTIAL).
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 69 89 2 (POTENTIAL).
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 103 124 3 (POTENTIAL).
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 142 166 4 (POTENTIAL).
CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 199 218 5 (POTENTIAL).
CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 236 260 6 (POTENTIAL).
CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 278 301 7 (POTENTIAL).
CC DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
CC DISULFID 101 178 BY SIMILARITY.
CC MOD RES 3 3 SULFATION (BY SIMILARITY).
CC MOD RES 10 10 SULFATION (BY SIMILARITY).
CC MOD RES 14 14 SULFATION (BY SIMILARITY).
CC MOD RES 15 15 SULFATION (BY SIMILARITY).
CC SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B861 CRC64;

Query Match 100.0%; Score 126; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFFS 22
DB 93 QWDFGNTMCQLLTGLYFIFGFFS 114

RESULT 15
CKR5_TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKRS5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.

```



OK NCBI\_TaxID=54180;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL: AF075442; AAD19854.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPSN.  
 DR PROSITE: PS00237; G-PROTEIN RECF\_F1\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN RECF\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;  
 Query Match 100.0%; Score 126; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTWCQLLTGLYFGFFS 22  
 Db 93 QWDFGNTWCQLLTGLYFGFFS 114  
 RESULT 16  
 ID -CKR5 TRAPH STANDARD; PRT; 352 AA.  
 AC O97879;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C-CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKBR5.  
 OS Trachypithecus phayrei (Phayre's leaf monkey).  
 NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;

Trachypithecus.  
 NCBI\_TaxID=61618;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL: AF075443; AAD19855.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODOPSN.  
 DR PROSITE: PS00237; G-PROTEIN RECF\_F1\_1; 1.  
 DR PROSITE: PS00262; G-PROTEIN RECF\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;  
 Query Match 100.0%; Score 126; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTWCQLLTGLYFGFFS 22  
 Db 93 QWDFGNTWCQLLTGLYFGFFS 114  
 RESULT 17  
 ID -CKR8 MOUSE STANDARD; PRT; 353 AA.  
 AC P56484;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 8 (C-C-CKR-8) (CCR-8).  
 GN CCR8 OR CMKBR8 OR TERL.  
 OS Mus musculus (Mouse).  
 NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zaballos A., Goya I.I., Gutierrez J., Varona R., Marquez G.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=98334001; PubMed=9670926;
RA Zingoni A., Soto H., Hedrick J.A., Stoppacciaro A., Storlazzi C.T.,
RA Sinigaglia F., D'Ambrosio D., O'Garra A., Robinson D., Rocchi M.,
RA Santoni A., Zlotnick A., Nepolitano M.;
RT "The chemokine receptor CCR8 is preferentially expressed in Th2 but
RT not Th1 cells.";
RL J. Immunol. 161:547-551(1998).
CC -!- FUNCTION: Receptor for the TCA-3 chemokine.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL: Z98206; CAB10896.1; --
DR DR EMBL: Z98205; CAB10895.1; --
DR DR EMBL: AF001277; AAC97598.1; --
DR DR MGD; MGI:1201402; Ccr8.
DR DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
DR DR GO; GO:0005515; F:protein binding; IPI.
DR DR GO; GO:0006935; P:chemotaxis; IDA.
DR DR InterPro; IPR004068; CC 8 receptor.
DR DR InterPro; IPR002276; GPCR_Rhodopsn.
DR DR Pfam; PF00001; 7tm1.1; 1.
DR DR PRINTS; PR01530; CHEMOKINERS.
DR DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR DR PROSITE; PS00237; G PROTEIN RECP FL1; 1.
DR DR PROSITE; PS00262; G PROTEIN RECP FL2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 61 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 62 71 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 72 91 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 92 105 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 106 127 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 128 144 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 145 169 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 170 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 220 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 221 236 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 237 261 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 262 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 302 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 303 353 BY SIMILARITY.
FT DISULFID 8 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 8
SQ SEQUENCE 353 AA; 40045 MW; 31EC4B642CDB9A5 CRC64;
Query Match 70.6%; Score 89; DB 1; Length 353;
Best Local Similarity 63.6%; Pred. No. 4e-06;
Matches 14; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
QY 1 QWDEGNTWCQLLYGFIQFFS 22
DB 96 QWVFGTAMKVVSLYIGFFS 117
RESULT 18
CCR2_HUMAN

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ID CCR2_HUMAN STANDARD; PRT; 374 AA.
AC P41597;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).
DE CCR2 OR CCR2B.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=94195821; PubMed=8146186;
RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,
RA Coughlin S.R.;
RT "Molecular cloning and functional expression of two monocyte
RT chemoattractant protein 1 receptors reveals alternative splicing of
RT the carboxyl-terminal tails.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756 (1994).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=94324942; PubMed=8048929;
RA Yamagami S., Tokuda Y., Ishii K., Tanaka H., Endo N.;
RT "cDNA cloning and functional expression of a human monocyte
RT chemoattractant protein 1 receptor.";
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=97150864; PubMed=8995400;
RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;
RT "Organization and differential expression of the human monocyte
RT chemoattractant protein 1 receptor gene. Evidence for the role of the
RT carboxyl-terminal tail in receptor trafficking.";
RL J. Biol. Chem. 272:1038-1045(1997).
RN [4]
RN SEQUENCE FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Guoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,
RA Porcel B.M., Dragan Y., Giacalone J., Rae A., Powell E.,
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A. AND VARIANTS ILE.64 AND GLU-355.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RN SULFATION OF TYR-26, AND N-GLYCOSYLATION.
RX MEDLINE=20501139; PubMed=11045064;
RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,
RA Chakravarty L., Kolatukudy P.B.;
RT "Monocyte chemoattractant protein-1 receptor CCR2B is a glycoprotein that
RT has tyrosine sulfation in a conserved extracellular N-terminal
RT region.";
RL J. Immunol. 165:5295-5303(2000).
CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.
CC Transduces a signal by increasing the intracellular calcium ions
CC level. Alternative coreceptor with CD4 for HIV-1 infection.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=A;
CC IsoId=P41597-1; Sequence=Displayed;
CC Name=B;
CC IsoId=P41597-2; Sequence=VSP_001893;
CC -!- PTM: N-glycosylated.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC

```

[illegible]

1 QMDPFGNTMCLLTGLTGLYFIFGF 21  
: ||| ||| ||| ||| ||| ||| :  
105 ENWFGNACMLTGLYHGVF 125

Db

Query Match  
Best Local Similarity 68.3%; Score 86; DB 1; Length 373;  
Pred. No. 1.2e-05;  
Mismatches 4; Indels 0; Gaps 0;

RESULT 19

| ID | CKR2 RAT                                                                                                                 | STANDARD; | PRT; | 373 AA. |
|----|--------------------------------------------------------------------------------------------------------------------------|-----------|------|---------|
| AC | 055193;                                                                                                                  |           |      |         |
| DT | 16-OCT-2001 (Rel. 40, Created)                                                                                           |           |      |         |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update)                                                                              |           |      |         |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update)                                                                            |           |      |         |
| DE | C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)                                                                    |           |      |         |
| GN | CCR2 OR CMKR2.                                                                                                           |           |      |         |
| OS | Rattus norvegicus (Rat).                                                                                                 |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                                                        |           |      |         |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.                                                    |           |      |         |
| OR | NCBI_TaxID=10116;                                                                                                        |           |      |         |
| RN | [1]                                                                                                                      |           |      |         |
| RP | SEQUENCE FROM N.A.                                                                                                       |           |      |         |
| RC | STRAIN=Sprague-Dawley;                                                                                                   |           |      |         |
| RC | MEDLINE=93318173; PubMed=9655467;                                                                                        |           |      |         |
| RA | Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,                                                      |           |      |         |
| RA | deribe C.M., Pennell N.A., Streit W.J., Harrison J.K.;                                                                   |           |      |         |
| RT | "Chemokine receptor expression in cultured glia and rat experimental                                                     |           |      |         |
| RT | allergic encephalomyelitis.;"                                                                                            |           |      |         |
| RL | J. Neuroimmunol. 86:1-12(1998).                                                                                          |           |      |         |
| CC | -1- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (PIC) and MCP-5                                                         |           |      |         |
| CC | chemokines. Transduces a signal by increasing the intracellular                                                          |           |      |         |
| CC | calcium ions level (By similarity).                                                                                      |           |      |         |
| CC | -1- SUBCELLULAR LOCATION: Integral membrane protein.                                                                     |           |      |         |
| CC | -1- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and                                                    |           |      |         |
| CC | macrophages.                                                                                                             |           |      |         |
| CC | -1- INDUCTION: In animals in which experimental allergic                                                                 |           |      |         |
| CC | encephalomyelitis (EAE) has been induced.                                                                                |           |      |         |
| CC | -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.                                                      |           |      |         |
| CC |                                                                                                                          |           |      |         |
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| CC | use by non-profit institutions as long as its content is in no way                                                       |           |      |         |
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| CC | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).                                        |           |      |         |
| CC |                                                                                                                          |           |      |         |
| DR | EMBL: U77349; AAC03242.1; -                                                                                              |           |      |         |
| DR | InterPro: IPR000276; GPCR_Rhodpsn.                                                                                       |           |      |         |
| DR | Pfam: PF00001; 7tm_1; 1.                                                                                                 |           |      |         |
| DR | PRINTS; PRO0237; GPCRHOOPS.                                                                                              |           |      |         |
| DR | PROSITE; PS00237; G PROTEIN RECP Fl.1; 1.                                                                                |           |      |         |
| DR | PROSITE; PS00262; G PROTEIN RECP Fl.2; 1.                                                                                |           |      |         |
| KW | G-protein coupled receptor; Transmembrane.                                                                               |           |      |         |
| FT | DOMAIN 1 60                                                                                                              |           |      |         |
| FT | TRANSMEM 61 81                                                                                                           |           |      |         |
| FT | DOMAIN 82 91                                                                                                             |           |      |         |
| FT | TRANSMEM 92 112                                                                                                          |           |      |         |
| FT | DOMAIN 113 128                                                                                                           |           |      |         |
| FT | TRANSMEM 129 149                                                                                                         |           |      |         |
| FT | DOMAIN 150 170                                                                                                           |           |      |         |
| FT | TRANSMEM 171 191                                                                                                         |           |      |         |
| FT | DOMAIN 192 220                                                                                                           |           |      |         |
| FT | TRANSMEM 221 241                                                                                                         |           |      |         |
| FT | DOMAIN 242 256                                                                                                           |           |      |         |
| FT | TRANSMEM 257 277                                                                                                         |           |      |         |
| FT | DOMAIN 278 301                                                                                                           |           |      |         |
| FT | TRANSMEM 302 322                                                                                                         |           |      |         |
| FT | DOMAIN 323 373                                                                                                           |           |      |         |
| FT | DISULFID 126 203                                                                                                         |           |      |         |
| FT | SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;                                                                       |           |      |         |

|                       |       |                    |       |             |
|-----------------------|-------|--------------------|-------|-------------|
| Query Match           | 68.3% | Score 86;          | DB 1; | Length 373; |
| Best Local Similarity | 66.7% | Pred. No. 1.2e-05; |       |             |
| 3. Mismatches         | 4.    | Indels             | 0:    | Gaps 0;     |

```
QY 1 QWDFGNTMCCLLTGLYFIFGFF 21
DB 118 EWVFGNIMCKLFTGLYHIGVF 138

RESULT 20
ID CKR5 RAT STANDARD; PRT; 354 AA.
AC O08556;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
DE CCR5 OR CWKBR5.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Brain;
RX MEDLINE=98334064; PubMed=9670989;
RA Speleiss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,
RA Berger M., Gebicke-Haerter P.J.;
RT "Cloning of rat HIV-1-chemokine coreceptor CKR5 from microglia and
RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";
RL J. Neurosci. Res. 53:16-28(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
RA Defiebre C.M., Pennell N.A., Streif W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis";
RL J. Neuroimmunol. 86:1-12(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; Y12009; AAC72737.1; -
CC DR EMBL; U77350; AAC03243.1; -
CC DR InterPro; IPR000276; GPCR_Rhodopn.
CC DR Pfam; PF00001; 7tm.1; 1.
CC DR PRINTS; PR00237; GPCRHHODOPSN.
CC DR PROSITE; PS00237; G PROTEIN RECF F1 1; 1.
CC DR PROSITE; PS0262; G PROTEIN RECF F1 2; 1.
CC DR G-protein coupled receptor; Transmembrane; Glycoprotein.
CC KW DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 1 32
CC FT TRANSMEM 33 60
CC FT DOMAIN 61 70
CC FT TRANSMEM 71 91
CC FT DOMAIN 92 104
CC FT TRANSMEM 105 126
CC FT DOMAIN 127 143
CC FT TRANSMEM 144 168
CC FT DOMAIN 169 200
CC FT TRANSMEM 201 220
CC FT DOMAIN 221 237
CC FT TRANSMEM 238 262
CC FT DOMAIN 263 279

QY 1 QWDFGNTMCCLLTGLYFIFGFF 21
DB 95 EWVFGNIMCKLFTGLYHIGVF 115

RESULT 21
ID VC03 SPVKA STANDARD; PRT; 269 AA.
AC P32229;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE G-protein coupled receptor homolog C3.
DE C3L.
GN Swinepox virus (strain Kasza) (SPV).
OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Suipoxvirus.
OC NCBI_TaxID=10277;
OX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94069924; PubMed=8249275;
RA Massung R.F., Jayarama V., Moyer R.W.;
RT "DNA sequence analysis of conserved and unique regions of swinepox
RT virus: identification of genetic elements supporting phenotypic
RT observations including a novel G protein-coupled receptor
RT homologue.";
RL Virology 197:511-528(1993).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; L22013; AAC37868.1; -
CC DR InterPro; IPR000276; GPCR_Rhodopn.
CC DR Pfam; PF00001; 7tm.1; 1.
CC DR PRINTS; PR00237; GPCRHHODOPSN.
CC DR PROSITE; PS00237; G PROTEIN RECF F1 1; 1.
CC DR PROSITE; PS0262; G PROTEIN RECF F1 2; 1.
CC DR G-protein coupled receptor; Transmembrane.
CC KW SEQUENCE 269 AA; 31509 MW; CEL192CCAB999A3 CRC64;
CC SQ SEQUENCE 269 AA; 31509 MW; CEL192CCAB999A3 CRC64;

Query Match 65.9%; Score 83; DB 1; Length 269;
Best Local Similarity 54.5%; Pred. No. 2.4e-05;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 QWDFGNTMCCLLTGLYFIFGFF 22
DB 20 QWTFGNILCKIMSVLYVGVFF 41

RESULT 22
ID VK02 SPVKA STANDARD; PRT; 370 AA.
AC Q08520;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
```

DE G-protein coupled receptor homolog K2.  
GN K2R.  
OS Swinepox virus (strain Kasza) (SPV).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Suipoxvirus.  
OX NCBI\_TaxID=10277;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94069924; PubMed=8249275;  
RA Messing R.F., Jayarama V., Moyer R.W.;  
RT "DNA sequence analysis of conserved and unique regions of swinepox  
RT virus: identification of genetic elements supporting phenotypic  
RT observations including a novel G protein-coupled receptor  
RT homologue.";  
RL Virology 137:511-528(1993).  
CC -1- FUNCTION: Putative chemokine receptor.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC  
CC EMBL; L21931; AAC37873.1; -  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHOPOPSN.  
DR PROSITE; PS00237; G-PROTEIN RECF\_F1\_1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECF\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
FT DOMAIN 1 61  
FT TRANSSEM 62 82  
FT DOMAIN 83 94  
FT TRANSSEM 95 115  
FT DOMAIN 116 131  
FT TRANSSEM 132 152  
FT DOMAIN 153 171  
FT TRANSSEM 172 192  
FT DOMAIN 193 223  
FT TRANSSEM 224 244  
FT DOMAIN 245 265  
FT TRANSSEM 266 286  
FT DOMAIN 287 300  
FT TRANSSEM 301 321  
FT DOMAIN 322 370  
FT CARBOHYD 6 6  
FT CARBOHYD 51 51  
FT SEQUENCE 370 AA; 43171 MW; 76D08613327B0CC0 CRC64;  
SQ  
Query Match 65.9%; Score 83; DB 1; Length 370;  
Best Local Similarity 54.5%; Pred. No. 3.3e-05;  
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
QY 1 QWDFGNMQLTGLYIFGRFS 22  
DB 121 QWIFGNILCKMSVLYVGRFS 142  
  
RESULT 23  
CKR2 MOUSE  
ID CKR2 MOUSE STANDARD; PRT; 373 AA.  
AC P51683; O61172;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)  
DE (JE/FIC receptor) (MCP-1 receptor).  
GN CCR2 OR CMKBR2.  
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96205938; PubMed=8631787;  
RA Boring L., Gosling J., Monteclaro F.S., Lusis A.J., Tsou C.-L.,  
RA Charo I.F.;  
RT "Molecular cloning and functional expression of murine JE (monocyte  
RT chemoattractant protein 1) and murine macrophage inflammatory protein  
RT alpha receptors: evidence for two closely linked C-C chemokine  
RT receptors on chromosome 9.";  
RL J. Biol. Chem. 271:7551-7558(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=BALB/C;  
RX MEDLINE=96216064; PubMed=8662823;  
RA Kurihara T., Bravo R.;  
RT "Cloning and functional expression of mCCR2, a murine receptor for  
RT the C-C chemokines JE and FIC.";  
RL J. Biol. Chem. 271:11603-11606(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97026720; PubMed=8872898;  
RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,  
RA Post T.W., Gerard C., Dorf M.E.;  
RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse  
RT transcriptase-polymerase chain reaction does not detect mRNA for the  
RT KC or new MCP-1 receptor.";  
RL J. Neurosci. Res. 45:382-391(1996).  
CC -1- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5  
CC chemokines. Transduces a signal by increasing the intracellular  
CC calcium ions level.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,  
CC but not in nonhematopoietic cell lines.  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC  
CC EMBL; U47035; AAC52453.1; -  
CC EMBL; U51717; AAC52557.1; -  
CC EMBL; U56819; AAC52784.1; -  
CC MGD; MGI:106185; Ccr2.  
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.  
CC GO; GO:0019955; F:cytokine binding; IPI.  
CC GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.  
CC GO; GO:0030037; P:hemoipoiesis; IMP.  
CC GO; GO:0006959; P:humoral immune response; IMP.  
CC GO; GO:0006954; P:inflammatory response; IMP.  
CC GO; GO:0030334; P:regulation of cell migration; IMP.  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm.1; 1.  
CC PRINTS; PR00237; GPCRHOPOPSN.  
CC PROSITE; PS00237; G-PROTEIN RECF\_F1\_1; 1.  
CC PROSITE; PS0262; G-PROTEIN RECF\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane.  
FT DOMAIN 1 55  
FT TRANSSEM 56 83  
FT DOMAIN 84 93  
FT TRANSSEM 94 114  
FT DOMAIN 115 127  
FT TRANSSEM 128 149  
FT DOMAIN 150 166  
FT TRANSSEM 167 191  
FT DOMAIN 192 219  
FT TRANSSEM 220 239



RESULT 25

CKR8 MACMU STANDARD; PRT; 356 AA.

AC 097665;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 8 (C-C CKR-8) (CC-CKR-8) (CCR-8).

GN CCR8.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI\_TaxID=9544;

RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RC MEDLINE=21354176; PubMed=11461684;

RA Margulies B.J., Hauer D.A., Clements J.E.;

RT "Identification and comparison of eleven rhesus macaque chemokine receptors.";

RT AIDS Res. Hum. Retroviruses 17:981-986 (2001).

RL AID-1 - FUNCTION: Receptor for the chemokines SCYAL/I-309, SCY44/MIP-1-beta and SCYAL1/TARC. May regulate monocyte chemotaxis and thymic cell line apoptosis (By similarity).

CC AID-1 - SUBCELLULAR LOCATION: Integral membrane protein.

CC AID-1 - SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; AF100205; AAC72403.1; -

DR InterPro; IPR004068; CC 8 receptor.

DR InterPro; IPR000276; GPCR\_Rhodopsn.

DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR01530; CHEMOKINER8.

DR PRINTS; PR00237; GPCR\_RHODOPSIN.

DR PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.

DR PROSITE; PS0262; G PROTEIN RECEPTOR FL 2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 35

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 36 63

FT DOMAIN 64 73

FT CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 74 93

FT DOMAIN 94 107

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 108 129

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 130 146

FT CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 147 172

FT DOMAIN 173 203

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 204 223

FT DOMAIN 224 239

FT CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 240 264

FT DOMAIN 265 281

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 282 305

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 306 356

FT DISULFID 106 184

FT BY SIMILARITY.

SQ SEQUENCE 356 AA; 41210 MW; 1979628DE84845B CRC64;

Query Match 65.1%; Score 82; DB 1; Length 356;

Best Local Similarity 54.5%; Pred. No. 4.6e-05;

Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QWDFGNWCOLLGLYIFGFS 22

Db 98 QWVFGTWCKVSGFYIGFYS 119

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**CC** -----  
**CC** EMBL; U47036; AAC52454.1; -;  
**CC** DR EMBL; X94151; CAA63867.1; -;  
**CC** DR EMBL; U68565; AAB37273.1; -;  
**CC** DR EMBL; U83327; AAC53386.1; -;  
**CC** DR EMBL; AF022990; AAC53389.1; -;  
**CC** DR EMBL; AF019772; AAB71183.1; -;  
**CC** DR EMBL; D83648; BAA12024.1; -;  
**CC** DR MGD; MG1107182; Ccr5.  
**CC** GO; GO:0016493; P:C-C chemokine receptor activity; IDA.  
**CC** GO; GO:000952; P:defense response; IMP.  
**CC** InferPro; IPR000276; GPCR\_Rhodopsn.  
**CC** Pfam; PF00001; 7tm 1; 1.  
**CC** PRINTS; PR00237; GPCR\_HODOPSN  
**CC** PROSITE; PS00237; G-PROTEIN RECP F1\_1; 1.  
**CC** PROSITE; PS0262; G-PROTEIN RECP F1\_2; 1.  
**KW** G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.  
**FT** DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).  
**FT** TRANSMEM 33 60 1 (POTENTIAL).  
**FT** DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).  
**FT** TRANSMEM 71 91 2 (POTENTIAL).  
**FT** DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).  
**FT** TRANSMEM 105 126 3 (POTENTIAL).  
**FT** DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).  
**FT** TRANSMEM 144 168 4 (POTENTIAL).  
**FT** DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).  
**FT** TRANSMEM 201 220 5 (POTENTIAL).  
**FT** DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).  
**FT** TRANSMEM 238 262 6 (POTENTIAL).  
**FT** DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).  
**FT** TRANSMEM 280 303 7 (POTENTIAL).  
**FT** DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).  
**FT** DISULFID 103 180 BY SIMILARITY.  
**FT** CARBOHYD 270 270 N-LINKED (GLCNAC... ) (POTENTIAL).  
**FT** VARIANT 11 11 I -> S.  
**FT** VARIANT 62 62 K -> R.  
**FT** VARIANT 66 66 V -> M.  
**FT** VARIANT 97 97 I -> V.  
**FT** VARIANT 109 109 V -> L.  
**FT** VARIANT 156 156 V -> A.  
**FT** VARIANT 160 160 P -> S.  
**FT** VARIANT 185 185 P -> L.  
**FT** VARIANT 213 213 I -> V.  
**FT** VARIANT 318 318 I -> M.  
**FT** VARIANT 337 337 V -> A.  
**FT** CONFLICT 3 3 F -> L (IN REF. 2).  
**FT** CONFLICT 80 80 L -> F (IN REF. 2).  
**FT** CONFLICT 145 145 N -> I (IN REF. 5).  
**FT** CONFLICT 190 190 H -> Y (IN REF. 3).  
**FT** CONFLICT 208 208 P -> S (IN REF. 1).  
**SQ** SEQUENCE 354 AA; 40863 MW; B4AGB942E8BF9CF0 CRC64;  
  
Query Match 63.5%; Score 80; DB 1; Length 354;  
Best Local Similarity 57.1%; Pred. No. 9,1e-05;  
Matches 12; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
  
**QY** 1 QWDFNTWCQLLTGTYFGIFG 21 : ||| ||: |:: ||: ||:  
**Db** 95 EWIFGNIMCKVFTGVYHIGYF 115  
  
**RESULT 28**  
**CCR3\_CAVPO** STANDARD; PRT; 358 AA.  
**ID** CCR3\_CAVPO  
**AC** Q92Z13;  
  
**SEQUENCE FROM N.A.**  
Guo B., Kuno K., Harada A., Matsushima K.;  
Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
**-!- FUNCTION:** Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
MIP-1-beta and RANTES and subsequently transduces a signal by  
increasing the intracellular calcium ions level.  
**-!- SUBCELLULAR LOCATION:** Integral membrane protein.  
**-!- TISSUE SPECIFICITY:** Detected in monocyte/macrophage cell lines,  
but not in nonhematopoietic cell lines.  
**-!- SIMILARITY:** Belongs to family 1 of G-protein coupled receptors.



RESULT 29

|                                                             |                                                                       |
|-------------------------------------------------------------|-----------------------------------------------------------------------|
| GO                                                          | GO:0016433; F:C-C chemokine receptor activity; IDA.                   |
| GO                                                          | GO:0005515; F:protein binding; IPI.                                   |
| GO                                                          | GO:0030595; P:immune cell chemotaxis; IDA.                            |
| GO                                                          | GO:0006954; P:inflammatory response; IMP.                             |
| GO                                                          | GO:0030099; P:myeloid blood cell differentiation; IMP.                |
| InterPro                                                    | IPR000276; GPCR_Rhodpsn.                                              |
| Pfam                                                        | PF00001; 7cm_1; 1.                                                    |
| PRINTS                                                      | PRO0237; GPCRHOOPS.                                                   |
| PROSITE                                                     | PS00237; G PROTEIN RECP Fl_1; 1.                                      |
| PROSITE                                                     | PS0262; G PROTEIN RECP Fl_2; 1.                                       |
| KEGG                                                        | G-protein coupled receptor; Transmembrane.                            |
| FT                                                          | DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).                                |
| FT                                                          | TRANSEM 35 60 1 (POTENTIAL).                                          |
| FT                                                          | DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).                                 |
| FT                                                          | TRANSEM 65 91 2 (POTENTIAL).                                          |
| FT                                                          | DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).                              |
| FT                                                          | TRANSEM 108 129 3 (POTENTIAL).                                        |
| FT                                                          | DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).                               |
| FT                                                          | TRANSEM 147 171 4 (POTENTIAL).                                        |
| FT                                                          | DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).                             |
| FT                                                          | TRANSEM 198 223 5 (POTENTIAL).                                        |
| FT                                                          | DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).                               |
| FT                                                          | TRANSEM 240 264 6 (POTENTIAL).                                        |
| FT                                                          | DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).                             |
| FT                                                          | TRANSEM 282 305 7 (POTENTIAL).                                        |
| FT                                                          | DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).                               |
| FT                                                          | DISULFID 106 183 BY SIMILARITY.                                       |
| FT                                                          | CONFLICT 55 55 M -> V (IN REF. 2 AND 3).                              |
| FT                                                          | CONFLICT 149 149 L -> F (IN REF. 3).                                  |
| FT                                                          | CONFLICT 278 278 H -> Q (IN REF. 3).                                  |
| SEQ                                                         | SEQUENCE 355 AA; 40901 MW; FCE39FF70E6F38B1 CRC64;                    |
| Query Match                                                 | 60.3%; Score 76; DB 1; Length 355;                                    |
| Best Local Similarity                                       | 52.4%; Pred. No. 0.00037;                                             |
| Matches 11; Conservative 6; Mismatches 4; Indels 0; Gaps 0; |                                                                       |
| QY                                                          | 2 WDFGNTWCQLLTGLYFIFGFFS 22                                           |
| Ddb                                                         | 99 WIFGDAMCKLLSGFYVLGLYS 119                                          |
| RESULT 30                                                   |                                                                       |
| CKR3 RAT                                                    |                                                                       |
| ID                                                          | CKR3_RAT STANDARD; PRT; 359 AA.                                       |
| AC                                                          | OS4814; O55169;                                                       |
| DT                                                          | 30-MAY-2000 (Rel. 39, Created)                                        |
| DT                                                          | 30-MAY-2000 (Rel. 39, Last sequence update)                           |
| DT                                                          | 10-OCT-2003 (Rel. 42, Last annotation update)                         |
| DE                                                          | C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)              |
| DE                                                          | (CKR3).                                                               |
| GN                                                          | CKR3 OR CMKBR3.                                                       |
| OS                                                          | Rattus norvegicus (Rat).                                              |
| OC                                                          | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |
| OC                                                          | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. |
| OX                                                          | NCBI_TaxID=10116;                                                     |
| XP                                                          | [1]                                                                   |
| RP                                                          | SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.                           |
| RC                                                          | STRAIN=Wistar; TISSUE=Spleen;                                         |
| RC                                                          | MEDLINE=9818173; PubMed=9655467;                                      |
| RA                                                          | Jiang Y., Salafraña M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., |
| RA                                                          | Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;              |
| RT                                                          | "Chemokine receptor expression in cultured glia and rat experimental  |
| RT                                                          | allergic encephalomyelitis.;"                                         |
| RL                                                          | J. Neuroimmunol. 86:11-12(1998).                                      |
| RP                                                          | [2]                                                                   |
| RP                                                          | SEQUENCE FROM N.A.                                                    |
| RC                                                          | STRAIN=Wistar; TISSUE=Spleen;                                         |
| RC                                                          | Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;            |
| RL                                                          | Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.               |
| CC                                                          | -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,    |
| CC                                                          | MCP-3, MCP-4 and RANTES and subsequently transduces a signal by       |
| CC                                                          | increasing the intracellular calcium ions level (By similarity).      |
| CC                                                          | -!- SUBCELLULAR LOCATION: Integral membrane protein.                  |

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:53:42 ; Search time 35.4694 Seconds  
(without alignments)  
195.701 Million cell updates/sec

Title: US-10-084-813-12

Perfect score: 126

Sequence: 1 QWDFGNTMQLLTGLYFIFGFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

SPTREMBL\_25.\*

1: sp\_archaea.\*

2: sp\_bacteria.\*

3: sp\_fungi.\*

4: sp\_human.\*

5: sp\_invertebrate.\*

6: sp\_mammal.\*

7: sp\_mhc.\*

8: sp\_organelle.\*

9: sp\_phage.\*

10: sp\_plant.\*

11: sp\_rodent.\*

12: sp\_virus.\*

13: sp\_vertebrate.\*

14: sp\_unclassified.\*

15: sp\_rvirus.\*

16: sp\_bacteriap.\*

17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 126   | 100.0       | 215    | 4  | 075303 homo sapien |
| 2          | 126   | 100.0       | 333    | 4  | 014694 homo sapien |
| 3          | 126   | 100.0       | 339    | 4  | Q9UN24             |
| 4          | 126   | 100.0       | 339    | 4  | Q9UN23 homo sapien |
| 5          | 126   | 100.0       | 339    | 4  | Q9UBJ7 homo sapien |
| 6          | 126   | 100.0       | 339    | 4  | Q9UN25 homo sapien |
| 7          | 126   | 100.0       | 339    | 4  | Q9UN27 homo sapien |
| 8          | 126   | 100.0       | 339    | 4  | Q9UBT9             |
| 9          | 126   | 100.0       | 339    | 4  | Q9UN28             |
| 10         | 126   | 100.0       | 339    | 6  | Q9TQW0             |
| 11         | 126   | 100.0       | 339    | 6  | Q9TUX1             |
| 12         | 126   | 100.0       | 339    | 6  | Q9TUX8             |
| 13         | 126   | 100.0       | 339    | 6  | Q9TUX4 macaca neme |
| 14         | 126   | 100.0       | 339    | 6  | Q9TUX9             |
| 15         | 126   | 100.0       | 339    | 6  | Q9TUX8 cercopithec |
| 16         | 126   | 100.0       | 339    | 6  | Q9TQW4 pan troglod |

|    |     |       |     |   |        |
|----|-----|-------|-----|---|--------|
| 17 | 126 | 100.0 | 339 | 6 | Q9TUM4 |
| 18 | 126 | 100.0 | 339 | 6 | Q9TQU7 |
| 19 | 126 | 100.0 | 339 | 6 | Q9TUU3 |
| 20 | 126 | 100.0 | 339 | 6 | Q9TUR3 |
| 21 | 126 | 100.0 | 339 | 6 | Q9TQT0 |
| 22 | 126 | 100.0 | 339 | 6 | Q9TUT9 |
| 23 | 126 | 100.0 | 339 | 6 | Q9TSN2 |
| 24 | 126 | 100.0 | 339 | 6 | Q9TUS6 |
| 25 | 126 | 100.0 | 339 | 6 | Q9TQV6 |
| 26 | 126 | 100.0 | 339 | 6 | Q9TUM6 |
| 27 | 126 | 100.0 | 339 | 6 | Q9TQU9 |
| 28 | 126 | 100.0 | 339 | 6 | Q9TSN3 |
| 29 | 126 | 100.0 | 339 | 6 | Q9TUU7 |
| 30 | 126 | 100.0 | 339 | 6 | Q9TQV0 |
| 31 | 126 | 100.0 | 339 | 6 | Q9TQU5 |
| 32 | 126 | 100.0 | 339 | 6 | Q9TUS7 |
| 33 | 126 | 100.0 | 339 | 6 | Q9TUM7 |
| 34 | 126 | 100.0 | 339 | 6 | Q9TUM3 |
| 35 | 126 | 100.0 | 339 | 6 | Q9TUS5 |
| 36 | 126 | 100.0 | 339 | 6 | Q9TUU0 |
| 37 | 126 | 100.0 | 339 | 6 | Q9TQV2 |
| 38 | 126 | 100.0 | 339 | 6 | Q9TQV3 |
| 39 | 126 | 100.0 | 339 | 6 | Q9TQU8 |
| 40 | 126 | 100.0 | 339 | 6 | Q9TQW2 |
| 41 | 126 | 100.0 | 339 | 6 | Q9TUU1 |
| 42 | 126 | 100.0 | 339 | 6 | Q9TUT6 |
| 43 | 126 | 100.0 | 339 | 6 | Q9TSQ4 |
| 44 | 126 | 100.0 | 339 | 6 | Q9TUT3 |
| 45 | 126 | 100.0 | 339 | 6 | Q9TUT0 |
| 46 | 126 | 100.0 | 339 | 6 | Q9TQR2 |
| 47 | 126 | 100.0 | 339 | 6 | Q9TUT8 |
| 48 | 126 | 100.0 | 339 | 6 | Q9TUT1 |
| 49 | 126 | 100.0 | 339 | 6 | Q9TUT0 |
| 50 | 126 | 100.0 | 339 | 6 | Q9TUM5 |
| 51 | 126 | 100.0 | 339 | 6 | Q9TUS3 |
| 52 | 126 | 100.0 | 339 | 6 | Q9TQT2 |
| 53 | 126 | 100.0 | 339 | 6 | Q9TQT1 |
| 54 | 126 | 100.0 | 339 | 6 | Q9TUT5 |
| 55 | 126 | 100.0 | 339 | 6 | Q9TUT2 |
| 56 | 126 | 100.0 | 339 | 6 | Q9TUS8 |
| 57 | 126 | 100.0 | 339 | 6 | Q9TUU4 |
| 58 | 126 | 100.0 | 339 | 6 | Q9TUS6 |
| 59 | 126 | 100.0 | 339 | 6 | Q9TUR7 |
| 60 | 126 | 100.0 | 339 | 6 | Q9TQU4 |
| 61 | 126 | 100.0 | 339 | 6 | Q9TUT7 |
| 62 | 126 | 100.0 | 339 | 6 | Q9TUX0 |
| 63 | 126 | 100.0 | 339 | 6 | Q9TUU5 |
| 64 | 126 | 100.0 | 339 | 6 | Q9TUT1 |
| 65 | 126 | 100.0 | 339 | 6 | Q9TUS9 |
| 66 | 126 | 100.0 | 340 | 6 | Q9TUU2 |
| 67 | 126 | 100.0 | 344 | 6 | Q9TQR8 |
| 68 | 126 | 100.0 | 344 | 6 | 077833 |
| 69 | 126 | 100.0 | 352 | 6 | Q9TSK1 |
| 70 | 126 | 100.0 | 352 | 6 | Q9SNC5 |
| 71 | 126 | 100.0 | 352 | 6 | Q9TV48 |
| 72 | 126 | 100.0 | 352 | 6 | Q9TV49 |
| 73 | 126 | 100.0 | 352 | 6 | Q9XT14 |
| 74 | 126 | 100.0 | 352 | 6 | 018771 |
| 75 | 126 | 100.0 | 352 | 6 | Q9TV47 |
| 76 | 126 | 100.0 | 352 | 6 | Q9SNC1 |
| 77 | 126 | 100.0 | 352 | 6 | 018770 |
| 78 | 126 | 100.0 | 352 | 6 | 018772 |
| 79 | 126 | 100.0 | 352 | 6 | Q9SNC6 |
| 80 | 126 | 100.0 | 352 | 6 | Q9SNC8 |
| 81 | 126 | 100.0 | 352 | 6 | Q9SNC0 |
| 82 | 126 | 100.0 | 352 | 6 | Q9SNC5 |
| 83 | 126 | 100.0 | 352 | 6 | Q9SNC5 |
| 84 | 126 | 100.0 | 352 | 6 | Q9XT12 |
| 85 | 126 | 100.0 | 352 | 6 | Q9TV42 |
| 86 | 126 | 100.0 | 352 | 6 | Q9XT13 |
| 87 | 126 | 100.0 | 352 | 6 | Q9XT13 |
| 88 | 126 | 100.0 | 352 | 6 | Q9MZA3 |
| 89 | 126 | 100.0 | 352 | 6 | Q9TV46 |

90 126 100.0 352 6 Q9TSQ7  
 91 126 100.0 352 6 Q9WZA2  
 92 126 100.0 352 6 Q9TV50  
 93 126 100.0 352 6 Q9X599  
 94 126 100.0 352 6 Q9TV45  
 95 126 100.0 352 6 Q9SNE1  
 96 126 100.0 352 6 Q9TV43  
 97 126 100.0 352 6 Q9TV43  
 98 126 100.0 352 6 Q9TV43  
 99 126 100.0 352 6 Q9TV43  
 100 122 96.8 339 6 Q9TVU6

## ALIGNMENTS

RESULT 1  
 Q75303  
 ID 075303 PRELIMINARY; PRT; 215 AA.  
 AC Q75303;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE CC-chemokine receptor.  
 GN CCR-5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tse L., Ehrenberg P.K., Chang G., Michael N.L.;  
 RT "Genomic Organization and Functional Characterization of the Complete  
 Transcription Unit for the Chemokine Receptor CCR-5, a Major Entry Co-  
 Receptor for HIV-1.";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF009962; AAC23944.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm1.1;  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 215 AA; 23946 MW; 3C9146C768A416F7 CRC64;  
 Query Match 100.0%; Score 126; DB 4; Length 215;  
 Best Local Similarity 100.0%; Pred. NO. 1.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTMCOQLTGLYFIGFFS 22  
 DB 93 QWDFGNTMCOQLTGLYFIGFFS 114  
 RESULT 2  
 Q14694  
 ID Q14694 PRELIMINARY; PRT; 333 AA.  
 AC Q14694;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE CCR5 receptor (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";  
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).  
 DR EMBL; AF011504; AAB65704.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm1.1;  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 339 339  
 SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;  
 Query Match 100.0%; Score 126; DB 4; Length 333;  
 Best Local Similarity 100.0%; Pred. NO. 3e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTMCOQLTGLYFIGFFS 22  
 DB 74 QWDFGNTMCOQLTGLYFIGFFS 95  
 RESULT 3  
 Q9UN24  
 ID Q9UN24 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN24;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161919; AAD47676.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm1.1;  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;  
 Query Match 100.0%; Score 126; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. NO. 3.1e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QWDFGNTMCOQLTGLYFIGFFS 22  
 DB 86 QWDFGNTMCOQLTGLYFIGFFS 107  
 RESULT 4  
 Q9UN23

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ID Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 9C3369FF1F2F27A CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161918; AAD47675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 10FE05F85371D4B3 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RESULT 7
Q9UN27
ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CBAEC2 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 8
Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CBAEC2 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 9
Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6B1A6 CRC64;

Query Match 100.0%; Score 126; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
Db 86 QWDFGNTWCQLLTGLYFIFGFFS 107

RESULT 10
Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.

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DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAP2614D35C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIIGFFS 107

RESULT 11
Q9TUX1 ID Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF161887; AAD47644.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIIGFFS 107

RESULT 12
Q9TUX8 ID Q9TUX8 PRELIMINARY; PRT; 339 AA.
AC Q9TUX8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.

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OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF161894; AAD47651.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIIGFFS 22
DB 86 QWDFGNTMCQLLTGLYFIIGFFS 107

RESULT 13
Q9TUT4 ID Q9TUT4 PRELIMINARY; PRT; 339 AA.
AC Q9TUT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF161979; AAD47734.1; -.
GO: GO:0016021; C:integral to membrane; IEA.
GO: GO:0004872; F:receptor activity; IEA.
GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548B0703C CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFS 22
Db 86 QWDFGNTMCLLTGLYFIFGFS 107

RESULT 14
Q9TUW9
ID Q9TUW9 PRELIMINARY; PRT; 339 AA.
AC Q9TUW9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
DR NON_TER 339
DR SEQUENCE 339 AA; 39024 MW; BC4CE48DEEF107E CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFS 22
Db 86 QWDFGNTMCLLTGLYFIFGFS 107

RESULT 15
Q9TUU8
ID Q9TUU8 PRELIMINARY; PRT; 339 AA.
AC Q9TUU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
DR NON_TER 339
DR SEQUENCE 339 AA; 39049 MW; 6DIA93F66270F3ED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFS 22
Db 86 QWDFGNTMCLLTGLYFIFGFS 107

RESULT 16
Q9TQW4
ID Q9TQW4 PRELIMINARY; PRT; 339 AA.
AC Q9TQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR NON_TER 1
DR NON_TER 339
DR SEQUENCE 339 AA; 39129 MW; 4A88F8BB601D46A4 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFS 22
Db 86 QWDFGNTMCLLTGLYFIFGFS 107

RESULT 17
Q9TUW4
ID Q9TUW4 PRELIMINARY; PRT; 339 AA.

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AC Q9TUM4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39159 MW; 8E699E882BAC0E84 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNWTCQLLTGLYFIFGFFS 22
DB 86 QWDFGNWTCQLLTGLYFIFGFFS 107
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|||||

RESULT 18
Q9TQV7
ID Q9TQV7 PRELIMINARY; PRT; 339 AA.
AC Q9TQV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

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DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92BB03E6E2 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNWTCQLLTGLYFIFGFFS 22
DB 86 QWDFGNWTCQLLTGLYFIFGFFS 107
|||||
|||||

RESULT 19
Q9TUU3
ID Q9TUU3 PRELIMINARY; PRT; 339 AA.
AC Q9TUU3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161961; AAD47716.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39121 MW; AFB6E3EE4D6D3484 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNWTCQLLTGLYFIFGFFS 22
DB 86 QWDFGNWTCQLLTGLYFIFGFFS 107
|||||
|||||

RESULT 20
Q9TUR9
ID Q9TUR9 PRELIMINARY; PRT; 339 AA.
AC Q9TUR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saginus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=100754;

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RN 11
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD4770.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMQLLTGLYFIQFFS 22
Db 86 QWDFGNTMQLLTGLYFIQFFS 107

RESULT 21
Q9TQT0 PRELIMINARY; PRT; 339 AA.
AC Q9TQT0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD4770.1; -.
DR EMBL; AF161952; AAD4770.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QWDFGNTMQLLTGLYFIQFFS 22
Db 86 QWDFGNTMQLLTGLYFIQFFS 107

RESULT 22
Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161972; AAD4772.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCB5BA96C2F9E CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMQLLTGLYFIQFFS 22
Db 86 QWDFGNTMQLLTGLYFIQFFS 107

RESULT 23
Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wollinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD4770.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO: 0004872; P:receptor activity; IEA.
DR GO: 0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39137 MW; 98626ED3288607C1 CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFS 107

RESULT 24
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39178 MW; 9DF2A6F446C5AED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFS 107

RESULT 25
ID Q9TQV6 PRELIMINARY; PRT; 339 AA.
AC Q9TQV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47760.1; -.
DR EMBL; AF162000; AAD47755.1; -.
DR EMBL; AF162001; AAD47756.1; -.
DR EMBL; AF162002; AAD47757.1; -.
DR EMBL; AF162003; AAD47758.1; -.
DR EMBL; AF162004; AAD47759.1; -.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
DB 86 QWDFGNTWCQLLTGLYFIFGFS 107

RESULT 26
ID Q9TQW6 PRELIMINARY; PRT; 339 AA.
AC Q9TQW6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161900; AAD47657.1; -.
DR GO: 0016021; C:integral to membrane; IEA.
DR GO: 0004872; F:receptor activity; IEA.
DR GO: 0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PS00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

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DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39103 MW; 4038C132D024C5A4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 126; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCLLTGLYFIFGFFS 107

RESULT 27
Q9TUQ9
ID Q9TUQ9 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5
OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36226;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161951; AAD47707.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1. 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39098 MW; F0132E8BC44EF829 CRC64;

Query Match
Best Local Similarity 100.0%; Score 126; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCLLTGLYFIFGFFS 107

RESULT 28
Q9TSN3
ID Q9TSN3 PRELIMINARY; PRT; 339 AA.
AC Q9TSN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.

DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39019 MW; 7176F940AF1F3ED CRC64;

Query Match
Best Local Similarity 100.0%; Score 126; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFFS 22
DB 86 QWDFGNTMCLLTGLYFIFGFFS 107

RESULT 29
Q9TUU7
ID Q9TUU7 PRELIMINARY; PRT; 339 AA.
AC Q9TUU7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9542;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161955; AAD47711.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1. 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39057 MW; C576E7AA492D7080 CRC64;

Query Match
Best Local Similarity 100.0%; Score 126; DB 6; Length 339;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCLLTGLYFIFGFFS 22
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DB 86 QWDFGNTWCQLLTGLYFIFGFFS 107
|||||
RESULT 30
Q9TQV0 PRELIMINARY; PRT; 339 AA.
AC Q9TQV0
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Papio papio (Guinea baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
OX NCBI_TaxID=100937;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161989; AAD47744.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.
DR PROSITE; PS0262; G PROTEIN RECP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39113 MW; 7F9803EA0E0AF9ED CRC64;

Query Match 100.0%; Score 126; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22
|||||
DB 86 QWDFGNTWCQLLTGLYFIFGFFS 107

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Search completed: March 4, 2004, 18:02:55  
Job time : 36.4694 secs

|                                                                                                                                                                                                    |                                                                                                                                                                                                                                                                                       |                                                                                          |        |                   |                    |  |  |  |  |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------|--------|-------------------|--------------------|--|--|--|--|
| GenCore version 5.1.6                                                                                                                                                                              |                                                                                                                                                                                                                                                                                       |                                                                                          |        |                   |                    |  |  |  |  |
| Copyright (c) 1993 - 2004 CompuGen Ltd.                                                                                                                                                            |                                                                                                                                                                                                                                                                                       |                                                                                          |        |                   |                    |  |  |  |  |
| OM protein - protein search, using sw model                                                                                                                                                        |                                                                                                                                                                                                                                                                                       |                                                                                          |        |                   |                    |  |  |  |  |
| Run on:                                                                                                                                                                                            | March 4, 2004, 17:55:22                                                                                                                                                                                                                                                               | ; Search time 14.1429 Seconds<br>(without alignments)<br>80.307 Million cell updates/sec |        |                   |                    |  |  |  |  |
| Title:                                                                                                                                                                                             | US-10-084-813-12                                                                                                                                                                                                                                                                      |                                                                                          |        |                   |                    |  |  |  |  |
| Perfect score:                                                                                                                                                                                     | 126                                                                                                                                                                                                                                                                                   |                                                                                          |        |                   |                    |  |  |  |  |
| Sequence:                                                                                                                                                                                          | 1 QWDFGNMCOQLTGLYFIFGFS 22                                                                                                                                                                                                                                                            |                                                                                          |        |                   |                    |  |  |  |  |
| Scoring table:                                                                                                                                                                                     | BLOSUM62                                                                                                                                                                                                                                                                              |                                                                                          |        |                   |                    |  |  |  |  |
| Gapop                                                                                                                                                                                              | 10.0 , Gapext 0.5                                                                                                                                                                                                                                                                     |                                                                                          |        |                   |                    |  |  |  |  |
| Searched:                                                                                                                                                                                          | 389414 seqs, 51625971 residues                                                                                                                                                                                                                                                        |                                                                                          |        |                   |                    |  |  |  |  |
| Total number of hits satisfying chosen parameters:                                                                                                                                                 | 389414                                                                                                                                                                                                                                                                                |                                                                                          |        |                   |                    |  |  |  |  |
| Minimum DB seq length:                                                                                                                                                                             | 0                                                                                                                                                                                                                                                                                     |                                                                                          |        |                   |                    |  |  |  |  |
| Maximum DB seq length:                                                                                                                                                                             | 2000000000                                                                                                                                                                                                                                                                            |                                                                                          |        |                   |                    |  |  |  |  |
| Post-processing:                                                                                                                                                                                   | Minimum Match 0%<br>Maximum Match 100%<br>Listing first 100 summaries                                                                                                                                                                                                                 |                                                                                          |        |                   |                    |  |  |  |  |
| Database :                                                                                                                                                                                         | Issued Patents AA.*<br>1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*<br>2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*<br>3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*<br>4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*<br>5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep.*<br>6: /cgn2_6/prodata/2/iaa/backfiles1.pep.* |                                                                                          |        |                   |                    |  |  |  |  |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. |                                                                                                                                                                                                                                                                                       |                                                                                          |        |                   |                    |  |  |  |  |
| SUMMARIES                                                                                                                                                                                          |                                                                                                                                                                                                                                                                                       |                                                                                          |        |                   |                    |  |  |  |  |
| Result No.                                                                                                                                                                                         | Score                                                                                                                                                                                                                                                                                 | Query Match                                                                              | Length | ID                | Description        |  |  |  |  |
| 1                                                                                                                                                                                                  | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 184    | US-08-833-752-4   | Sequence 4, Appli  |  |  |  |  |
| 2                                                                                                                                                                                                  | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 215    | US-09-087-232A-17 | Sequence 17, Appli |  |  |  |  |
| 3                                                                                                                                                                                                  | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 215    | US-08-833-752-6   | Sequence 6, Appli  |  |  |  |  |
| 4                                                                                                                                                                                                  | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-08-466-343D-2  | Sequence 2, Appli  |  |  |  |  |
| 5                                                                                                                                                                                                  | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-09-087-232A-13 | Sequence 13, Appli |  |  |  |  |
| 6                                                                                                                                                                                                  | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-08-861-105-14  | Sequence 14, Appli |  |  |  |  |
| 7                                                                                                                                                                                                  | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-08-575-967A-2  | Sequence 2, Appli  |  |  |  |  |
| 8                                                                                                                                                                                                  | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-09-045-583-52  | Sequence 52, Appli |  |  |  |  |
| 9                                                                                                                                                                                                  | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-09-517-605-5   | Sequence 5, Appli  |  |  |  |  |
| 10                                                                                                                                                                                                 | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-09-534-185-52  | Sequence 52, Appli |  |  |  |  |
| 11                                                                                                                                                                                                 | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-08-833-752-5   | Sequence 5, Appli  |  |  |  |  |
| 12                                                                                                                                                                                                 | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-09-502-783A-2  | Sequence 2, Appli  |  |  |  |  |
| 13                                                                                                                                                                                                 | 126                                                                                                                                                                                                                                                                                   | 100.0                                                                                    | 352    | US-09-796-202-1   | Sequence 1, Appli  |  |  |  |  |
| 14                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 344    | US-08-466-343D-9  | Sequence 9, Appli  |  |  |  |  |
| 15                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 347    | US-08-461-244-3   | Sequence 3, Appli  |  |  |  |  |
| 16                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 360    | US-08-450-393A-4  | Sequence 4, Appli  |  |  |  |  |
| 17                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 360    | US-08-446-669-4   | Sequence 4, Appli  |  |  |  |  |
| 18                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 360    | US-09-045-583-50  | Sequence 50, Appli |  |  |  |  |
| 19                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 360    | US-09-534-185-50  | Sequence 50, Appli |  |  |  |  |
| 20                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 360    | US-08-833-752-7   | Sequence 7, Appli  |  |  |  |  |
| 21                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 360    | US-09-131-827A-2  | Sequence 2, Appli  |  |  |  |  |
| 22                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 360    | US-09-131-827A-20 | Sequence 20, Appli |  |  |  |  |
| 23                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 360    | PCT-US95-00476-4  | Sequence 4, Appli  |  |  |  |  |
| 24                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 374    | US-08-450-393A-2  | Sequence 2, Appli  |  |  |  |  |
| 25                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 374    | US-08-446-669-2   | Sequence 2, Appli  |  |  |  |  |
| 26                                                                                                                                                                                                 | 87                                                                                                                                                                                                                                                                                    | 69.0                                                                                     | 374    | PCT-US95-00476-2  | Sequence 2, Appli  |  |  |  |  |
| 27                                                                                                                                                                                                 | 83                                                                                                                                                                                                                                                                                    | 65.9                                                                                     | 269    | US-08-307-499-30  | Sequence 30, Appli |  |  |  |  |

## ALIGNMENTS

## RESULT 1

US-08-833-752-4  
; Sequence 4, Application US/08833752  
; Patent No. 6448375  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; APPLICANT: PARMENTIER, MARC  
; APPLICANT: VASSART, GILBERT  
; APPLICANT: LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/833,752  
; FILING DATE: 9-APR-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E.  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 184 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-833-752-4

Query Match 100.0%; Score 126; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22  
Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

## RESULT 2

US-09-087-232A-17  
; Sequence 17, Application US/09087232A  
; Patent No. 6153431  
; GENERAL INFORMATION:  
; APPLICANT: Quillent et al.  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR  
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/087,232A  
; FILING DATE: 28 MAY 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/048,057  
; FILING DATE: 30 MAY 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOLE, LISA B.  
; REGISTRATION NUMBER: 35,225  
; REFERENCE/DOCKET NUMBER: AP 31115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 408-2628  
; TELEFAX: (212) 765-2519  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-087-232A-17

Query Match 100.0%; Score 126; DB 3; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22  
Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114

## RESULT 3

US-08-833-752-6  
; Sequence 6, Application US/08833752  
; Patent No. 6448375  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; APPLICANT: PARMENTIER, MARC  
; APPLICANT: VASSART, GILBERT  
; APPLICANT: LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/833,752  
; FILING DATE: 9-APR-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E.  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER:  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 215 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-833-752-6

Query Match 100.0%; Score 126; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 1.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 4  
US-08-466-343D-2  
; Sequence 2, Application US/08466343D  
; Patent No. 6025154  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN  
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGRN10 (AS AMENDED)  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,343D  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-466-343D-2

Query Match 100.0%; Score 126; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 5  
US-09-087-232A-13  
; Sequence 13, Application US/09087232A  
; Patent No. 6153431  
; GENERAL INFORMATION:  
; APPLICANT: Quillient et al.  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR  
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA

ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/087,232A  
; FILING DATE: 28 MAY 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/048,057  
; FILING DATE: 30 MAY 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOLE, LISA B.  
; REGISTRATION NUMBER: 35,225  
; REFERENCE/DOCKET NUMBER: AP 31115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 408-2628  
; TELEFAX: (212) 765-2519  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-087-232A-13

Query Match 100.0%; Score 126; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 6  
US-08-861-105-14  
; Sequence 14, Application US/08861105  
; Patent No. 6258527  
; GENERAL INFORMATION:  
; APPLICANT: LITTMAN, DAN R.  
; APPLICANT: DENG, HONGKUI  
; APPLICANT: ELMIEBER, WILFRIED  
; APPLICANT: LANDAU, NATHANIEL R.  
; APPLICANT: LIU, RONG  
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH  
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,105  
; FILING DATE:  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/666,020  
; FILING DATE: 19-JUN-1996  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:



APPLICATION NUMBER: US 08/227,319  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1049-1-004 N1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-861-105-14

Query Match 100.0%; Score 126; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22  
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 7  
US-08-575-967A-2  
Sequence 2, Application US/08575967A  
Patent No. 6265184  
GENERAL INFORMATION:  
APPLICANT: Gray et al.  
TITLE OF INVENTION: Chemokine Receptor Materials and Methods  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/575,967A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6265184and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32918  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-485-1900  
TELEFAX: 206-485-1662  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: /= "86C amino acid sequence"  
US-08-575-967A-2

Query Match 100.0%; Score 126; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QWDFGNTMCQLLTGLYFIFGFS 22  
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 8  
US-09-045-583-52  
Sequence 52, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: NO. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-045-583-52

Query Match 100.0%; Score 126; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22  
DB 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 9  
US-09-517-605-5  
Sequence 5, Application US/09517605  
Patent No. 6391567  
GENERAL INFORMATION:  
APPLICANT: Littman, Dan R.  
APPLICANT: Kwon, Douglas S.  
APPLICANT: van Kooyk, Yvette  
APPLICANT: Geijtenbeek, Ineo  
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO  
CELLS  
FILE REFERENCE: 1049-1-017  
CURRENT APPLICATION NUMBER: US/09/517,605

;; CURRENT FILING DATE: 2000-03-02  
;; NUMBER OF SEQ ID NOS: 17  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 352  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-517-605-5

Query Match 100.0%; Score 126; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLTGLYFIGFFS 22  
Db 93 QWDFGNTMCQLTGLYFIGFFS 114

## RESULT 10

US-09-534-185-52  
; Sequence 52, Application US/09534185  
; Patent No. 6403767  
; GENERAL INFORMATION:

;; APPLICANT: Graham, Gerard J. et al.  
;; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
;; Heptahelical Receptor Superfamily and Uses  
Therefor

;; NUMBER OF SEQUENCES: 56  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSER: LAHIVE & COCKFIELD, LLP  
;; STREET: 28 State Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02109

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/534,185  
;; FILING DATE: 24-Mar-2000  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/045,583  
;; FILING DATE: <Unknown>

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mandragouras, Amy E.  
;; REGISTRATION NUMBER: 36,207  
;; REFERENCE/DOCKET NUMBER: MWI-044  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617)227-7400  
;; TELEFAX: (617)742-4214

;; INFORMATION FOR SEQ ID NO: 52:  
;; SEQUENCE CHARACTERISTICS:  
;; TYPE: amino acid  
;; LENGTH: 352 amino acids  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-09-534-185-52

Query Match 100.0%; Score 126; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLTGLYFIGFFS 22  
Db 93 QWDFGNTMCQLTGLYFIGFFS 114

## RESULT 11

US-08-833-752-5  
; Sequence 5, Application US/08833752  
; Patent No. 6448375  
; GENERAL INFORMATION:

;; APPLICANT: SAMSON, MICHEL  
;; APPLICANT: PARMENTIER, MARC  
;; APPLICANT: VASSART, GILBERT  
;; APPLICANT: LIBERT, FREDERICK  
;; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
;; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
;; NUMBER OF SEQUENCES: 17  
;; CORRESPONDENCE ADDRESS:

;; ADDRESSER: Knobbe, Martens, Olson & Bear  
;; STREET: 620 Newport Center Drive 16th Floor  
;; CITY: Newport Beach  
;; STATE: CA  
;; COUNTRY: U.S.A.  
;; ZIP: 92660

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/833,752  
;; FILING DATE: 9-APR-1997  
;; CLASSIFICATION: 536

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Altman, Daniel E  
;; REGISTRATION NUMBER: 34,115  
;; REFERENCE/DOCKET NUMBER:  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 352 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein

US-08-833-752-5

Query Match 100.0%; Score 126; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QWDFGNTMCQLTGLYFIGFFS 22  
Db 93 QWDFGNTMCQLTGLYFIGFFS 114

## RESULT 12

US-09-502-783A-2  
; Sequence 2, Application US/09502783A  
; Patent No. 6511826  
; GENERAL INFORMATION:

;; APPLICANT: Ruben, Steven M.  
;; APPLICANT: Li, Yi  
;; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)  
;; TITLE OF INVENTION: HDGnr10  
;; FILE REFERENCE: 1488.1150006  
;; CURRENT APPLICATION NUMBER: US/09/502,783A  
;; CURRENT FILING DATE: 2001-08-23  
;; PRIOR APPLICATION NUMBER: 08/466,343  
;; PRIOR FILING DATE: 1995-06-06  
;; NUMBER OF SEQ ID NOS: 9  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 2  
;; TYPE: PRT  
;; LENGTH: 352  
;; ORGANISM: Homo sapiens  
US-09-502-783A-2

Query Match 100.0%; Score 126; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 2.5e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFFS 22

Db 93 QWDFGNTWCQLLTGLYFIIGFFS 114

## RESULT 13

US-09-796-202-1  
; Sequence 1, Application US/09796202

; Patent No. 6548636

; GENERAL INFORMATION:

; APPLICANT: Dragic, Tatjana

; APPLICANT: Olson, William

; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION

; FILE REFERENCE: 2048/61010/JPW/SHS

; CURRENT APPLICATION NUMBER: US/09/796.202

; CURRENT FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 352

; TYPE: PRT

; ORGANISM: human

US-09-796-202-1

Query Match 100.0%; Score 126; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.5e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFFS 22

Db 93 QWDFGNTWCQLLTGLYFIIGFFS 114

## RESULT 14

US-08-466-343D-9

; Sequence 9, Application US/08466343D

; Patent No. 6025154

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN

; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVE., NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466.343D

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: STEFFE, ERIC K.

; REGISTRATION NUMBER: 36,688

; REFERENCE/DOCKET NUMBER: 1488.1150000/BKS/KLM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 344 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-466-343D-9

Query Match 69.0%; Score 87; DB 3; Length 344;

Best Local Similarity 66.7%; Pred. No. 1.9e-05;

Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFF 21

Db 88 EWVFGNAMCKLFTGLYHIGYF 108

## RESULT 15

US-08-461-244-3

; Sequence 3, Application US/08461244

; Patent No. 5776729

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.

; APPLICANT: Yi, Li

; APPLICANT: Ruben, Steven M.

; APPLICANT: Rosen, Craig A.

; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

; ADDRESSEE: STUART & OLSTEIN

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461.244

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Ferraro, Gregory D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-445

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 347 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-461-244-3

Query Match 69.0%; Score 87; DB 1; Length 347;

Best Local Similarity 66.7%; Pred. No. 2e-05;

Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIIGFF 21

Db 92 EWVFGNAMCKLFTGLYHIGYF 112

## RESULT 16

US-08-450-393A-4

; Sequence 4, Application US/08450393A

; Patent No. 5707815

; GENERAL INFORMATION:

; APPLICANT: Charo, Israel

; APPLICANT: Coughlin, Shaun

; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT

TITLE OF INVENTION: PROTEIN RECEPTORS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
STREET: 5 Palo Alto Square  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306-2155  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,393A  
FILING DATE: May 25, 1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Cseri, Luann  
REGISTRATION NUMBER: 31,822  
REFERENCE/DOCKET NUMBER: UCAL-237/02US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-843-5165  
TELEFAX: 415-8857-0663  
TELEX: 380816COOLEYPA  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-450-393A-4

Query Match 69.0%; Score 87; DB 1; Length 360;  
Best Local Similarity 66.7%; Pred. No. 2e-05;  
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNWCOLLTGLYFIGFF 21  
DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 17  
US-08-446-669-4  
Sequence 4, Application US/08446669  
Patent No. 6132987  
GENERAL INFORMATION:  
APPLICANT: Charo, Israel  
APPLICANT: Coughlin, Shaun  
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
REFERENCE/DOCKET NUMBER: PROTEIN RECEPTORS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
STREET: 5 Palo Alto Square  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306-2155  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,669  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Neeley, Richard  
REGISTRATION NUMBER: 30,092  
REFERENCE/DOCKET NUMBER: UCAL-237/01US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-843-5000  
TELEFAX: 415-857-0663  
TELEX: 380816COOLEYPA  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-669-4

Query Match 69.0%; Score 87; DB 3; Length 360;  
Best Local Similarity 66.7%; Pred. No. 2e-05;  
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNWCOLLTGLYFIGFF 21  
DB 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 18  
US-09-045-583-50  
Sequence 50, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-045-583-50

Query Match 69.0%; Score 87; DB 3; Length 360;  
Best Local Similarity 66.7%; Pred. No. 2e-05;  
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNWCOLLTGLYFIGFF 21  
DB 105 EWVFGNACKLFTGLYHIGYF 125

```
RESULT 19
US-09-534-185-50
; Sequence 50, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Hepatahelical Receptor Superfamily and Uses
; Therefor
;
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-534-185-50

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. NO. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 20
US-09-534-185-50
; Sequence 7, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
```

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ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6448375e
US-08-833-752-7

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. NO. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 21
US-09-131-827A-2
; Sequence 2, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
; APPLICANT: Carrington, Mary
; TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A
; FILE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE
; FILE REFERENCE: 14014.0333
; CURRENT APPLICATION NUMBER: US/09/131,827A
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/055,659
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-131-827A-2

Query Match 69.0%; Score 87; DB 4; Length 360;
Best Local Similarity 66.7%; Pred. NO. 2e-05;
Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIQFF 21
Db 105 EWVFGNAMCKLFTGLYHIGYF 125

RESULT 22
US-09-131-827A-20
; Sequence 20, Application US/09131827A
; Patent No. 6600030
; GENERAL INFORMATION:
; APPLICANT: Dean, Michael
; APPLICANT: O'Brien, Stephen J.
; APPLICANT: Smith, Michael
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Qy 1 QWDFGNTMCQLLTGLYFIGFF 21
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Db 105 EWVFGNAMCKLFTGLYHIGYF 125

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RESULT 25
US-08-446-669-2
; Sequence 2, Application US/08446669
; Patent No. 6132987
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSSE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/446,669  
 FILING DATE: May 25, 1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Neeley, Richard  
 REGISTRATION NUMBER: 30,092  
 REFERENCE/DOCKET NUMBER: UCAL-237/01US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-843-5000  
 TELEFAX: 415-857-0663  
 TELEX: 380916CooleyPA  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 374 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-446-669-2

Query Match 69.0%; Score 87; DB 3; Length 374;  
 Best Local Similarity 66.7%; Pred. No. 2.1e-05;  
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLTLGLYFIQFF 21  
 Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 26  
 PCT-US95-00476-2  
 Sequence 2, Application PC/TUS9500476  
 GENERAL INFORMATION:  
 APPLICANT: The Regents of the University of California  
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
 TITLE OF INVENTION: PROTEIN RECEPTORS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Robbins, Berliner & Carson  
 STREET: 201 N. Figueroa Street, 5th Floor  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90012-2628  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/00476  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Berliner, Robert  
 REGISTRATION NUMBER: 20,121  
 REFERENCE/DOCKET NUMBER: 5555-291  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 310-977-1001  
 TELEFAX: 310-977-1003  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 374 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-00476-2

Query Match 69.0%; Score 87; DB 5; Length 374;  
 Best Local Similarity 66.7%; Pred. No. 2.1e-05;  
 Matches 14; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLTLGLYFIQFF 21  
 Db 105 EWVFGNACKLFTGLYHIGYF 125

RESULT 27  
 US-08-307-499-30  
 Sequence 30, Application US/08307499  
 Patent No. 5651972  
 GENERAL INFORMATION:  
 APPLICANT: Moyer, Richard W.  
 APPLICANT: Vi uela, Eladio  
 APPLICANT: Gibbs, E.P.J.  
 TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a  
 TITLE OF INVENTION: Live Vaccine Vector  
 NUMBER OF SEQUENCES: 60  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: David R. Saliwanchik  
 STREET: 2421 N.W. 41st Street, Suite A-1  
 CITY: Gainesville  
 STATE: Florida  
 COUNTRY: U.S.A.  
 ZIP: 32606  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/307,499  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/908,241  
 FILING DATE: 1-JUL-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/908,630  
 FILING DATE: 29-JUN-1992  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/342,212  
 FILING DATE: 21-APR-1992  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Saliwanchik, David R.  
 REGISTRATION NUMBER: 31,794  
 REFERENCE/DOCKET NUMBER: UF35.1.FWCCI  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 904-375-8100  
 TELEFAX: 904-372-5800  
 INFORMATION FOR SEQ ID NO: 30:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 269 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-307-499-30

Query Match 65.9%; Score 83; DB 1; Length 269;  
 Best Local Similarity 54.5%; Pred. No. 6e-05;  
 Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 QWDFGNTMCKLTLGLYFIQFFS 22  
 Db 20 QWIFGNILCKIMSVLYTVGFFS 41

RESULT 28  
 US-09-299-268-30  
 Sequence 30, Application US/09299268  
 Patent No. 6217882  
 GENERAL INFORMATION:

APPLICANT: Moyer, Richard W.  
APPLICANT: Vi uela, Eladio  
APPLICANT: Gibbs, E.P.J.  
TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a  
TITLE OF INVENTION: Live Vaccine Vector  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David R. Saliwanchik  
STREET: 2421 N.W. 41st Street, Suite A-1  
CITY: Gainesville  
STATE: Florida  
COUNTRY: U.S.A.  
ZIP: 32606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/299,268  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/901,127  
FILING DATE:  
APPLICATION NUMBER: US 07/908,241  
FILING DATE: 1-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/908,630  
FILING DATE: 29-JUN-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/342,212  
FILING DATE: 21-APR-1992  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Saliwanchik, David R.  
REGISTRATION NUMBER: 31,794  
REFERENCE/DOCKET NUMBER: UF35.1.FWCC1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 904-375-8100  
TELEFAX: 904-372-5800  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 269 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-299-268-30

Query Match 65.9%; Score 83; DB 3; Length 269;  
Best Local Similarity 54.5%; Pred. No. 6e-05;  
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QWDFGNTMQLTGLYFGFSS 22  
Db 20 QWIRGNILCKIMSVLYVGFSS 41

RESULT 29  
US-08-461-244-2  
Sequence 2, Application US/08461244  
Patent No. 5776729  
GENERAL INFORMATION:  
APPLICANT: Soppet, Daniel R.  
APPLICANT: Yi, Li  
APPLICANT: Ruben, Steven M.  
APPLICANT: Rosen, Craig A.  
TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARRELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
STUART & OLSTEIN

STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,244  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferraro, Gregory D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-445  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-244-2

Query Match 65.1%; Score 82; DB 1; Length 355;  
Best Local Similarity 54.5%; Pred. No. 0.00011;  
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QWDFGNTMQLTGLYFGFSS 22  
Db 98 QWFGTVMCKVSGFYIGFYS 119

RESULT 30  
US-09-045-583-56  
Sequence 56, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 56:



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-045-583-56
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Query Match 65.1%; Score 82; DB 3; Length 355;
Best Local Similarity 54.5%; Pred. No. 0.00011;
Matches 12; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
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Db 98 QWVFGTVMCKWVSGFYIGFYS 119
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Job time : 15.1429 secs
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 18:03:03 ; Search time 29.4082 Seconds  
(without alignments) 157.962 Million cell updates

**Title:** US-10-084-813-12

Perfect score:

Sequence: 1 QWDFGNTMCQLLTGLYFIFGFS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum

Minimum Match 0%  
Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:\*

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| 2:  | /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*  |
| 3:  | /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*  |
| 4:  | /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*  |
| 5:  | /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*  |
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| 18: | /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*  |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Query % |       | Length | DB  | ID                | Description       |
|------------|---------|-------|--------|-----|-------------------|-------------------|
|            | Score   | Match |        |     |                   |                   |
| 1          | 136     | 100.0 | 22     | 14  | US-10-084-813-12  | Sequence 12, Appl |
| 2          | 136     | 100.0 | 22     | 184 | US-09-938-719-4   | Sequence 4, Appl  |
| 3          | 136     | 100.0 | 184    | 9   | US-09-938-719-4   | Sequence 4, Appl  |
| 4          | 136     | 100.0 | 184    | 9   | US-09-938-726-4   | Sequence 4, Appl  |
| 5          | 136     | 100.0 | 215    | 9   | US-09-938-703-4   | Sequence 4, Appl  |
| 6          | 136     | 100.0 | 215    | 9   | US-09-938-719-6   | Sequence 6, Appl  |
| 7          | 136     | 100.0 | 215    | 9   | US-09-939-226-6   | Sequence 6, Appl  |
| 8          | 136     | 100.0 | 215    | 9   | US-09-938-703-6   | Sequence 6, Appl  |
| 9          | 136     | 100.0 | 352    | 14  | US-10-095-876A-2  | Sequence 2, Appl  |
| 10         | 136     | 100.0 | 352    | 9   | US-09-725-285-2   | Sequence 2, Appl  |
| 11         | 136     | 100.0 | 352    | 9   | US-09-759-841-2   | Sequence 2, Appl  |
| 12         | 136     | 100.0 | 352    | 9   | US-09-779-879A-2  | Sequence 2, Appl  |
| 13         | 136     | 100.0 | 352    | 9   | US-09-779-879A-22 | Sequence 22, Appl |
| 14         | 136     | 100.0 | 352    | 9   | US-09-779-880A-2  | Sequence 2, Appl  |
| 15         | 136     | 100.0 | 352    | 9   | US-09-779-880A-22 | Sequence 22, Appl |
| 16         | 136     | 100.0 | 352    | 9   | US-09-779-880A-22 | Sequence 15, Appl |
| 17         | 136     | 100.0 | 352    | 9   | US-09-813-653-15  | Sequence 15, Appl |

89 71 56.3 355 15 US-10-452-015-2 Sequence 2, Appli  
90 71 56.3 375 14 US-10-219-834-78 Sequence 78, Appl  
91 69 54.8 355 9 US-09-938-719-9 Sequence 9, Appl  
92 69 54.8 355 9 US-09-939-226-9 Sequence 9, Appl  
93 69 54.8 355 9 US-09-938-703-9 Sequence 9, Appl  
94 67 53.2 332 13 US-10-001-835-140 Sequence 140, App  
95 67 53.2 355 9 US-09-931-381A-16 Sequence 16, Appl  
96 67 53.2 355 9 US-09-922-895-1 Sequence 1, Appl  
97 67 53.2 355 11 US-09-826-509-475 Sequence 475, App  
98 67 53.2 355 13 US-10-106-623-4 Sequence 4, Appl  
99 67 53.2 355 14 US-10-225-567A-64 Sequence 64, Appl  
100 67 53.2 355 14 US-10-283-028-2 Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-10-084-813-12  
; Sequence 12, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215975  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-12

Query Match 100.0%; Score 126; DB 14; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.2e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22  
Db 1 QWDFGNTWCQLLTGLYFIFGFFS 22

RESULT 2  
US-09-938-719-4  
; Sequence 4, Application US/09938719  
; Patent No. US20020106742A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; PARMENTIER, MARC  
; VASSART, GILBERT  
; LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/939,226  
; FILING DATE: 24-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/626,939  
; FILING DATE: 2000-07-27  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: <Unknown>  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 184 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/938,719  
; FILING DATE: 24-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/626,939  
; FILING DATE: 27-JULY-2000  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: <Unknown>  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 184 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-938-719-4  
  
Query Match 100.0%; Score 126; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 QWDFGNTWCQLLTGLYFIFGFFS 22  
Db 93 QWDFGNTWCQLLTGLYFIFGFFS 114  
  
RESULT 3  
US-09-939-226-4  
; Sequence 4, Application US/09939226  
; Patent No. US20020110805A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; PARMENTIER, MARC  
; VASSART, GILBERT  
; LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/939,226  
; FILING DATE: 24-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/626,939  
; FILING DATE: 2000-07-27  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: <Unknown>  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 184 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-939-226-4

Query Match 100.0%; Score 126; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 4

US-09-938-703-4  
; Sequence 4, Application US/09938703  
; Patent No. US20020110870A1  
; GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,703

FILING DATE: 24-Aug-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939

FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-938-703-4

Query Match 100.0%; Score 126; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 5

US-09-938-719-6  
; Sequence 6, Application US/09938719  
; Patent No. US20020106742A1  
; GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,719

FILING DATE: 24-Aug-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939

FILING DATE: 27-JULY-2000

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: &lt;Unknown&gt;

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-938-719-6

Query Match 100.0%; Score 126; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22  
DB 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 6

US-09-939-226-6

; Sequence 6, Application US/09939226

; Patent No. US20020110805A1

; GENERAL INFORMATION:

APPLICANT: SAMSON, MICHEL

PARMENTIER, MARC

VASSART, GILBERT

LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/939,226

FILING DATE: 24-Aug-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

```

/ APPLICATION NUMBER: 09/626,939
/
/ FILING DATE: 2000-07-27
/
/ ATTORNEY/AGENT INFORMATION:
/
/ NAME: Altman, Daniel E
/
/ REGISTRATION NUMBER: 34,115
/
/ REFERENCE/DOCKET NUMBER: <Unknown>
/
/ INFORMATION FOR SEQ ID NO: 6:
/
/ SEQUENCE CHARACTERISTICS:
/
/ LENGTH: 215 amino acids
/
/ TYPE: amino acid
/
/ TOPOLOGY: linear
/
/ MOLECULE TYPE: protein
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6:
/
/ US-09-939-226-6

```

```
Query Match 100.0%; Score 126; DB 9; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 QWDFGNTMCQLLTGLYFIGFFS 22  
db 93 QWDFGNTMCQLLTGLYFIGFFS 114

```

RESULT 7
US-09-338-703-6
; Sequence 6, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
;
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;
; NUMBER OF SEQUENCES: 17
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U. S. A.

```

Query Match 100.0%; Score 126; DB 9; Length 215;  
Best Local Similarity 100.0%; Pred. No. 2.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22

Db 93 QWDFGNTMCQLLTGLYFICGFFS 114

```

RESULT 8
US-10-095-876A-2
; Sequence 2, Application US/10095876A
; Publication No. US20030148294A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Bandman, Olga
; APPLICANT: Coleman, Roger; Wilde, Craig G.
; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS
; FILE REFERENCE: PP-0050-1 CON
; CURRENT APPLICATION NUMBER: US/10/095,876A
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 08/638,081
; PRIOR FILING DATE: 1996-04-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRN
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861
US-10-095-876A-2

```

|                       |                 |                    |           |             |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match           | 100.0%;         | Score 126;         | DB 14;    | Length 332; |
| Best Local Similarity | 100.0%;         | Pred. No. 3.3e-10; |           |             |
| Matches 22;           | Conservative 0; | Mismatches 0;      | Indels 0; | Gaps 0;     |

Qy 1 QWDFGNTMCQLLTGLYFIFGFFS 22  
Db 84 QWDFGNTMCQLLTGLYFIFGFFS 105

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RESULT 9
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US2001000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNE10
; TITLE OF INVENTION: (CCRS Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

```

```
Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 QWDFGNTMCQLLTGLYFIGFFS 22  
|||  
p'b 93 QWDFGNTMCQLLTGLYFIGFFS 114

RESULT 12

RESULT 14  
JS-09-779-880A-22

/ APPLICANT: Ruben, Steven, M.  
 /  
 / TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)  
 /  
 / FILE REFERENCE: 1488.1150002  
 /  
 / CURRENT APPLICATION NUMBER: US/09/195,662A  
 /  
 / CURRENT FILING DATE: 1998-11-18  
 /  
 / PRIOR APPLICATION NUMBER: 08/466,343  
 /

```

; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-195-662A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 19
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 20
US-09-338-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 21
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 22
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
```

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; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 27-JULY-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-719-5

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 21
US-09-939-226-5
; Sequence 5, Application US/09939226
; Patent No. US20020110805A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIFGFS 22
Db 93 QWDFGNTWCQLLTGLYFIFGFS 114

RESULT 22
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
```



```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-939-226-5

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 22
US-09-938-703-5
; Sequence 5, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-938-703-5

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 23
US-09-502-783A-2
; Sequence 2, Application US/09502783A
; Patent No. US20020132269A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR
; TITLE OF INVENTION: HDGNR10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-502-783A-2

Query Match 100.0%; Score 126; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFIFGFS 22
Db 93 QWDFGNTMCQLLTGLYFIFGFS 114

RESULT 24
US-09-734-221A-14
; Sequence 14, Application US/09734221A
; Publication No. US20030096221A1
; GENERAL INFORMATION:
; APPLICANT: LITTMAN, DAN R.
; DENG, HONGKUI
; EILMEIER, WILFRIED
; LANDAU, NATHANIEL R.
; LIU, RONG
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
; MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
; USES THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/734,221A
; FILING DATE: 11-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,020
; FILING DATE: 19-JUN-1996
; APPLICATION NUMBER: US 08/227,319
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-004 N2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
```

```

;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

Query Match 100.0%; Score 126; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFGFFS 114

RESULT 25
US-09-826-509-477
; Sequence 477, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 477
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-477

Query Match 100.0%; Score 126; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFGFFS 114

RESULT 26
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:

```

```

;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match 100.0%; Score 126; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTMCQLLTGLYFGFFS 22
Db 93 QWDFGNTMCQLLTGLYFGFFS 114

RESULT 27
US-10-106-623-20
; Sequence 20, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:

```

SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-106-623-20

Query Match 100.0%; Score 126; DB 13; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22  
DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

## RESULT 28

US-10-232-686-2  
; Sequence 2, Application US/10232686  
; Publication No. US20030023044A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.115000N  
; CURRENT APPLICATION NUMBER: US/10/232,686  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: 09/339,912  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 09/195,662  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/466,343  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-232-686-2

Query Match 100.0%; Score 126; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22  
DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

## RESULT 29

US-10-086-814-1  
; Sequence 1, Application US/10086814  
; Publication No. US2003002632A1  
; GENERAL INFORMATION:  
; APPLICANT: Dragic, Tatjana  
; APPLICANT: Olson, William C.  
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
; FILE REFERENCE: 61010-AB-1  
; CURRENT APPLICATION NUMBER: US/10/086,814  
; CURRENT FILING DATE: 2002-02-28  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-086-814-1

Query Match 100.0%; Score 126; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22  
DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

## RESULT 30

US-10-067-800-2  
; Sequence 2, Application US/10067800  
; Publication No. US20030100059A1  
; GENERAL INFORMATION:  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.115000I  
; CURRENT APPLICATION NUMBER: US/10/067,800  
; CURRENT FILING DATE: 2002-02-08  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: PCT/US01/04153  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 09/779,880  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/297,257  
; PRIOR FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: 60/310,458  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/328,447  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/341,725  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-800-2

Query Match 100.0%; Score 126; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QWDFGNTWCQLLTGLYFIGFFS 22  
DB 93 QWDFGNTWCQLLTGLYFIGFFS 114

Search completed: March 4, 2004, 18:22:51  
Job time : 29.4082 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 42.7959 Seconds  
(without alignments)  
118.840 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQYQFWKNPQTKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: A\_Geneseq\_23Jan04:\*

2: Geneseqp1980s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 96    | 100.0       | 18     | 4  | AAB88954           |
| 2          | 96    | 100.0       | 18     | 4  | AAB88995           |
| 3          | 96    | 100.0       | 352    | 2  | AAW27407 Human CCR |
| 4          | 96    | 100.0       | 352    | 2  | AAW27123 Human che |
| 5          | 96    | 100.0       | 352    | 2  | AAW07602 Human G-P |
| 6          | 96    | 100.0       | 352    | 2  | AAW23835 Human CC  |
| 7          | 96    | 100.0       | 352    | 2  | AAW88232 HIV-1 co- |
| 8          | 96    | 100.0       | 352    | 3  | AAW80128 Human G-P |
| 9          | 96    | 100.0       | 352    | 4  | AAW07046 Amino aci |
| 10         | 96    | 100.0       | 352    | 4  | AAW07048 Human G-P |
| 11         | 96    | 100.0       | 352    | 4  | AAW07048 Human G-P |
| 12         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |
| 13         | 96    | 100.0       | 352    | 4  | AAW07037 Human che |
| 14         | 96    | 100.0       | 352    | 4  | AAW07037 Human G-P |
| 15         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |
| 16         | 96    | 100.0       | 352    | 4  | AAW07037 Human G-P |
| 17         | 96    | 100.0       | 352    | 4  | AAW07037 Human HDG |
| 18         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |
| 19         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |
| 20         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |
| 21         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |
| 22         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |
| 23         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |
| 24         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |
| 25         | 96    | 100.0       | 352    | 4  | AAW07037 Human CCR |

|    |    |       |     |   |           |
|----|----|-------|-----|---|-----------|
| 26 | 96 | 100.0 | 352 | 5 | ABG92880  |
| 27 | 96 | 100.0 | 352 | 5 | AAE25808  |
| 28 | 96 | 100.0 | 352 | 5 | AAE25811  |
| 29 | 96 | 100.0 | 352 | 5 | ABE81054  |
| 30 | 96 | 100.0 | 352 | 5 | ABE808343 |
| 31 | 96 | 100.0 | 352 | 5 | ABG75540  |
| 32 | 96 | 100.0 | 352 | 6 | ABF58602  |
| 33 | 96 | 100.0 | 352 | 6 | AAO29514  |
| 34 | 96 | 100.0 | 352 | 6 | ABU61654  |
| 35 | 96 | 100.0 | 352 | 6 | ABP97728  |
| 36 | 96 | 100.0 | 352 | 6 | ABP81933  |
| 37 | 96 | 100.0 | 352 | 7 | ADC03341  |
| 38 | 96 | 100.0 | 371 | 2 | AAW23834  |
| 39 | 96 | 100.0 | 439 | 2 | AAW41280  |
| 40 | 93 | 96.9  | 352 | 2 | AAW27125  |
| 41 | 93 | 96.9  | 352 | 7 | ADC03359  |
| 42 | 82 | 85.4  | 21  | 2 | AAW50141  |
| 43 | 82 | 85.4  | 22  | 4 | AAW80087  |
| 44 | 82 | 85.4  | 32  | 2 | AAW43018  |
| 45 | 82 | 85.4  | 32  | 2 | AAW39912  |
| 46 | 78 | 81.2  | 18  | 4 | AAW88953  |
| 47 | 78 | 81.2  | 32  | 4 | AAW80086  |
| 48 | 78 | 81.2  | 138 | 5 | ABG32539  |
| 49 | 78 | 81.2  | 157 | 5 | ABG32540  |
| 50 | 75 | 78.1  | 18  | 4 | AAW88955  |
| 51 | 74 | 77.1  | 14  | 6 | ABP82819  |
| 52 | 74 | 77.1  | 20  | 4 | AAW83314  |
| 53 | 74 | 77.1  | 21  | 7 | AAE38756  |
| 54 | 74 | 77.1  | 354 | 7 | AAW54037  |
| 55 | 74 | 77.1  | 354 | 7 | ADD44859  |
| 56 | 74 | 77.1  | 354 | 7 | ADD44863  |
| 57 | 60 | 62.5  | 18  | 4 | AAW88952  |
| 58 | 60 | 62.5  | 27  | 2 | AAW46983  |
| 59 | 60 | 62.5  | 27  | 2 | AAW46985  |
| 60 | 60 | 62.5  | 27  | 2 | AAW46986  |
| 61 | 60 | 62.5  | 27  | 2 | AAW46990  |
| 62 | 60 | 62.5  | 27  | 2 | AAW46984  |
| 63 | 60 | 62.5  | 27  | 2 | AAW46982  |
| 64 | 60 | 62.5  | 27  | 6 | ABG75973  |
| 65 | 60 | 62.5  | 27  | 6 | ABU09550  |
| 66 | 54 | 56.2  | 27  | 2 | AAW46987  |
| 67 | 54 | 56.2  | 27  | 2 | AAW46988  |
| 68 | 52 | 54.2  | 27  | 2 | AAW46989  |
| 69 | 47 | 49.0  | 18  | 4 | AAW88956  |
| 70 | 47 | 49.0  | 31  | 2 | AAW40027  |
| 71 | 47 | 49.0  | 355 | 2 | AAW29179  |
| 72 | 47 | 49.0  | 355 | 7 | ADD45360  |
| 73 | 46 | 47.9  | 27  | 2 | AAW46991  |
| 74 | 45 | 46.9  | 314 | 7 | ADC01243  |
| 75 | 45 | 46.9  | 429 | 3 | AAW41644  |
| 76 | 45 | 46.9  | 436 | 3 | AAW41643  |
| 77 | 45 | 46.9  | 447 | 3 | AAW41642  |
| 78 | 44 | 45.8  | 332 | 2 | AAW26766  |
| 79 | 44 | 45.8  | 467 | 6 | ABU26719  |
| 80 | 44 | 45.8  | 616 | 4 | AAW88551  |
| 81 | 44 | 45.8  | 616 | 5 | AAU91482  |
| 82 | 43 | 44.8  | 24  | 2 | AAW23837  |
| 83 | 43 | 44.8  | 25  | 4 | AAW18971  |
| 84 | 43 | 44.8  | 25  | 4 | AAW38144  |
| 85 | 43 | 44.8  | 25  | 4 | AAW31572  |
| 86 | 43 | 44.8  | 25  | 4 | AAW23352  |
| 87 | 43 | 44.8  | 25  | 4 | AAW71293  |
| 88 | 43 | 44.8  | 25  | 4 | AAW58780  |
| 89 | 43 | 44.8  | 25  | 4 | ABG53004  |
| 90 | 43 | 44.8  | 25  | 5 | ABG41093  |
| 91 | 43 | 44.8  | 38  | 4 | ABW39710  |
| 92 | 43 | 44.8  | 38  | 4 | AAW33287  |
| 93 | 43 | 44.8  | 38  | 4 | AAW73068  |
| 94 | 43 | 44.8  | 38  | 4 | AAW60428  |
| 95 | 43 | 44.8  | 38  | 4 | ABG54782  |
| 96 | 43 | 44.8  | 38  | 5 | ABG42912  |
| 97 | 43 | 44.8  | 209 | 5 | ABP25707  |
| 98 | 43 | 44.8  | 232 | 2 | AAW36078  |

99 43 44.8 233 4 AAM39001 Human pol  
100 43 44.8 233 4 AAG89186 Human sec

ALIGNMENTS

```

RESULT 1
AAB88954
ID AAB88954 standard; peptide; 18 AA.
XX
AC AAB88954;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #47.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
PT WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
and binds to HIV gp120 under physiological conditions.
XX
PS Claim 21; Page 38; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
bind to HIV glycoprotein 120 (gp120). These are similar to the human
chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
useful in the treatment of HIV, as they prevent replication of the virus.
XX
CC The present sequence is an example of a peptide of the invention
Sequence 18 AA;
XX
SQ
Query Match 100.0%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKMFQTLKIVILG 18
DB 1 SOYQFWKMFQTLKIVILG 18

RESULT 2
AAB88995
ID AAB88995 standard; peptide; 18 AA.
XX
AC AAB88995;
XX
DT 23-MAY-2001 (first entry)
XX
DE HIV gp120 protein binding peptide #88.
XX
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
KW replication; CCR5; CXCR4; CD4; STRL33.
XX
OS Homo sapiens.
XX
PN WO200116182-A2.
XX
PD 08-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023505.
XX
PR 27-AUG-1999; 99US-0151270P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Saxinger C;
XX
PT WPI; 2001-244398/25.
XX
PT Novel polypeptides useful for treating HIV infection, have homology to
regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
and binds to HIV gp120 under physiological conditions.
XX
PS Example 1; Page 37; 114pp; English.
XX
CC The present invention describes a number of peptides which are able to
bind to HIV glycoprotein 120 (gp120). These are similar to the human
chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
useful in the treatment of HIV, as they prevent replication of the virus.
XX
CC The present sequence is an example of a peptide of the invention
Sequence 18 AA;
XX
SQ
Query Match 100.0%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKMFQTLKIVILG 18
DB 1 SOYQFWKMFQTLKIVILG 18

RESULT 3
AAM27407
ID AAM27407 standard; protein; 352 AA.
XX
AC AAM27407;
XX
DT 14-APR-1998 (first entry)
XX
DE Human CCR5.
XX
KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;
type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;
KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;
KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;
KW atherosclerosis; autoimmune disorder.
XX
OS Homo sapiens.
XX
PN WO9732019-A2.
XX
PD 04-SEP-1997.
XX
PF 28-FEB-1997; 97WO-BE000023.
XX
PR 01-MAR-1996; 96EP-00870021.
XX
PR 06-AUG-1996; 96EP-00870102.
XX
PA (EURO-) EUROSREEN SA.
XX
PI Samson M, Parmentier M, Vassart G, Libert F;
XX
PT WPI; 1997-479829/44.
XX
DR N-PSDB; AAT90117.
XX
PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful

```

PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune  
 PT disease and viral infection.  
 XX  
 PS Claim 4; Fig 1b-c; 94pp; English.  
 XX  
 CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),  
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but  
 CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3,  
 CC interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha)  
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency  
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to  
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid  
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and  
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,  
 CC atherosclerosis and autoimmune disorders  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFKNFQTLKIVILG 18  
 DB 185 SQYQFKNFQTLKIVILG 202  
 RESULT 4  
 AAW27123  
 ID AAW27123 standard; protein; 352 AA.  
 XX  
 AC AAW27123;  
 XX  
 DT 14-DEC-1997 (first entry)  
 XX  
 DE Human chemokine receptor 88C.  
 XX  
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;  
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;  
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;  
 KW modulator; antibody; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..32  
 FT /label= Extracellular\_domain  
 FT Domain 56..67  
 FT /label= Intracellular\_domain  
 FT Domain 89..112  
 FT /label= Extracellular\_domain  
 FT Domain 125..145  
 FT /label= Intracellular\_domain  
 FT Domain 166..191  
 FT /label= Extracellular\_domain  
 FT Domain 213..235  
 FT /label= Intracellular\_domain  
 FT Domain 259..280  
 FT /label= Extracellular\_domain  
 FT Domain 301..352  
 FT /label= Intracellular\_domain  
 XX  
 FN WO9722698-A2.  
 XX  
 PD 26-JUN-1997.  
 XX  
 XX 20-DEC-1996; 96WO-US020759.  
 XX  
 PR 20-DEC-1995; 95US-00575967.  
 PR 07-JUN-1996; 96US-00661393.  
 XX  
 PA (ICOS-) ICOS CORP.  
 XX

PI Gray PW, Schweickart VL, Raport CJ;  
 XX  
 DR WPI; 1997-341689/31.  
 DR N-PSDB; AAT85161.  
 XX  
 PT New nucleic acid encoding chemokine receptors 88-2B and 88C - used to  
 PT modulate leukocyte trafficking, e.g. for treatment of inflammation,  
 PT tumours, viral infections, auto-immune diseases, etc.  
 XX  
 XX Claim 16; Page 47-48; 65pp; English.  
 XX  
 CC This polypeptide sequence comprises novel human chemokine receptor 88C, a  
 CC G protein coupled receptor that is involved in leukocyte trafficking. Its  
 CC amino sequence was deduced from a cDNA clone (AAT85161) isolated from a  
 CC macrophage library. It shows 62% identity to CCR1. Chemokine receptor  
 CC 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors  
 CC and their polypeptide fragments can be produced in transformed host  
 CC cells. The receptors, peptides comprising one or more of the  
 CC extracellular or intracellular domains, and anti-receptor antibodies can  
 CC be used to modulate receptor activities, particularly ligand and G  
 CC protein binding, and are potentially useful in the treatment  
 CC of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral  
 CC infection, AIDS, inflammatory conditions, pathological immune response,  
 CC abnormal haematopoietic processes etc  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFKNFQTLKIVILG 18  
 DB 185 SQYQFKNFQTLKIVILG 202  
 RESULT 5  
 AAW07602  
 ID AAW07602 standard; protein; 352 AA.  
 XX  
 AC AAW07602;  
 XX  
 DT 26-FEB-1997 (first entry)  
 XX  
 DE Human G-protein chemokine receptor HDGNR10.  
 XX  
 KW G-protein chemokine receptor; HDGNR10; signal transduction;  
 KW haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;  
 KW therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9639437-A1.  
 XX  
 PD 12-DEC-1996.  
 XX  
 PF 06-JUN-1995; 95WO-US007173.  
 XX  
 PR 06-JUN-1995; 95WO-US007173.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Li Y, Ruben SM;  
 XX  
 DR WPI; 1997-043072/04.  
 DR N-PSDB; AAT44042.  
 XX  
 PT Human G-protein chemokine receptor, HDGNR10 - useful to identify  
 PT (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and  
 PT acute inflammation, rheumatoid arthritis, etc.  
 XX  
 PS Claim 1; Page 44-46; 61pp; English.  
 XX

CC Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7  
 CC -transmembrane protein involved in signal transduction. Its amino acid  
 CC sequence was deduced from a cDNA clone (AAT44042) isolated from a human  
 CC monocyte library. Isolation of the cDNA allows prodn. of recombinant  
 CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant  
 CC receptor can be used to identify agonists or antagonists of the receptor;  
 CC such cpds. can be used to treat conditions related to the under- and over  
 CC -expression of G-protein chemokine receptors  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQQFWKFNFTLKIVILG 18  
 DB 185 SQQFWKFNFTLKIVILG 202  
 RESULT 6  
 AAW23835  
 ID AAW23835 standard; protein; 352 AA.  
 XX  
 AC AAW23835;  
 XX  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Human CC chemokine receptor 5 (CCR5).  
 XX  
 KW CC chemokine receptor 5; CCR5; G-protein coupled receptor;  
 KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 29..55  
 FT /label= I  
 FT /note= "transmembrane domain"  
 FT 104..126  
 FT /label= III  
 FT /note= "transmembrane domain"  
 FT 109..120  
 FT /note= "extracellular loop-1 (Claim 19)"  
 FT 143..171  
 FT /label= IV  
 FT /note= "transmembrane domain"  
 FT 187..210  
 FT /note= "extracellular loop-2 (Claim 19)"  
 FT 194..219  
 FT /label= V  
 FT /note= "transmembrane domain"  
 FT 238..258  
 FT /label= VI  
 FT /note= "transmembrane domain"  
 FT 261..276  
 FT /note= "extracellular loop-3 (Claim 19)"  
 FT 277..300  
 FT /label= VII  
 FT /note= "transmembrane domain"  
 XX  
 PN W09745543-A2.  
 XX  
 PD 04-DEC-1997.  
 XX  
 PF 28-MAY-1997; 97WO-US009586.  
 XX  
 PR 28-MAY-1996; 96US-0018508P.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Combadriere C, Feng Y, Berger EA, Alkhatib G, Murphy PM,  
 PI Broder CC, Kennedy PE;

XX WPI; 1998-032650/03.  
 DR N-PSDB; AAT76920.  
 XX  
 CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion  
 FT between HIV and a target cell.  
 XX  
 PS Claim 68; Fig 1C; 70pp; English.  
 XX  
 CC This protein sequence comprises of a novel human macrophage-selective CC  
 CC chemokine receptor that has been designated CCR5. The sequence was  
 CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant  
 CC (see W238340 of CCR5 was also identified. The susceptibility of human  
 CC macrophages to HIV infection depends on cell surface expression of CD4  
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-  
 CC protein coupled cell surface molecules. It plays an essential role in the  
 CC membrane fusion step of infection by some HIV isolates. The establishment  
 CC of stable, non-human cell lines and transgenic mammals having cells that  
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV  
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding  
 CC agents capable of blocking membrane fusion between HIV and target cells  
 CC represent potential anti-HIV therapeutics for macrophage tropic strains  
 CC of HIV  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQQFWKFNFTLKIVILG 18  
 DB 185 SQQFWKFNFTLKIVILG 202  
 RESULT 7  
 AAW88232  
 ID AAW88232 standard; protein; 352 AA.  
 XX  
 AC AAW88232;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE HIV-1 co-receptor CCR5.  
 XX  
 KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;  
 KW gene therapy; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 32..56  
 FT /note= "transmembrane domain 1"  
 FT 67..87  
 FT /note= "transmembrane domain 2"  
 FT Misc-difference 101  
 FT /note= "corresponds to TGT (Cys) in wild-type CCR5, TGA  
 FT (Stop) in CCR5m303"  
 FT 103..124  
 FT /note= "transmembrane domain 3"  
 FT 142..167  
 FT /note= "transmembrane domain 4"  
 FT 200..223  
 FT /note= "transmembrane domain 5"  
 FT 236..260  
 FT /note= "transmembrane domain 6"  
 FT 275..301  
 FT /note= "transmembrane domain 7"  
 XX  
 PN W09854317-A1.  
 XX  
 PD 03-DEC-1998.  
 XX

PF 29-MAY-1998; 98WO-EP003437.  
 XX  
 PR 30-MAY-1997; 97US-0048057P.  
 XX  
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.  
 XX  
 XX Beretta A, Quillent C, Arenzana Siededros F, Braun J;  
 XX WPI; 1999-059835/05.  
 DR N-PSDB; AAV84126.  
 XX  
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing  
 PT resistance of CCR5-expressing cells to HIV-1 infection.  
 PT Disclosure; Page 34-35; 55pp; English.  
 XX  
 XX This is the amino acid sequence of wild-type human CCR5, which serves as  
 CC a co-receptor for infection by macrophage-tropic (M-tropic) strains of  
 CC HIV-1. The invention relates to the identification of a CCR5 variant (see  
 CC AAV84126), designated CCR5m303, comprising the first two transmembrane  
 CC domains of wild-type CCR5, but lacking transmembrane domains 3-7. The  
 CC presence of the CCR5m303 variant with the wild type CCR5 allele shows a  
 CC positive correlation with resistance to infection with M-tropic HIV-1  
 CC strains, and may indicate slower progression of the disease. The  
 CC detection of CCR5 variants may be used to identify individuals at lower  
 CC risk of infection relative to the general population who, if infected,  
 CC may exhibit slower progression to AIDS. Probes and primers (see AAV84127-  
 CC 36) are provided for use in diagnostic methods for detecting the presence  
 CC of such variants. A method is provided for inhibiting HIV-1 infection of  
 CC a cell expressing the CCR5 receptor. This involves introducing a nucleic  
 CC acid encoding a CCR5 variant into the cell, thereby reducing the number  
 CC of functional CCR5 molecules present on the cell surface  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 96; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 Db 185 SQYQFWKNFQTLKIVILG 202  
 |||||  
 RESULT 8  
 AAY80128  
 ID AAY80128 standard; protein; 352 AA.  
 XX  
 AC AAY80128;  
 XX  
 DT 19-MAY-2000 (first entry)  
 XX  
 DE Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.  
 XX  
 KW Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;  
 KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;  
 KW tumour; infection; leukaemia; psoriasis; allergy;  
 KW T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;  
 KW inflammation; allergic reaction; silicosis; sarcoidosis;  
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US6025154-A.  
 XX  
 XX 15-FEB-2000.  
 XX  
 PF 06-JUN-1995; 95US-00466343.  
 XX  
 PR 06-JUN-1995; 95US-00466343.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX

PI Li Y, Ruben SM;  
 XX  
 DR WPI; 2000-181807/16.  
 DR N-PSDB; AAZ91481.  
 XX  
 PT Isolated nucleic acid encoding human G-protein chemokine receptor useful  
 PT for diagnostic assays, scientific research and screening for compounds  
 PT which bind to and activate or inhibit activation of the receptor  
 PT polypeptides.  
 XX  
 XX Claim 1; Fig 1; 22pp; English.  
 XX  
 XX The present sequence represents a human G-protein chemokine receptor  
 CC designated HDGNR10. HDGNR10 polynucleotides are useful in methods of  
 CC screening for compounds which bind to and either: (1) activate the  
 CC HDGNR10 polypeptides causing stimulation of haematopoiesis, wound  
 CC healing, coagulation, and angiogenesis; treatment of solid tumours,  
 CC chronic infections, leukaemia, T-cell mediated autoimmune diseases,  
 CC parasitic infections, psoriasis, and to stimulate growth factor activity;  
 CC or (2) inhibit activation of the HDGNR10 polypeptides which is useful for  
 CC preventing and/or treating allergy, atherosclerosis, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin  
 CC E-mediated allergic reactions, prostaglandin-independent fever, bone  
 CC marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and  
 CC hyper-eosinophilia syndrome. The polynucleotides are also useful for  
 CC diagnostic assays for detecting diseases related to mutations in the  
 CC nucleic acid sequences encoding the polypeptides and for detecting an  
 CC altered level of the soluble form of the receptor polypeptides. The  
 CC polynucleotides are also useful for in vitro purposes related to  
 CC scientific research, synthesis of DNA and manufacture of DNA vectors  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 96; DB 3; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 Db 185 SQYQFWKNFQTLKIVILG 202  
 |||||  
 RESULT 9  
 AAG79089  
 ID AAG79089 standard; protein; 352 AA.  
 XX  
 AC AAG79089;  
 XX  
 DT 10-DEC-2001 (first entry)  
 XX  
 DE Amino acid sequence of human CCR5 protein.  
 XX  
 KW Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;  
 KW C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200164752-A2.  
 XX  
 XX 07-SEP-2001.  
 XX  
 XX 28-FEB-2001; 2001WO-US006322.  
 XX  
 PR 02-MAR-2000; 2000US-00517605.  
 XX  
 XX (UTNY ) UNIV NEW YORK STATE.  
 XX (UTNY-) UNIV NIJMEGEN.  
 XX  
 PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;  
 XX WPI; 2001-602565/68.  
 DR  
 XX An antibody for the treatment or prevention of HIV-infection comprises a



PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of  
 PT DC-SIGN due to concomitant conformational change.

XX Disclosure; Page 118-119; 131pp; English.

CC The specification describes an antibody which is specific for an  
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or  
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant  
 CC conformational change. DC-SIGN is a receptor that is specifically  
 CC expressed on dendritic cells and facilitates infection of T lymphocytes  
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC  
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)  
 CC with high affinity. The antibody of the invention inhibits the trans  
 CC enhancement of HIV entry into a T cell or macrophage facilitated by  
 CC dendritic cells. The antibody is useful to treat or prevent HIV  
 CC infection. The present sequence represents a human CCR5 protein, which is  
 CC a translocation promoting agent that interacts with CD4. This receptor  
 CC functions in HIV-1 entry into cells

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18  
 |||||  
 Db 185 SQYQWKNFQTLKIVILG 202

RESULT 10

AAE07046  
 ID AAE07046 standard; protein; 352 AA.

XX AAE07046;

DT 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;  
 KW cytostatic; immunosuppressive; neutropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX Key Location/Qualifiers

FT 1..36 /label= Extracellular\_domain  
 FT 37..305 /label= Transmembrane\_domain  
 FT 37..58 /label= Transmembrane\_domain  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 1"  
 FT 59..67 /label= Intracellular\_loop\_1  
 FT 68..88 /label= Transmembrane\_domain  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 2"  
 FT 89..102 /label= Extracellular\_loop\_1  
 FT 103..124 /label= Transmembrane\_domain  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 3"  
 FT 125..141 /label= Intracellular\_loop\_2  
 FT 142..166 /label= Intracellular\_loop\_2

FT /label= Transmembrane\_domain  
 FT /note= "Segment 4"  
 FT 167..195 /label= Extracellular\_loop\_2  
 FT 196..223 /label= Transmembrane\_domain  
 FT /note= "Segment 5"  
 FT 224..235 /label= Intracellular\_loop\_3  
 FT 236..260 /label= Transmembrane\_domain  
 FT /note= "Segment 6"  
 FT 261..274 /label= Extracellular\_loop\_3  
 FT 287..305 /label= Transmembrane\_domain  
 FT /note= "Segment 7"  
 FT 306..352 /label= Intracellular\_domain

WO200158916-A2.

16-AUG-2001.

09-FEB-2001; 2001WO-US004153.

09-FEB-2000; 2000US-0181258P.

09-MAR-2000; 2000US-0187999P.

22-SEP-2000; 2000US-0234336P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Roschke V, Li Y, Ruben SM;

WPI; 2001-48866/53.

N-PDDB; AAD13282.

Isolated nucleic acid encoding a human G-protein chemokine receptor  
 (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 neurodegenerative disorders.

Claim 102; Fig 1; 518pp; English.

The invention relates to human G-protein chemokine receptor (CCR5)  
 CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are  
 CC useful for treating, preventing or ameliorating a disease or disorder  
 CC associated with inflammation, defective or aberrant chemotaxis of immune  
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's  
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell  
 CC interaction. The disease or disorder may also be an infectious disease  
 CC (e.g. a viral infection such as an early stage HIV infection, a  
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune  
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The  
 CC disease or disorder may be associated with aberrant CCR5 expression, lack  
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand  
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative  
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful  
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,  
 CC protein, antibodies, agonists and antagonists are also useful in the  
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal  
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,  
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)  
 CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The  
 CC present sequence is human CCR5 HDGNR10 protein

Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18  
DB 185 SOYQFWKFNFTLKIVILG 202

RESULT 11  
AAE07048  
ID AAE07048 standard; protein; 352 AA.  
XX  
AC AAE07048;  
XX  
DT 16-OCT-2001 (first entry)  
XX  
DE Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;  
XX human immunodeficiency virus; antimicrobial; vasodilator; vulnery;  
KW cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;  
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.  
OS  
XX WO200158916-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 09-FEB-2001; 2001WO-US004153.  
XX  
XX 09-FEB-2000; 2000US-0181259P.  
PR  
XX 09-MAR-2000; 2000US-0187999P.  
PR  
XX 22-SEP-2000; 2000US-0234336P.  
PR  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX

PI Rosen CA, Roschke V, Li Y, Ruben SM;  
XX  
XX WPI; 2001-488966/53.  
DR  
XX N-PSDB; AAD13299.  
DR  
XX

PT Isolated nucleic acid encoding a human G-protein chemokine receptor  
PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune  
PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
PT neurodegenerative disorders.

XX Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)  
CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are  
CC useful for treating, preventing or ameliorating a disease or disorder  
CC associated with inflammation, defective or aberrant chemotaxis of immune  
CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's  
CC sarcoma) or defective or aberrant T-cell antigen presenting cell  
CC interaction. The disease or disorder may also be an infectious disease  
CC (e.g. a viral infection such as an early stage HIV infection, a  
CC cytomegalovirus infection, or a poxvirus infection), an autoimmune  
CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The  
CC disease or disorder may be associated with aberrant CCR5 expression, lack  
CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand  
CC function. CCR5 HDGMR10 protein is used as a food additive or preservative  
CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful  
CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA, a  
CC protein, antibodies, agonists and antagonists are also useful in the  
CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal  
CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,  
CC urogenital); immune disorders (Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)

CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The  
CC present sequence is human CCR5 HDGMR10 protein  
XX  
SQ Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18  
DB 185 SOYQFWKFNFTLKIVILG 202

RESULT 12  
AAG80111  
ID AAG80111 standard; protein; 352 AA.  
XX  
AC AAG80111;  
XX  
DT 17-JAN-2002 (first entry)  
XX  
DE Human CCR5 protein.  
XX  
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
KW anti-inflammatory; antiasthmatic; immunosuppressive; dermatological;  
KW antirheumatic; antiarthritic.

XX Homo sapiens.  
OS  
XX WO200172830-A2.  
XX  
XX 04-OCT-2001.  
XX

XX 02-APR-2001; 2001WO-EP003708.  
XX  
XX 31-MAR-2000; 2000DB-01016013.  
XX

PA (IPFP-) IPF PHARM GMBH.  
PA (FORS/) FORSSMANN U.  
XX

PI Forssmann W, Adermann K, Heitland A, Spodsborg N;  
XX

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful  
PT for detecting tumors, inflammation etc., also therapeutic use of ligand  
PT inhibitors.

XX Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least  
CC two different ligands (I) for receptors (II) that are implicated in  
CC disease. (A) are used for the diagnosis of tumors (especially colorectal  
CC or prostatic), organ rejection, inflammation and autoimmune diseases.  
CC Also inhibitors of (I) are used therapeutically against tumors (and their  
CC metastases), inflammation (particularly bronchial asthma or chronic bowel  
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
CC endocrine, motor or urogenital systems or skin are affected, and bone  
CC marrow diseases. The products of the invention are chemokine derivatives  
CC which have cytostatic, antiinflammatory, antiasthmatic,  
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.  
CC Chemokines act on specific tumor and inflammatory cells through a  
CC constellation of chemokine receptors (CR), which control migration and  
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
CC fragments used to illustrate the method of the invention

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKIVILG 18  
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 13

AAE04321  
ID AAE04321 standard; protein; 352 AA.

AC AAE04321;

DT 04-SEP-2001 (first entry)

XX Human chemokine receptor (CCR), CC-CR-5 related protein #2.

XX Human; transformed mammalian cell; CD4; reporter gene; translocation;  
KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;  
KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;  
KW CC-CR-5; envelope glycoprotein; anti-HIV.

XX Homo sapiens.

XX US6258527-B1.

XX 10-JUL-2001.

XX 21-MAY-1997; 97US-00861105.

XX 20-MAY-1996; 96US-0017157P.

XX 19-JUN-1996; 96US-0020043P.

XX 19-MAY-1997; 97US-00858660.

XX (AARO-) AARON DIAMOND AIDS RES CENT.

XX (UNYV) UNIV NEW YORK STATE.

XX Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;

XX WPI; 2001-417127/44.

XX N-PSDB; AAD08577.

XX Transformed mammalian cell (1) that contains a CD4 gene, reporter gene  
PT and HIV LTR for identification of drugs and antibodies for treatment of  
PT HIV.

XX Disclosure; Col 47-50; 37pp; English.

XX The present invention relates to a transformed mammalian cell that  
CC contains a gene encoding CD4, a construct encoding a reporter gene under  
CC the regulation of an human immuno deficiency virus (HIV) long terminal  
CC repeat (LTR) and that has been transduced with a vector encoding a human  
CC chemokine receptor (CCR) where the CD4 and the CCR are present on the  
CC cell surface of transformed mammalian cell. The invention is useful for  
CC identifying drugs or antibodies that interfere with the translocation of  
CC HIV into transformed mammalian cell or for identifying a human chemokine  
CC receptor that facilitates the infection of a particular HIV strain into  
CC the transformed mammalian cell. Compounds identified can be used to treat  
CC cellular dysfunction and to prevent or combat HIV infection. The present  
CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.  
CC CC-CR-5 is the principal cofactor for entry mediated by the envelope  
CC glycoproteins of primary macrophage-tropic strains of HIV-1

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKIVILG 18  
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 14

AAE07037

ID AAE07037 standard; protein; 352 AA.

XX AAE07037;

XX 16-OCT-2001 (first entry)

XX Human G-protein chemokine receptor (CCR5) HDGMR10 protein #1.

XX Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;  
KW human immunodeficiency virus; antineoplastic; vasodilator; vulnery;  
KW cytostatic; immunosuppressive; neotropic; neuroprotective; gene therapy;  
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX Key

XX Domain 1..36

XX /label= Extracellular\_domain

XX Domain 37..305

XX /label= Transmembrane\_domain

XX Domain 37..58

XX /label= Transmembrane\_domain

XX Domain 59..67

XX /label= Intracellular\_loop\_1

XX Domain 68..88

XX /label= Transmembrane\_domain

XX Domain 89..102

XX /label= Extracellular\_loop\_1

XX Domain 103..124

XX /label= Transmembrane\_domain

XX Domain 125..141

XX /label= Intracellular\_loop\_2

XX Domain 142..166

XX /label= Transmembrane\_domain

XX Domain 167..195

XX /label= Extracellular\_loop\_2

XX Domain 196..223

XX /label= Transmembrane\_domain

XX Domain 224..235

XX /label= Intracellular\_loop\_3

XX Domain 236..260

XX /label= Transmembrane\_domain

XX Domain 261..274

XX /label= Extracellular\_loop\_3

XX Domain 287..305

XX /label= Transmembrane\_domain

XX Domain 306..352

XX /label= Intracellular\_domain

XX WO200158915-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004152.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

PR 22-SEP-2000; 2000US-0234336P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX WPI; 2001-488965/53.  
 DR N-PSDB; AAD13181.  
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor  
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 PT neurodegenerative disorders.  
 XX Claim 102; Fig 1; 495pp; English.  
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10  
 CC protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No. 97193. CCR5  
 CC HDGNR10 antibodies are useful for treating, preventing or ameliorating a  
 CC disease or disorder associated with inflammation, defective or aberrant  
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii  
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen  
 CC presenting cell interaction. The disease or disorder may also be an  
 CC infectious disease (e.g. a viral infection such as an early stage HIV  
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an  
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative  
 CC disorder. The disease or disorder may be associated with aberrant CCR5  
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or  
 CC lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food  
 CC additive or preservative to increase or decrease storage capabilities.  
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene  
 CC therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists  
 CC are also useful in the diagnosis, treatment and prevention of cancer  
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,  
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,  
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound  
 CC healing  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 96; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SOYQFWKNFQTLKIVILG 18  
 |||||  
 DB 185 SOYQFWKNFQTLKIVILG 202  
 RESULT 15  
 AAEO7039  
 ID AAE07039 standard; protein; 352 AA.  
 AC AAE07039;  
 XX 16-OCT-2001 (first entry)  
 DT Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.  
 DE  
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;  
 KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.  
 XX Homo sapiens.  
 OS  
 XX

PN WO200158915-A2.  
 XX 16-AUG-2001.  
 XX 09-FEB-2001; 2001WO-US004152.  
 XX 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX WPI; 2001-488965/53.  
 DR N-PSDB; AAD13198.  
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor  
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 PT neurodegenerative disorders.  
 XX Example 40; Page 486-487; 495pp; English.  
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10  
 CC protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or  
 CC ameliorating a disease or disorder associated with inflammation,  
 CC defective or aberrant chemotaxis of immune cells, HIV infection (such as  
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or  
 CC aberrant T-cell antigen presenting cell interaction. The disease or  
 CC disorder may also be an infectious disease (e.g. a viral infection such  
 CC as an early stage HIV infection, a cytomegalovirus infection, or a  
 CC poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or  
 CC a neurodegenerative disorder. The disease or disorder may be associated  
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5  
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein  
 CC is used as a food additive or preservative to increase or decrease  
 CC storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome  
 CC identification and in gene therapy. CCR5 HDGNR10 DNA, protein,  
 CC antibodies, agonists and antagonists are also useful in the diagnosis,  
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,  
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune  
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,  
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple  
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular  
 CC disorders (myocardial ischaemias) and wound healing  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 96; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SOYQFWKNFQTLKIVILG 18  
 |||||  
 DB 185 SOYQFWKNFQTLKIVILG 202  
 RESULT 16  
 AAB46858  
 ID AAB46858 standard; protein; 352 AA.  
 XX AAB46858;  
 XX 16-AUG-2001 (revised)  
 DT 02-AUG-2001 (revised)  
 DT 04-MAY-2001 (first entry)  
 XX Human HDGNR10 protein.  
 DE  
 XX HDGNR10; human; G-protein chemokine receptor; antiinflammatory;  
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;  
 KW cytostatic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;

KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;  
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;  
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;  
 KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;  
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;  
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;  
 KW hyper-eosinophilic syndrome; vulnery.

OS Homo sapiens.  
 XX  
 XX US2001000241-A1.  
 PN  
 XX  
 XX 12-APR-2001.  
 PD  
 XX  
 XX 29-NOV-2000; 2000US-00725285.  
 PF  
 XX  
 XX 06-JUN-1995; 95US-00466343.  
 PR  
 XX 18-NOV-1998; 98US-00195662.  
 PR  
 XX 25-JUN-1999; 99US-00339912.  
 PR  
 XX (LIVY/) LI Y.  
 PA (RUBE/) RUBEN S M.  
 PA  
 XX  
 XX Li Y, Ruben SM;  
 PI  
 XX WPI; 2001-226317/23.  
 DR N-PSDB; AAF26390.  
 DR  
 XX  
 XX New human G-protein chemokine receptor polypeptides and polynucleotides,  
 PT useful for identifying (ant)agonists to the G-protein chemokine receptor.  
 PT  
 XX  
 XX Claim 1a; Page 15; 22pp; English.

XX This invention describes a novel receptor polypeptide (I) selected from  
 CC (i) a fully defined 323 amino acid sequence (II) fully disclosed in the  
 CC specification; and (ii) a polypeptide encoded by the cDNA contained in a  
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The  
 CC products of the invention have antiinflammatory, immunomodulatory,  
 CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic,  
 CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic  
 CC activity and can be used for gene therapy. The G-protein chemokine  
 CC receptors, HDGRI0, (I) are useful for screening for compounds which  
 CC activate or inhibit activation of (I). The products of the invention can  
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,  
 CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-  
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and  
 CC stimulating growth factor activity. HDGRI0 is useful for treating  
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic  
 CC reactions, prostaglandin-independent fever, bone marrow failure,  
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-  
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct  
 CC errors in the keyword formatting)

XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 17  
 ABB56342  
 ID ABB56342 standard; protein; 352 AA.  
 XX  
 AC ABB56342;  
 XX  
 XX 18-FEB-2002 (first entry)  
 DT  
 XX

DE Non-endogenous human GPCR protein, SEQ ID NO: 477.  
 XX  
 XX Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;  
 KW constitutively activated GPCR; agonist; disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Synthetic.  
 XX  
 XX WO200177172-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX  
 XX 05-APR-2001; 2001WO-US011098.  
 PF  
 XX  
 XX 07-APR-2000; 2000US-0195747P.  
 PR  
 XX (AREN-) ARENA PHARM INC.  
 PA  
 XX Lehmann-Bruinsma K, Liaw CW, Lin I;  
 PI  
 XX WPI; 2001-648759/74.  
 DR N-PSDB; ABI97978.  
 DR  
 XX  
 XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in  
 PT disease treatment, comprises contacting candidate compounds with versions  
 PT of GPCRs.  
 PT  
 XX  
 XX Claim 1; Page 277-278; 394pp; English.

XX The invention relates to G protein-coupled receptors (GPCRs) for which  
 CC the endogenous ligand has been identified. Non-endogenous constitutively  
 CC activated versions of known GPCRs are used in the invention for the  
 CC direct identification of candidate compounds as receptor agonists,  
 CC inverse agonists or partial agonists. Such agonists are useful as  
 CC therapeutic agents for diseases or disorders associated with GPCRs. The  
 CC present sequence is a non-endogenous version of a known human GPCR  
 XX Sequence 352 AA;

Query Match 100.0%; Score 96; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 18  
 AAB83354  
 ID AAB83354 standard; protein; 352 AA.

XX AAB83354;

XX 09-OCT-2001 (first entry)

XX Human CCR5 protein sequence.

XX Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;  
 KW human immunodeficiency virus; anti-inflammatory disease; human.

XX Homo sapiens.

XX EP1118858-A2.

XX 25-JUL-2001.

XX 03-JAN-2001; 2001EP-00300020.

XX 12-JAN-2000; 2000GB-00000659.

XX 12-JAN-2000; 2000GB-00000661.

XX 12-JAN-2000; 2000GB-00000663.

PA (PFIZ ) PFIZER LTD.  
 XX (PFIZ ) PFIZER INC.  
 PI Dobbs S, Perros M, Rickett GA;  
 XX  
 DR WPI: 2001-477088/52.  
 DR N-PSDB; AAF87099.  
 XX  
 PT Determining if an agent can modulate CCR5-gp120 interaction, comprises  
 PT incubating the agent with CCR5 and gp120 and determining if the agent  
 PT modulates the interaction.  
 XX  
 PS Claim 1; Page 110; 113pp; English.  
 XX  
 CC This sequence represents the human CCR5 protein sequence. The invention  
 CC relates to a method for determining whether an agent is capable of  
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)  
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and  
 CC determining whether the agent modulates the interaction, where gp120 is  
 CC associated with CD4, and where the interaction is a low affinity binding.  
 CC The method is used to identify an agent capable of modulating the  
 CC interaction of CCR5 with gp120. An agent identified by the method is used  
 CC to prepare a pharmaceutical composition for the treatment of a disease or  
 CC condition associated with CCR5 and gp120 interaction, to treat a subject  
 CC with a disease or condition associated with CCR5 and gp120 interaction,  
 CC and for preparing a pharmaceutical for treating human immunodeficiency  
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method  
 CC is commercially useful, amenable to high throughput screening, and  
 CC detects interaction of gp120 with cells expressing only CCR5  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 Db 185 SQYQFWKNFQTLKIVILG 202  
 RESULT 19  
 AAB82948  
 ID AAB82948 standard; protein; 352 AA.  
 AC AAB82948;  
 DT 21-DEC-2001 (first entry)  
 XX  
 DE Human HIV-1 co-receptor CCR5.  
 XX  
 CC CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;  
 KW infection; therapy; vaccine; anti-HIV-1.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Binding-site 2..18  
 FT /note= "binds to HIV-1 gp120"  
 XX  
 PN W0200164710-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US006699.  
 XX  
 PR 29-FEB-2000; 2000US-0185667P.  
 PR 19-MAY-2000; 2000US-0205839P.  
 PR 07-FEB-2001; 2001US-0267231P.  
 XX  
 PA (PROG-) PROGENICS PHARM INC.  
 PA (AARO-) ARON DIAMOND AIDS RES CENT.  
 XX

PI Dragic T, Olson WC;  
 XX  
 DR WPI: 2001-611273/70.  
 DR N-PSDB; AAH26903.  
 XX  
 PT Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-  
 PT receptor) amino terminal domain including negatively charged and two  
 PT sulfated tyrosine residues is useful for treating HIV infection in  
 PT humans.  
 XX  
 PS Claim 1; Page 30; 163pp; English.  
 XX  
 CC The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids  
 CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding  
 CC site that determines the specificity of the interaction between CCR5 and  
 CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the  
 CC CCR5 N-terminus is required for gp120 binding and may critically modulate  
 CC the susceptibility of target cells to HIV-1 infection in vivo. The  
 CC invention provides claimed sulfated peptides (see AAB82947) that are  
 CC based on the CCR5 N-terminal region and which are effective for  
 CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed  
 CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+  
 CC cells from becoming infected with HIV, of treating a subject whose CD4+  
 CC cells are infected with HIV, and of identifying an agent which inhibits  
 CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried  
 CC out in a subject, especially a human, infected (therapeutic method), not  
 CC infected with HIV (prophylactic method), or in a subject who is not  
 CC infected with, but has been exposed to, HIV  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 Db 185 SQYQFWKNFQTLKIVILG 202  
 RESULT 20  
 AAU97150  
 ID AAU97150 standard; protein; 352 AA.  
 XX  
 AC AAU97150;  
 XX  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.  
 XX  
 CC Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;  
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;  
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;  
 KW hyperproliferative disease; neurological disease; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002048786-A1.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 09-FEB-2001; 2001US-00779879.  
 XX  
 PR 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 XX  
 CC (ROSE/) ROSEN C A.  
 PA (ROSC/) ROSCHKE V.  
 PA (LIY/) LI Y.  
 PA (RUBE/) RUBEN S M.  
 XX  
 PI Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2002-434754/46.  
 DR N-PSDB; ABK51853.  
 XX  
 PT New nucleic acid encoding an antibody specific for the G-protein  
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.  
 PT inflammation.  
 XX  
 XX Claim 61; Fig 1; 180pp; English.  
 XX  
 CC The present invention relates to the isolation of a novel human G-protein  
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide  
 CC sequences encoding it. The invention also describes antibodies that bind  
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide  
 CC sequences encoding the antibodies. The antibodies are useful for treating  
 CC or preventing inflammation, defective or aberrant chemotaxis of immune  
 CC cells and T-cell/antigen-presenting cell interactions, infections and  
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral  
 CC infections (especially early-stage human immune deficiency virus (HIV),  
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions  
 CC associated with aberrant or deficient expression of the CCR5 receptor or  
 CC its ligands. The antibodies are also useful to determine CCR5 expression,  
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other  
 CC hyperproliferative diseases. The polynucleotide sequences encoding human  
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the  
 CC recombinant receptor, and in the treatment of a wide range of diseases  
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.  
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The  
 CC present sequence represents human G-protein chemokine receptor (CCR5)  
 CC HDGNR10 #1.  
 XX  
 XX Sequence 352 AA;  
 SQ

Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18  
 |||||  
 Db 185 SOYQFWKFNFTLKIVILG 202

RESULT 21  
 AAU97152  
 ID AAU97152 standard; protein; 352 AA.  
 XX  
 AC AAU97152;  
 XX  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 #2.  
 XX  
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;  
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;  
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;  
 KW hyperproliferative disease; neurological disease; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002048786-A1.  
 XX  
 PD 25-APR-2002.  
 XX  
 XX 09-FEB-2001; 2001US-00779879.  
 XX  
 PR 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 XX  
 XX (ROSE/) ROSEN C A.  
 PA (ROSC/) ROSCHKE V.  
 PA (LIY/) LI Y.  
 PA (RUBE/) RUBEN S M.

XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX WPI; 2002-434754/46.  
 DR N-PSDB; ABK51870.  
 XX  
 PT New nucleic acid encoding an antibody specific for the G-protein  
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.  
 PT inflammation.  
 XX  
 XX Disclosure; Page 165-166; 180pp; English.  
 XX  
 CC The present invention relates to the isolation of a novel human G-protein  
 CC chemokine receptor (CCR5) designated HDGNR10, and polynucleotide  
 CC sequences encoding it. The invention also describes antibodies that bind  
 CC human G-protein chemokine receptor (CCR5) HDGNR10 and polynucleotide  
 CC sequences encoding the antibodies. The antibodies are useful for treating  
 CC or preventing inflammation, defective or aberrant chemotaxis of immune  
 CC cells and T-cell/antigen-presenting cell interactions, infections and  
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral  
 CC infections (especially early-stage human immune deficiency virus (HIV),  
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions  
 CC associated with aberrant or deficient expression of the CCR5 receptor or  
 CC its ligands. The antibodies are also useful to determine CCR5 expression,  
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other  
 CC hyperproliferative diseases. The polynucleotide sequences encoding human  
 CC G-protein chemokine receptor (CCR5) HDGNR10 can be used to produce the  
 CC recombinant receptor, and in the treatment of a wide range of diseases  
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.  
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The  
 CC present sequence represents human G-protein chemokine receptor (CCR5)  
 CC HDGNR10 #2.  
 XX  
 XX Sequence 352 AA;  
 SQ

Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKFNFTLKIVILG 18  
 |||||  
 Db 185 SOYQFWKFNFTLKIVILG 202

RESULT 22  
 AAMS2829  
 ID AAMS2829 standard; protein; 352 AA.  
 XX  
 AC AAMS2829;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Human CCR5 Gln 55 variant.  
 XX  
 KW CCR5; CC chemokine receptor 5; human; HIV infection;  
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
 KW drug screening; identification; variant.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 55 /note= "Glu replaces wild-type Leu; encoded by CTG"  
 FT FT Misc-difference 58 /note= "Encoded by AGC"  
 FT FT  
 XX WO200171346-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 XX 21-MAR-2001; 2001WO-US009155.  
 XX  
 PR 21-MAR-2000; 2000US-0190946P.

PR 21-MAR-2000; 2000US-0190996P.  
 PR 21-MAR-2000; 2000US-0191299P.  
 PR 20-MAR-2001; 2001US-00813448.  
 PR 20-MAR-2001; 2001US-00813651.  
 PR 20-MAR-2001; 2001US-00813653.  
 XX  
 PA (CONS-) CONSENSUS PHARM INC.  
 XX  
 PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;  
 XX  
 PI WPI; 2002-010610/01.  
 DR N-PSDB; ABA02318.  
 XX  
 PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
 PT comprises binding a molecule from library to a molecule having binding  
 PT property corresponding to CCR5 and identifying bound molecule.  
 XX  
 PS Example 3; Fig 4B; 50pp; English.  
 XX  
 CC The invention relates to a method for identifying a binding compound for  
 CC of chemokine receptor 5 (CCR5). The method involves screening a library  
 CC of test molecules (particularly peptides) with immobilised CCR5, and then  
 CC identifying those molecules which bind. The invention also relates to  
 CC CCR5-binding molecules identified using the method of the invention,  
 CC methods for identifying consensus motifs for CCR5-binding peptides, a  
 CC transfer vector encoding tagged CCR5, a computer-aided methods for  
 CC determining the relative binding affinity of a test molecule to CCR5 and  
 CC a computer aided drug screening assay that utilises the three-dimensional  
 CC structure of CCR5. Compounds identified using the methods of the  
 CC invention are useful for treating or preventing HIV (human  
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency  
 CC syndrome) in a patient. The methods of the invention may also be used to  
 CC identify agonists or antagonists of the interaction of CCR5 with its  
 CC natural ligand, and to determine a binding motif for CCR5. The present  
 CC sequence represents a naturally occurring variant of human CCR5 in which  
 CC there is a glutamine, rather than a leucine, at position 55  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 Db 185 SQYQFWKNFQTLKIVILG 202  
 |||||  
 RESULT 23  
 AAM52828  
 ID AAM52828 standard; protein; 352 AA.  
 XX  
 AC AAM52828;  
 XX  
 DE 22-FEB-2002 (first entry)  
 XX  
 DE Human CC chemokine receptor 5 (CCR5).  
 XX  
 KW CCR5; CC chemokine receptor 5; human; HIV infection;  
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
 KW drug screening; identification.  
 XX  
 OS Homo sapiens.  
 XX  
 KW W0200171346-A2.  
 PN  
 XX  
 PD 27-SEP-2001.  
 XX  
 XX 21-MAR-2001; 2001WO-US009155.  
 XX  
 XX 21-MAR-2000; 2000US-0190946P.  
 PR  
 PR 21-MAR-2000; 2000US-0190996P.  
 PR 21-MAR-2000; 2000US-0191299P.

PR 20-MAR-2001; 2001US-00813448.  
 PR 20-MAR-2001; 2001US-00813651.  
 PR 20-MAR-2001; 2001US-00813653.  
 XX  
 PA (CONS-) CONSENSUS PHARM INC.  
 XX  
 PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;  
 XX  
 PI WPI; 2002-010610/01.  
 DR N-PSDB; ABA02317.  
 XX  
 PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
 PT comprises binding a molecule from library to a molecule having binding  
 PT property corresponding to CCR5 and identifying bound molecule.  
 XX  
 PS Example 3; Fig 4A; 50pp; English.  
 XX  
 CC The invention relates to a method for identifying a binding compound for  
 CC of chemokine receptor 5 (CCR5). The method involves screening a library  
 CC of test molecules (particularly peptides) with immobilised CCR5, and then  
 CC identifying those molecules which bind. The invention also relates to  
 CC CCR5-binding molecules identified using the method of the invention,  
 CC methods for identifying consensus motifs for CCR5-binding peptides, a  
 CC transfer vector encoding tagged CCR5, a computer-aided methods for  
 CC determining the relative binding affinity of a test molecule to CCR5 and  
 CC a computer aided drug screening assay that utilises the three-dimensional  
 CC structure of CCR5. Compounds identified using the methods of the  
 CC invention are useful for treating or preventing HIV (human  
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency  
 CC syndrome) in a patient. The methods of the invention may also be used to  
 CC identify agonists or antagonists of the interaction of CCR5 with its  
 CC natural ligand, and to determine a binding motif for CCR5. The present  
 CC sequence represents human CCR5  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 Db 185 SQYQFWKNFQTLKIVILG 202  
 |||||  
 RESULT 24  
 ABG70597  
 ID ABG70597 standard; protein; 352 AA.  
 XX  
 AC ABG70597;  
 XX  
 DE 03-DEC-2002 (first entry)  
 XX  
 DE Human G-protein chemokine receptor, HDGNR10.  
 XX  
 KW Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;  
 KW haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;  
 KW chronic infection; leukaemia; T-cell mediated autoimmune disease;  
 KW parasitic infection; psoriasis; growth factor activity; allergy;  
 KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;  
 KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;  
 KW prostaglandin-independent fever; bone marrow failure; shock;  
 KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;  
 KW immunosuppressive; antiparasitic; antipsoriatic; antiallergic;  
 KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;  
 KW antipyretic; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002099176-A1.  
 XX  
 PD 25-JUL-2002.



PF 25-JUN-1999; 99US-00339912.  
 XX  
 PR 06-JUN-1995; 95US-00466343.  
 XX  
 PA (LIYY/) LI Y.  
 PA (RUBE/) RUBEN S M.  
 XX  
 PI Li Y, Ruben SM;  
 XX  
 DR WPI; 2002-690494/74.  
 XX N-PSDB; ABS54272.  
 DR  
 XX Novel human G-protein chemokine receptor polypeptide useful for  
 PT identifying modulators for stimulating hematopoiesis, wound healing,  
 PT leukemia, for treating allergy, rheumatoid arthritis, shock and as  
 PT research agents.  
 XX  
 PS Claim 7; Fig 1; 22pp; English.  
 XX  
 CC The present invention relates to the isolation of human G-protein  
 CC chemokine receptor, HDGMR10 (CCR5 receptor), and the polynucleotide  
 CC sequence encoding it. HDGMR10 polypeptide and polynucleotide sequences  
 CC are useful for diagnosing a disease or a susceptibility to a disease  
 CC related to underexpression of HDGMR10. They are useful for identifying  
 CC modulators for stimulating hematopoiesis, wound healing, coagulation,  
 CC angiogenesis, to treat solid tumors, chronic infections, leukaemia, T-  
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, or  
 CC for stimulating growth factor activity. The sequences are also useful for  
 CC preventing and/or treating allergy, atherosclerosis, anaphylaxis,  
 CC malignancy, chronic and acute inflammation, histamine and immunoglobulin  
 CC E (IgE)-mediated allergic reactions, prostaglandin-independent fever,  
 CC bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-  
 CC eosinophilic syndrome. Polynucleotide sequences encoding HDGMR10 can be  
 CC used in gene therapy to treat conditions related to underexpression of  
 CC HDGMR10. The present sequence represents human G-protein chemokine  
 CC receptor, HDGMR10  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKQFQTLKIVLG 18  
 |||||  
 Db 185 SQYQFWKQFQTLKIVLG 202  
 RESULT 25  
 ABG92883  
 ID ABG92883 standard; protein; 352 AA.  
 AC ABG92883;  
 XX  
 DT 19-NOV-2002 (first entry)  
 XX  
 DE Human immunoglobulin variable heavy domain #1.  
 XX  
 KW Immunoglobulin; variable heavy chain; variable light chain; human;  
 KW G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;  
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;  
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;  
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;  
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;  
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;  
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;  
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;  
 KW lymphocytopenia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200264612-A2.  
 XX

PD 22-AUG-2002.  
 XX  
 PF 08-FEB-2002; 2002WO-US003634.  
 XX  
 PR 09-FEB-2001; 2001US-00779880.  
 PR 09-FEB-2001; 2001WO-US004153.  
 PR 12-JUN-2001; 2001US-0297257P.  
 PR 08-AUG-2001; 2001US-0310458P.  
 PR 12-OCT-2001; 2001US-0328447P.  
 PR 21-DEC-2001; 2001US-0341725P.  
 XX  
 FA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Roschke V, Rosen CA, Ruben SM;  
 XX N-PSDB; ABS68606.  
 DR WPI; 2002-643455/69.  
 DR  
 DR  
 XX New human G-protein Chemokine Receptor gene (HDGMR10) useful for  
 PT treating, preventing, ameliorating or monitoring diseases or disorders  
 PT associated with aberrant expression of HDGMR10 e.g. cancer.  
 XX  
 PS Example 55; Fig 4; 562pp; English.  
 XX  
 CC The invention describes an isolated polynucleotide encoding a first  
 CC antibody at least 95-100% identical to a second antibody consisting of an  
 CC amino acid sequence comprising at least one, two or three CDR regions of  
 CC a variable heavy (VH) or variable light (VL) domain of the antibody  
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,  
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,  
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody  
 CC is useful treating, preventing, ameliorating, prognosing or monitoring  
 CC cancers or other diseases or disorders e.g. immunologic deficiency  
 CC syndromes such as blood protein disorders and ataxia telangiectasia.  
 CC inflammation associated disorders such as endotoxin lethality, nephritis  
 CC and inflammatory bowel disease, conditions associated with an increase in  
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant  
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,  
 CC an infectious disease, an autoimmune disease such as Addison's disease,  
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative  
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or  
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,  
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a  
 CC disease or disorder associated with aberrant expression of novel human G-  
 CC protein chemokine receptor (CCR5) HDGMR10. This is the amino acid  
 CC sequence of human immunoglobulin sequence associated with the antibodies  
 CC against HDGMR10  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKQFQTLKIVLG 18  
 |||||  
 Db 185 SQYQFWKQFQTLKIVLG 202  
 RESULT 26  
 ABG92880  
 ID ABG92880 standard; protein; 352 AA.  
 XX  
 AC ABG92880;  
 XX  
 DT 19-NOV-2002 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5) HDGMR10 #1.  
 XX  
 KW Immunoglobulin; variable heavy chain; variable light chain; human;  
 KW G-protein chemokine receptor; CCR5; HDGMR10; cancer; inflammation;  
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;  
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;

KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;  
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergy;  
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;  
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;  
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;  
 KW lymphocytopenia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200264612-A2.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PF 08-FEB-2002; 2002WO-US003634.  
 XX  
 PR 09-FEB-2001; 2001US-00779880.  
 PR 09-FEB-2001; 2001WO-US004153.  
 PR 12-JUN-2001; 2001US-0297257P.  
 PR 08-AUG-2001; 2001US-0310458P.  
 PR 12-OCT-2001; 2001US-0328447P.  
 PR 21-DEC-2001; 2001US-0341725P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Roschke V, Rosen CA, Ruben SM;  
 XX  
 XX WPI; 2002-643455/69.  
 DR N-PSDB; ABS68553.  
 XX  
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for  
 PT treating, preventing, ameliorating or monitoring diseases or disorders  
 PT associated with aberrant expression of HDGNR10 e.g. cancer.  
 XX  
 PS Disclosure; Fig 1A-B; 562pp; English.  
 XX  
 CC The invention describes an isolated polynucleotide encoding a first  
 CC antibody at least 95-100% identical to a second antibody consisting of an  
 CC amino acid sequence comprising at least one, two or three CDR regions of  
 CC a variable heavy (VH) or variable light (VL) domain of the antibody  
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,  
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.1B5,  
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody  
 CC is useful treating, preventing, ameliorating, prognosing or monitoring  
 CC cancers or other diseases or disorders e.g. immunologic deficiency  
 CC syndromes such as blood protein disorders and ataxia telangiectasia,  
 CC inflammation associated disorders such as endotoxin lethality, nephritis  
 CC and inflammatory bowel disease, conditions associated with an increase in  
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant  
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,  
 CC an infectious disease, an autoimmune disease such as Addison's disease,  
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative  
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or  
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,  
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a  
 CC disease or disorder associated with aberrant expression of novel human G-  
 CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence  
 CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 DB 185 SQYQFWKNFQTLKIVILG 202  
 RESULT 27  
 AAE25808  
 ID AAE25808 standard; protein; 352 AA.  
 XX

AC AAE25808;  
 XX 24-FEB-2003 (first entry)  
 DT  
 XX Human G-protein chemokine receptor (CCR5), HDGNR10 #1.  
 DE  
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;  
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;  
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;  
 KW hyperproliferative disease; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002061834-A1.  
 XX  
 PD 23-MAY-2002.  
 XX  
 PF 09-FEB-2001; 2001US-00779880.  
 XX  
 PR 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 XX  
 PA (ROSE/) ROSEN C A.  
 PA (ROSC/) ROSCHKE V.  
 PA (LIYI/) LI Y.  
 PA (RUBE/) RUBEN S M.  
 XX  
 PI Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX  
 XX WPI; 2002-499674/53.  
 DR N-PSDB; AAD42409.  
 XX  
 XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,  
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also  
 PT related antibodies.  
 PT  
 PS Claim 61; Page 163-164; 186pp; English.  
 XX  
 CC The invention relates to human G-protein chemokine receptor (CCR5),  
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5  
 CC antibodies are used for the treatment or prevention of inflammation,  
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-  
 CC presenting cell interaction, viral infections (specifically human immune  
 CC deficiency (including its early stages), cytomegalovirus or pox viruses),  
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis  
 CC carinii infection, Kaposi's sarcoma or any condition associated with  
 CC aberrant expression of CCR5 or their ligands. They are also used for the  
 CC detection, diagnosis, prognosis and monitoring of cancers or other  
 CC hyperproliferative diseases. The present sequence is human G-protein  
 CC chemokine receptor (CCR5), HDGNR10 DNA  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 DB 185 SQYQFWKNFQTLKIVILG 202  
 RESULT 28  
 AAE25811  
 ID AAE25811 standard; protein; 352 AA.  
 XX  
 AC AAE25811;  
 XX  
 DT 24-FEB-2003 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5), HDGNR10 #2.  
 XX

KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;  
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;  
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;  
 KW hyperproliferative disease; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002061834-A1.  
 PN  
 XX  
 XX 23-MAY-2002.  
 PD  
 XX  
 XX 09-FEB-2001; 2001US-00779880.  
 PF  
 XX  
 XX 09-FEB-2000; 2000US-0181258P.  
 PR  
 XX  
 XX 09-MAR-2000; 2000US-0187999P.  
 PR  
 XX  
 XX 22-SEP-2000; 2000US-0234336P.  
 XX  
 XX (ROSE/) ROSEN C A.  
 PA  
 XX (ROSC/) ROSCHKE V.  
 PA  
 XX (LIYY/) LI Y.  
 PA  
 XX (RUBE/) RUBEN S M.  
 XX  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 PI  
 XX WPI: 2002-499674/53.  
 DR  
 XX N-PSDB; RAD42426.  
 DR  
 XX  
 XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,  
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also  
 PT related antibodies.  
 PT  
 XX Disclosure; Page 170; 186pp; English.  
 PS  
 XX The invention relates to human G-protein chemokine receptor (CCR5),  
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5  
 CC antibodies are used for the treatment or prevention of inflammation,  
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-  
 CC presenting cell interaction, viral infections (specifically human immune  
 CC deficiency (including its early stages), cytomegalovirus or pox viruses),  
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis  
 CC carinii infection, Kaposi's sarcoma or any condition associated with  
 CC aberrant expression of CCR5 or their ligands. They are also used for the  
 CC detection, diagnosis, prognosis and monitoring of cancers or other  
 CC hyperproliferative diseases. The present sequence is human G-protein  
 CC chemokine receptor (CCR5), HDGNR10 DNA  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 Db 185 SQYQFWKNFQTLKIVILG 202  
 RESULT 29  
 ABB81054  
 ID ABB81054 standard; protein; 352 AA.  
 XX  
 AC ABB81054;  
 XX  
 XX 05-NOV-2002 (first entry)  
 DT  
 XX G-protein chemokine receptor, HDGNR10.  
 DE  
 XX 7-transmembrane receptor; G-protein coupled receptor; GPCR; HDGNR10;  
 KW G-protein chemokine receptor; haematopoietic; immunosuppressant;  
 KW antiparasitic; antipsoriatic; anti-allergic; anti-inflammatory; cytostatic;  
 KW antirheumatic; antiarthritic; gene therapy; human; receptor.  
 XX  
 OS Homo sapiens.  
 XX

XX US2002076745-A1.  
 PN  
 XX 20-JUN-2002.  
 PD  
 XX  
 XX 18-NOV-1998; 98US-00195662.  
 PF  
 XX  
 XX 06-JUN-1995; 95US-00466343.  
 PR  
 XX  
 XX (LIYY/) LI Y.  
 PA  
 XX (RUBE/) RUBEN S M.  
 XX  
 XX Li Y, Ruben SM;  
 PI  
 XX WPI: 2002-598724/64.  
 DR  
 XX N-PSDB; AEN86542.  
 DR  
 XX New polynucleotide encoding a human G protein chemokine receptor HDGNR10,  
 PT useful e.g. for treating tumors.  
 PT  
 XX Claim 7; Fig 1; 22pp; English.  
 PS  
 XX The invention relates to a novel human 7-transmembrane receptor, HDGNR10,  
 CC which has been identified as a G-protein chemokine receptor. The GPCR  
 CC HDGNR10 polypeptide can be expressed by standard recombinant methodology.  
 CC Compounds that activate or inhibit the receptor polypeptide, optionally  
 CC expressed from DNA in gene therapy vectors, are used to treat diseases  
 CC that require: (a) activation of the receptor (e.g. stimulation of  
 CC haematopoiesis, treatment of solid tumours, T-cell mediated autoimmune  
 CC diseases, parasitic infections, psoriasis etc.); or (b) inhibition of the  
 CC receptor (e.g. allergy, inflammation, rheumatoid arthritis, silicosis  
 CC etc.). The present sequence represents the human HDGNR10 receptor  
 CC polypeptide  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 Db 185 SQYQFWKNFQTLKIVILG 202  
 RESULT 30  
 ABB08343  
 ID ABB08343 standard; protein; 352 AA.  
 XX  
 AC ABB08343;  
 XX  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX Human chemokine (C-C motif) receptor 5 polypeptide.  
 DE  
 XX Human chemokine C-C motif receptor 5; CCR5; haplotype pair; isogene;  
 KW single nucleotide polymorphism; SNP; human immunodeficiency virus 1;  
 KW HIV-1 infection; acquired immunodeficiency syndrome; AIDS; antiviral;  
 KW genotype; polymorphic variant; transgenic; drug screening; gene therapy;  
 KW chromosome 3p21.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 55 /label= Leu, Gln  
 FT  
 FT Misc-difference 182 /label= Phe, Leu  
 FT  
 FT Misc-difference 223 /label= Arg, Gln  
 FT  
 XX WO200177125-A2.  
 PN  
 XX

PD 18-OCT-2001.  
 XX  
 PF 04-APR-2001; 2001WO-US010708.  
 XX  
 PR 05-APR-2000; 2000US-0194361P.  
 XX  
 PA (GENA-) GENAISSANCE PHARM INC.  
 XX  
 PI Choi JY, Kliem SE, Koshy B;  
 XX  
 DR WPI; 2002-041282/05.  
 DR N-PSDB; ABA97318, ABA97319.  
 XX  
 PT New haplotypes of the human chemokine (C-C motif) receptor 5 gene, useful  
 PT to diagnose and treat diseases associated with its abnormal expression or  
 PT function, including human immunodeficiency virus-1 infection.  
 XX  
 PS Claim 29; Fig 3; 61pp; English.  
 XX  
 CC The present sequence is that of a polypeptide encoded by the human  
 CC chemokine (C-C motif) receptor 5 (CCR5) gene of the invention (see  
 CC ABA97318, ABA97319). The specification describes haplotyping the CCR5  
 CC gene of an individual by determining if the individual has one of the  
 CC CCR5 haplotypes or haplotype pairs fully defined in the specification.  
 CC The specification also describes an isolated polynucleotide comprising a  
 CC nucleotide sequence which is a polymorphic variant of the reference CCR5  
 CC gene sequence and comprises an isogene defined by a haplotype described  
 CC in the specification and its encoded polypeptide. The methods of the  
 CC invention are useful to diagnose and develop treatment for diseases  
 CC associated with abnormal expression or function of the gene. The CCR5  
 CC isogenes and the screened compounds are useful for treating human  
 CC immunodeficiency virus (HIV)-1 infection and the progression to acquired  
 CC immunodeficiency syndrome (AIDS). The invention has antiviral  
 CC applications. The specification describes genotyping the CCR5 gene of an  
 CC individual; predicting a haplotype pair for the CCR5 gene of an  
 CC individual; identifying an association between a trait and a haplotype or  
 CC haplotype pair of the CCR5 gene. The specification describes a  
 CC composition comprising a genotyping oligonucleotide for detecting a CCR5  
 CC polymorphism; a recombinant non-human organism transformed with CCR5  
 CC polynucleotide expressing a CCR5 protein encoded by the variant sequence;  
 CC an isolated antibody specific for the CCR5 polypeptide and a method for  
 CC screening drugs targeting the CCR5 polypeptide  
 XX  
 SQ Sequence 352 AA;  
  
 Query Match 100.0%; Score 96; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 SQYQFWNFKQTLKIVILG 18  
 Db 185 SQYQFWNFKQTLKIVILG 202  
  
 Search completed: March 4, 2004, 17:59:23  
 Job time : 44.7959 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 9.18367 Seconds  
(without alignments)  
188.535 Million cell updates/sec

Title: US-10-084-813-13  
Perfect score: 96  
Sequence: 1 SQQFWNFQTLKVLIG 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 78:\*\*

1: Pir1:\*\*  
2: Pir2:\*\*  
3: Pir3:\*\*  
4: Pir4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 96    | 100.0       | 352    | 2 A43113 | chemokine (C-C) re |
| 2          | 47    | 49.0        | 355    | 2 I49339 | macrophage inflam  |
| 3          | 46    | 47.9        | 196    | 2 T22609 | hypothetical prote |
| 4          | 45    | 46.9        | 177    | 2 S34499 | hypothetical prote |
| 5          | 45    | 46.9        | 302    | 2 A75203 | 2-phosphoglycerate |
| 6          | 45    | 46.9        | 314    | 2 G85575 | hypothetical prote |
| 7          | 45    | 46.9        | 314    | 2 G90724 | hypothetical prote |
| 8          | 45    | 46.9        | 1289   | 2 S67200 | hypothetical prote |
| 9          | 44.5  | 46.4        | 301    | 2 C71236 | probable 2-phospho |
| 10         | 44    | 45.8        | 467    | 2 A81263 | probable integral  |
| 11         | 44    | 45.8        | 616    | 1 I64056 | secretion protein  |
| 12         | 43    | 44.8        | 237    | 2 C95399 | nitroreductase fam |
| 13         | 43    | 44.8        | 237    | 2 A98066 | NADPH-flavin oxido |
| 14         | 43    | 44.8        | 242    | 2 A86719 | oxidoreductase ybg |
| 15         | 43    | 44.8        | 344    | 2 JC5942 | chemokine receptor |
| 16         | 43    | 44.8        | 475    | 2 G98183 | periplasmic sorbit |
| 17         | 43    | 44.8        | 3587   | 2 T40486 | surfactin syntheta |
| 18         | 42    | 43.8        | 241    | 2 S30843 | UTR4 protein - yea |
| 19         | 42    | 43.8        | 350    | 2 E81303 | probable branched- |
| 20         | 42    | 43.8        | 383    | 2 D90528 | FAD-dependent mono |
| 21         | 42    | 43.8        | 421    | 2 AB2915 | hypothetical prote |
| 22         | 42    | 43.8        | 421    | 2 E97689 | hypothetical prote |
| 23         | 42    | 43.8        | 496    | 2 C84678 | hypothetical prote |
| 24         | 41.5  | 43.2        | 159    | 2 H81442 | hypothetical prote |
| 25         | 41.5  | 43.2        | 334    | 2 S16296 | hypothetical prote |
| 26         | 41.5  | 43.2        | 334    | 2 A85558 | ferric enterobacti |
| 27         | 41.5  | 43.2        | 334    | 2 E90707 | ferric enterobacti |
| 28         | 41    | 42.7        | 46     | 2 I37047 | NADH2 dehydrogenas |
| 29         | 41    | 42.7        | 118    | 2 H83734 | hypothetical prote |

hypothetical prote  
envelope-like prot  
oligopeptide ABC t  
hypothetical prote  
NADH2 dehydrogenas  
hypothetical prote  
hypothetical prote  
pre-mRNA splicing  
probable zinc-fing  
related to TOM1 pr  
DNA-damage-inducib  
DNA-damage-inducib  
hypothetical prote  
hypothetical prote  
hypothetical prote  
alcohol sulfotrans  
hypothetical prote  
hypothetical prote  
chemokine (C-C) re  
hypothetical prote  
uncharacterized pr  
transposase - frui  
argininosuccinate  
hypothetical prote  
heat shock protein  
acetate-CoA ligase  
hypothetical prote  
Ig heavy chain - C  
hypothetical prote  
hypothetical prote  
hypothetical prote  
competence protein  
hypothetical prote  
hypothetical prote  
transposase all708  
cell division prot  
alanine racemase (  
tyrosine-TRNA liga  
hypothetical prote  
galactosyl transfe  
UDP-N-acetylmuramo  
DNA modification m  
DNA methyltransfer  
neurotrophin-3 rec  
hypothetical prote  
RF1 protein - saim  
electron transfer  
hypothetical prote  
hypothetical prote  
leukotoxin express  
hypothetical prote  
bo-type ubiquinol  
conserved hypothet  
probable type-1 se  
NADH2 dehydrogenas  
penicillin-binding  
hypothetical prote  
neurotrophin-3 rec  
sensory transducti  
cation transprotin  
tyrosine kinase C  
integral membrane  
hypothetical prote  
hypothetical prote  
probable membrane  
epimerase/dehydrat  
cation efflux syst  
hypothetical prote

## ALIGNMENTS

RESULT 1  
A43113  
chemokine (C-C) receptor 5 - human  
N;Alternate names: C-C CKR-5; CCR5  
C;Species: Homo sapiens (man)  
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000  
C;Accession: A43113; S71808; A58834; A58832; G02653; A58833  
R;Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
Biochemistry 35, 3362-3367, 1996  
A;Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
A;Reference number: A43113; MUID:96241590; PMID:8639485  
A;Accession: A43113  
A;Molecule type: mRNA  
A;Residues: 1-352 <SAM1>  
A;Cross-references: GB:X91492; NID:gl262810; PIDN:CAA62796.1; PID:gl262811  
R;Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Lienard, C.; Farber, C.M.; Saragosti  
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Pa  
Nature 382, 722-725, 1996  
A;Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles o  
A;Reference number: S71808; MUID:96345670; PMID:8751444  
A;Accession: S71808  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 182-206;207-230 <SAM2>  
A;Accession: A58834  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-184, 'TKSHLGAGPAAAGCHLLGNPKNSASVK' <SAM3>  
A;Cross-references: GB:X99393; NID:gl524062; PIDN:CAA67767.1; PID:gl524063  
A;Note: This frameshift mutation results in a non-functional receptor but confers a dege  
nd may have had a selective advantage by conferring resistance to Yersinia plague infect  
R;Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.  
J. Leukoc. Biol. 60, 147-152, 1996  
A;Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine rec  
A;Reference number: A58832; MUID:96295970; PMID:8699119  
A;Accession: A58832  
A;Molecule type: mRNA  
A;Residues: 1-352 <COM1>  
A;Cross-references: GB:U57840; NID:gl502408; PIDN:AA817071.1; PID:gl502409  
A;Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
R;Combadiere, C.  
submitted to the EMBL Data Library, May 1996  
A;Reference number: H01541  
A;Accession: G02653  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-89, 'L', 91-352 <COM2>  
A;Cross-references: EMBL:U57840  
R;Rapport, C.J.; Goelling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
J. Biol. Chem. 271, 17161-17166, 1996  
A;Title: Molecular cloning and functional characterization of a novel human CC chemokine  
A;Reference number: A58833; MUID:96291862; PMID:8663314  
A;Accession: A58833  
A;Molecule type: mRNA  
A;Residues: 1-352 <RAP>  
A;Cross-references: GB:U54994; NID:gl457945; PIDN:AA650598.1; PID:gl457946  
C;Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see  
C;Comment: Macrophage- and dual-tropic strains of HIV-1 bind to a complex of chemokine  
C;Genetics:  
A;Gene: GDB:CMKBR5; CCR5; CXCR-5; CC-CCR-5; CXCR5; ChemR13  
A;Cross-references: GDB:1230510; OMIM:601373  
A;Map position: 3p21-3p21  
C;Function:  
A;Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES  
A;Note: probably acts to control granulocyte proliferation and differentiation  
C;Superfamily: vertebrate rhodopsin  
Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembran  
F;32-56/Domain: transmembrane #status predicted <TM1>  
F;67-87/Domain: transmembrane #status predicted <TM2>  
F;103-124/Domain: transmembrane #status predicted <TM3>

F;142-166/Domain: transmembrane #status predicted <TM4>  
F;193-218/Domain: transmembrane #status predicted <TM5>  
F;236-257/Domain: transmembrane #status predicted <TM6>  
F;285-300/Domain: transmembrane #status predicted <TM7>  
F;20-269,101-178/Disulfide bonds: #status predicted  
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted  
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted  
Query Match 100.0%; Score 96; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 5.6e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SOYQFMKNFQTLKIVILG 18  
DB 185 SOYQFMKNFQTLKIVILG 202  
RESULT 2  
I49339  
macrophage inflammatory protein-1 alpha receptor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 13-Aug-1999  
C;Accession: I49339  
R;Gao, J.L.; Murphy, P.M.  
J. Biol. Chem. 270, 17494-17501, 1995  
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemok  
A;Reference number: I49339; MUID:95340546; PMID:7542241  
A;Accession: I49339  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-355 <RES>  
A;Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548  
C;Superfamily: vertebrate rhodopsin  
Query Match 49.0%; Score 47; DB 2; Length 355;  
Best Local Similarity 61.5%; Pred. No. 5.6;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 6 WKNFQTLKIVILG 18  
DB 195 WKNFQTLKIVILG 207  
RESULT 3  
T22609  
hypothetical protein F54B11.8 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 04-Mar-2000  
C;Accession: T22609  
R;Swinburne, J.  
submitted to the EMBL Data Library, March 1996  
A;Reference number: Z19588  
A;Accession: T22609  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-196 <WIL>  
A;Cross-references: EMBL:Z70208; PIDN:CAA94143.1; GSPDB:GN00028; CESP:F54B11.8  
A;Experimental source: clone F54B11  
C;Genetics:  
A;Gene: CESP:F54B11.8  
A;Map position: X  
A;Introns: 26/1; 60/1; 94/3; 122/3  
C;Superfamily: Caenorhabditis elegans hypothetical protein F54B11.8  
Query Match 47.9%; Score 46; DB 2; Length 196;  
Best Local Similarity 66.7%; Pred. No. 4.5;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 6 WKNFQTLKIVIL 17  
DB 36 WKNFQTLKIVIL 47

```

RESULT 4
S34499
hypothetical protein 177 (psbc 3' region) - Euglena gracilis chloroplast
C:Species: chloroplast Euglena gracilis
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 11-Apr-1995
C:Accession: S34499; S34867
R:Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.; Monfort, A.; Orsat, B.; Spielmann,
submitted to the EMBL Data Library, January 1993
A:Description: The complete sequence of the Euglena gracilis chloroplast genome (tentati
A:Reference number: S34494
A:Accession: S34499
A:Molecule type: DNA
A:Residues: 1-177 <HAL1>
A:Cross-references: EMBL:X70810
R:Hallick, R.B.; Hong, L.; Drager, R.G.; Favreau, M.R.; Monfort, A.; Orsat, B.; Spielman
Nucleic Acids Res. 21, 3537-3544, 1993
A:Title: Complete sequence of Euglena gracilis chloroplast DNA.
A:Reference number: S34862; MUID:93347989; PMID:8346031
A:Accession: S34867
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-177 <HAL2>
A:Cross-references: EMBL:X70810
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C:Genetics:
A:Genome: chloroplast
C:Keywords: chloroplast

Query Match 46.9%; Score 45; DB 2; Length 177;
Best Local Similarity 55.6%; Pred. No. 5.9;
Matches 10; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 4 QFW-----KNFQTLKIVIL 17
 :|||:|:|:|:|:|
Db 60 KFWDSQIKNFMTLKIIL 77

RESULT 5
A75203
2-phosphoglycerate kinase, PAB2253 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: A75203
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: A75203
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-302 <KAW>
A:Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49072.1; PID:g545758
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2253
C:Superfamily: 2-phosphoglycerate kinase

Query Match 46.9%; Score 45; DB 2; Length 302;
Best Local Similarity 37.5%; Pred. No. 10;
Matches 6; Conservative 6; Mismatches 6; Indels 4; Gaps 0;

QY 2 QYQFWKNFQTLKIVIL 17
 :|||:|:|:|:|
Db 77 RYLFWRFRKMKVPLL 92

RESULT 6
G85575
hypothetical protein Z0898 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: G85575

```

```

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Pocamocsis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85575
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <STO>
A:Cross-references: GB:AE005174; NID:gl2513664; PIDN:AAG55067.1; GSPDB:GN00145; UWGP:Z08
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z0898

```

```

Query Match 46.9%; Score 45; DB 2; Length 314;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVI 16
 :|||:|:|:|:|
Db 289 SQYRFFKMTNLALVI 304

RESULT 7
G90724
hypothetical protein ECs0767 [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: G90724
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kubara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: G90724
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA034190.1; PID:gl33360226; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs0767

```

```

Query Match 46.9%; Score 45; DB 2; Length 314;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVI 16
 :|||:|:|:|:|
Db 289 SQYRFFKMTNLALVI 304

RESULT 8
S67200
hypothetical protein YOR296w - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O5623
C:Species: Saccharomyces cerevisiae
C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C:Accession: S67200
R:Ciepluch, C.; Jauniaux, J.C.; Kordes, E.; Poiry, R.; Pujol, A.; Tobiasch, E.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67194
A:Accession: S67200
A:Molecule type: DNA
A:Residues: 1-1289 <CZI>
A:Cross-references: EMBL:Z75204; NID:gl420655; PID:gl420656; GSPDB:GN00015; MIPS:YOR296w
A:Experimental source: strain S288c
C:Genetics:
A:Gene: MIPS:YOR296w
A:Cross-references: SGD:S0005822
A:Map position: 15R
C:Superfamily: Saccharomyces cerevisiae hypothetical protein YOR296w

```

Query Match 46.9%; Score 45; DB 2; Length 1289;  
 Best Local Similarity 43.8%; Pred. No. 44;  
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 QYQWKNFQTLKIVIL 17  
 DB 312 EYNLWKNVLELTANL 327

RESULT 9  
 C71236  
 probable 2-phosphoglycerate kinase - Pyrococcus horikoshii  
 C:Species: Pyrococcus horikoshii  
 C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 21-Jul-2000  
 C:Accession: C71236  
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki  
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
 DNA Res. 5, 55-76, 1998  
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
 A:Reference number: A71000; MUID:198344137; PMID:9679194  
 A:Accession: C71236  
 A:Molecule type: DNA  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Residues: 1-301 <XAW>  
 A:Cross-references: GB:AP000001; NID:93236128; PIDN:BAR29218.1; PID:93256535  
 A:Experimental source: strain OT3  
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C:Genetics:  
 A:Gene: PH0149  
 C:Superfamily: 2-phosphoglycerate kinase

Query Match 46.4%; Score 44.5; DB 2; Length 301;  
 Best Local Similarity 40.0%; Pred. No. 12;  
 Matches 8; Conservative 6; Mismatches 3; Indels 3; Gaps 1;

QY 2 QYQWKNFQTLK---IVILG 18  
 DB 77 RYFWRRKMKVFLILIG 96

RESULT 10  
 A81263  
 probable integral membrane protein Cj1660 [imported] - Campylobacter jejuni (strain NCTC  
 C:Species: Campylobacter jejuni  
 C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
 C:Accession: A81263  
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell  
 Nature 403, 665-668, 2000  
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp  
 A:Reference number: A81250; MUID:20150912; PMID:10688204  
 A:Accession: A81263  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-467 <PAR>  
 A:Cross-references: GB:AL139079; GB:AL111168; NID:96968971; PIDN:CAB73647.1; PID:9696907  
 A:Experimental source: serotype O2, strain NCTC 11168  
 C:Genetics:  
 A:Gene: Cj1660

Query Match 45.8%; Score 44; DB 2; Length 467;  
 Best Local Similarity 37.5%; Pred. No. 23;  
 Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 QYQWKNFQTLKIVILG 18  
 DB 77 FYFWKTEILNFIILG 92

RESULT 11  
 I64056  
 secretion protein secD - Haemophilus influenzae (strain Rd KW20)  
 C:Species: Haemophilus influenzae

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 28-Jul-2000  
 C:Accession: I64056  
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J  
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, L  
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.  
 Science 269, 496-512, 1995  
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,  
 A:Reference number: A64000; MUID:95350630; PMID:7542800  
 A:Accession: I64056  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-616 <TIGR>  
 A:Cross-references: GB:U32710; GB:L42023; NID:G1573200; PIDN:AAC21908.1; PID:G1573205; 7  
 C:Genetics:

A:Gene: secD  
 C:Superfamily: protein export membrane protein secD  
 C:Keywords: inner membrane; protein export; transmembrane protein  
 F10-30/Domain: transmembrane #status predicted <TM1>  
 F457-473/Domain: transmembrane #status predicted <TM2>  
 F478-498/Domain: transmembrane #status predicted <TM3>  
 F503-519/Domain: transmembrane #status predicted <TM4>  
 F565-581/Domain: transmembrane #status predicted <TM5>  
 F587-606/Domain: transmembrane #status predicted <TM6>

Query Match 45.8%; Score 44; DB 1; Length 616;  
 Best Local Similarity 38.9%; Pred. No. 30;  
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18  
 DB 3 NRYPLKMLVIFIVAIG 20

## RESULT 12

C95199  
 nitroreductase family protein [imported] - Streptococcus pneumoniae (strain TIGR4)  
 C:Species: Streptococcus pneumoniae  
 C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 24-Aug-2001  
 C:Accession: C95199

R:Testelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heic  
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,  
 non, T.; Hickey, E.K.; Holt, I.E.  
 Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
 A:Reference number: A95000; MUID:21357209; PMID:11463916  
 A:Accession: C95199

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-237 <KUR>  
 A:Cross-references: GB:AE005672; PIDN:AAK75788.1; PID:G14973205; GSPDB:GN00164; TIGR:SP4  
 A:Experimental source: strain TIGR4  
 C:Genetics:

A:Gene: SPI710  
 C:Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 44.8%; Score 43; DB 2; Length 237;  
 Best Local Similarity 41.7%; Pred. No. 17;  
 Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17  
 DB 40 WKNFQSYVIV 51

## RESULT 13

A98066  
 NADPH-flavin oxidoreductase (SC 1.6.99.-) homolog [imported] - Streptococcus pneumoniae  
 C:Species: Streptococcus pneumoniae  
 C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 02-Nov-2001  
 C:Accession: A98066  
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E



e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
Y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: A98066  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-237 <KUR>  
A:Cross-references: GB:AE007317; PIDN:AAL00358.1; PID:g15459219; GSPDB:GN00174  
C:Genetics:  
A:Gene: fip  
C:Superfamily: NADPH-flavin oxidoreductase homolog  
C:Keywords: oxidoreductase

Query Match 44.8%; Score 43; DB 2; Length 237;  
Best Local Similarity 41.7%; Pred. No. 17;  
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17  
||||| : : : :  
DB 40 WKNFQSYVIVV 51

RESULT 14  
A86719  
oxidoreductase yhgA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C:Accession: A86719  
R:Rolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: A86719  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-242 <STO>  
A:Cross-references: GB:AE005176; PID:g12723669; PIDN:AAK04851.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: yhgA  
C:Superfamily: NADPH-flavin oxidoreductase homolog

Query Match 44.8%; Score 43; DB 2; Length 242;  
Best Local Similarity 41.7%; Pred. No. 17;  
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17  
||||| : : : :  
DB 43 WKNFQSYVIVV 54

RESULT 15  
JC5942  
chemokine receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: JC5942  
R:Fan, P.; Kyaw, H.; Su, K.; Zeng, Z.; Augustus, M.; Carter, K.C.; Li, Y.  
Biochem. Biophys. Res. Commun. 243, 264-268, 1998  
A:Title: Cloning and characterization of a novel human chemokine receptor.  
A:Reference number: JC5942; MUID:98139902; PMID:9473515  
A:Accession: JC5942  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-344 <PAN>  
A:Cross-references: GB:U97123; NID:g2897070; PIDN:AAC39595.1; PID:g2897071  
C:Superfamily: vertebrate rhodopsin

Query Match 44.8%; Score 43; DB 2; Length 344;  
Best Local Similarity 66.7%; Pred. No. 24;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FWKNFQTLKIVI 16  
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DB 195 FWKHFLLTKNNI 206

RESULT 16  
G98183  
periplasmic sorbitol-binding protein, smoe (AF018073) [imported] - Agrobacterium tumefac  
C:Species: Agrobacterium tumefaciens  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 18-Nov-2002  
C:Accession: G98183  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Iappas, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: G98183  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-475 <KUR>  
A:Cross-references: GB:AE007870; PIDN:AAK88993.1; PID:g15158779; GSPDB:GN00170  
C:Genetics:  
A:Gene: AGR L 841  
A:Map position: linear chromosome

Query Match 44.8%; Score 43; DB 2; Length 475;  
Best Local Similarity 50.0%; Pred. No. 34;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 FWKNFQTLKIVILG 18  
||||| : : : :  
DB 34 FWEEDMTLKIVILG 47

RESULT 17  
I40486  
surfactin synthetase component II - Bacillus subtilis  
N:Alternate names: surfactin synthetase srfA2; surfactin synthetase/competence protein s  
N:Contains: acid-amino-acid ligase (EC 6.3.2.-)  
C:Species: Bacillus subtilis  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 03-Nov-2000  
C:Accession: I40486; S60866; C69718; S46968; S35518; S25558; S34986  
R:Cosmina, P.; Rodriguez, F.; de Terra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sindi  
Mol. Microbiol. 8, 821-831, 1993  
A:Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis  
A:Reference number: I40485; MUID:93360813; PMID:8355609  
A:Accession: I40486  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3587 <RES>  
A:Cross-references: EMBL:X70356; NID:g396480; PIDN:CAA49817.1; PID:g396482  
A:Experimental source: strain M168 derivative of JH642  
R:Hansen, L.W.; Behuis, H.; Jongbloed, J.; Venema, G.; van Sinderen, D.  
Mol. Microbiol. 15, 55-63, 1995  
A:Title: A small gene, designated comS, located within the coding region of the fourth a  
A:Reference number: S60866; MUID:95272393; PMID:7752896  
A:Accession: S60866  
A:Molecule type: DNA  
A:Residues: 977-1104 <HAM>  
R:Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C:Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
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A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mueel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,  
Rieger, M.; Rivolta, C.; Rocha, E.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,  
A:Authors: Schleich, S.; Schroeter, R.; Skoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A:Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
 A:Reference number: A69580; MUID:98044033; PMID:9384377  
 A:Accession: G69718  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-3587 <KUN>  
 A:Cross-references: GB:Z99105; GB:AL009126; NID:G2632457; PIDN:CAB12143.1; PID:G2632635  
 A:Experimental source: strain 168  
 R:Fabret, C.; Quentin, Y.; Guiseppi, A.; Busuttill, J.; Haiech, J.; Denizot, F.  
 submitted to the EMBL Data Library, March 1993  
 A:Reference number: S46967  
 A:Molecule type: DNA  
 A:Residues: 1-32, 'F', 34-41, 'G', 111-114, 'G', 116-138, 'V', 140-258, 'W', 260-308, 'A', 1756-1914, 'PK', 1917-2138, 'SRL', 2142, 'DSL', 2146-2444, 'Q', 2446-2712, 'H', 2714-2722, 'H', 2722-2729, 'H', 2731-2738, 'SRL', 2742, 'DSL', 2746-2944, 'Q', 2946-3088, 'W', 3090-3108, 'A', 3110-3118, 'G', 3120-3128, 'V', 3130-3138, 'SRL', 3142, 'DSL', 3146-3344, 'Q', 3346-3587, 'H', 3589-3597, 'H', 3599-3607, 'A', 3609-3617, 'G', 3619-3627, 'V', 3629-3637, 'A', 3639-3647, 'G', 3649-3657, 'V', 3659-3667, 'A', 3669-3677, 'G', 3679-3687, 'V', 3689-3697, 'A', 3699-3707, 'G', 3709-3717, 'V', 3719-3727, 'A', 3729-3737, 'G', 3739-3747, 'V', 3749-3757, 'A', 3759-3767, 'G', 3769-3777, 'V', 3779-3787, 'A', 3789-3797, 'G', 3799-3807, 'V', 3809-3817, 'A', 3819-3827, 'G', 3829-3837, 'V', 3839-3847, 'A', 3849-3857, 'G', 3859-3867, 'V', 3869-3877, 'A', 3879-3887, 'G', 3889-3897, 'V', 3899-3907, 'A', 3909-3917, 'G', 3919-3927, 'V', 3929-3937, 'A', 3939-3947, 'G', 3949-3957, 'V', 3959-3967, 'A', 3969-3977, 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A;Gene: A  
A;Map pos  
C;Superfa

N:Alternate names: ferriterobactin permease fepD  
 C:Species: Escherichia coli  
 C>Date: 04-Dec-1992 #sequence revision 04-Dec-1992 #text\_change 01-Mar-2002  
 C:Accession: S16296; S16305; D64792; S14841  
 R:Shea, C.M.; McIntosh, M.A.  
 Mol. Microbiol. 5, 1415-1428, 1991  
 A:Title: Nucleotide sequence and genetic organization of the ferric enterobactin transporter  
 A:Reference number: S16295; MUID:92157868; PMID:1838574  
 A:Accession: S16296  
 A:Molecule type: DNA  
 A:Residues: 1-334 <SHE>  
 A:Cross-references: EMBL:X57471; NID:g41429; PIDN:CRA40707.1; PID:g41430  
 R:Chenault, S.S.; Earhart, C.F.  
 Mol. Microbiol. 5, 1405-1413, 1991  
 A:Title: Organization of genes encoding membrane proteins of the Escherichia coli ferric enterobactin transporter  
 A:Reference number: S16305; MUID:92157867; PMID:1787794  
 A:Accession: S16305  
 A:Molecule type: DNA  
 A:Residues: 1-232, 'AL', 235-334 <CHE>  
 A:Cross-references: EMBL:X59402; NID:g41433; PIDN:CRA42043.1; PID:g41434  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: D64792  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-334 <BLAT>  
 A:Cross-references: GB:AE000164; GB:U00096; NID:g1786800; PIDN:AACT3691.1; PID:g1786805;  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: fepD  
 A:Map position: 14 min  
 C:Superfamily: vitamin B12 transport protein btuC  
 C:Keywords: transmembrane protein  
 F:16-32/Domain: transmembrane #status predicted <TM1>  
 F:65-81/Domain: transmembrane #status predicted <TM2>  
 F:94-110/Domain: transmembrane #status predicted <TM3>  
 F:121-137/Domain: transmembrane #status predicted <TM4>  
 F:156-172/Domain: transmembrane #status predicted <TM5>  
 F:198-214/Domain: transmembrane #status predicted <TM6>  
 F:240-256/Domain: transmembrane #status predicted <TM7>  
 F:284-300/Domain: transmembrane #status predicted <TM8>  
 F:310-326/Domain: transmembrane #status predicted <TM9>

Query Match 43.2%; Score 41.5; DB 2; Length 334;  
 Best Local Similarity 34.8%; Pred. No. 42;  
 Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;  
 QY 2 QYQFW-----KNFOTLKIVIL 17  
 DB 179 QLRFWQAGSLDIRNLHTLKVLI 201

RESULT 26  
 A85558  
 ferric enterobactin (enterochelin) transport [imported] - Escherichia coli (strain O157:H7)  
 C:Species: Escherichia coli  
 C>Date: 16-Feb-2001 #sequence revision 16-Feb-2001 #text\_change 17-May-2002  
 C:Accession: A85558  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamousis, K.; Apodaca, J.; Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: A85558  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-334 <STO>  
 A:Cross-references: GB:AE005174; NID:g12513480; PIDN:AAG54925.1; GSPDB:GN00145; UWGP:207  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:

A:Gene: fepD  
 C:Superfamily: vitamin B12 transport protein btuC  
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 Best Local Similarity 34.8%; Pred. No. 42;  
 Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;  
 QY 2 QYQFW-----KNFOTLKIVIL 17  
 DB 179 QLRFWQAGSLDIRNLHTLKVLI 201

RESULT 27  
 E90707  
 ferric enterobactin (enterochelin) transport ECs0629 [imported] - Escherichia coli (strain O157:H7)  
 C:Species: Escherichia coli  
 C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 17-May-2002  
 C:Accession: E90707  
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic organization of the ferric enterobactin transporter  
 A:Reference number: A99629; MUID:21156231; PMID:11258796  
 A:Accession: E90707  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-334 <HAY>  
 A:Cross-references: PIDN:BA000007; PIDN:BA034052.1; PID:g13360087; GSPDB:GN00154  
 A:Experimental source: strain O157:H7, substrain RIMD 050952  
 C:Genetics:  
 A:Gene: ECs0629  
 C:Superfamily: vitamin B12 transport protein btuC  
 Query Match 43.2%; Score 41.5; DB 2; Length 334;  
 Best Local Similarity 34.8%; Pred. No. 42;  
 Matches 8; Conservative 5; Mismatches 3; Indels 7; Gaps 1;  
 QY 2 QYQFW-----KNFOTLKIVIL 17  
 DB 179 QLRFWQAGSLDIRNLHTLKVLI 201

RESULT 28  
 I37047  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - siamang mitochondrion (fragment)  
 C:Species: mitochondrion Hylobates syndactylus (siamang)  
 C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 03-Jun-2002  
 C:Accession: I37047  
 R:Horai, S.; Satta, Y.; Hayasaka, K.; Kondo, R.; Inoue, T.; Ishida, T.; Hayashi, S.; Tajima, F.  
 J. Mol. Evol. 35, 32-43, 1992  
 A:Title: Man's place in Hominoidea revealed by mitochondrial DNA genealogy.  
 A:Reference number: I37047; MUID:92389366; PMID:1518083  
 A:Accession: I37047  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-46 <HOR>  
 A:Cross-references: GB:D38484; NID:g558513; PIDN:BA007494.1; PID:g558514  
 C:Genetics:  
 A:Gene: NDI  
 A:Genome: mitochondrion  
 A:Genetic code: SGC1  
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1  
 C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 42.7%; Score 41; DB 2; Length 46;  
 Best Local Similarity 46.7%; Pred. No. 6.7;  
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 3 QYQFWKNFOTLKIVIL 17  
 DB 15 YLLWKNFLPLTALL 29

## H83734

S03215

Search completed: March 4, 2004, 18:04:01  
Job time : 12.1837 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 5.87755 Seconds  
(without alignments)  
159.465 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQYQFWKFNQTLKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 96    | 100.0       | 352    | 1  | CKR5_CERAE  |
| 2          | 96    | 100.0       | 352    | 1  | CKR5_CERP   |
| 3          | 96    | 100.0       | 352    | 1  | CKR5_CERTO  |
| 4          | 96    | 100.0       | 352    | 1  | CKR5_GORGO  |
| 5          | 96    | 100.0       | 352    | 1  | CKR5_HUMAN  |
| 6          | 96    | 100.0       | 352    | 1  | CKR5_HYLE   |
| 7          | 96    | 100.0       | 352    | 1  | CKR5_HYLM   |
| 8          | 96    | 100.0       | 352    | 1  | CKR5_HYLSY  |
| 9          | 96    | 100.0       | 352    | 1  | CKR5_PANTR  |
| 10         | 96    | 100.0       | 352    | 1  | CKR5_PAPHA  |
| 11         | 96    | 100.0       | 352    | 1  | CKR5_PONPY  |
| 12         | 96    | 100.0       | 352    | 1  | CKR5_PYGBI  |
| 13         | 96    | 100.0       | 352    | 1  | CKR5_PYGNE  |
| 14         | 96    | 100.0       | 352    | 1  | CKR5_TPAFR  |
| 15         | 96    | 100.0       | 352    | 1  | CKR5_TPAFR  |
| 16         | 93    | 96.9        | 352    | 1  | CKR5_MACMU  |
| 17         | 74    | 77.1        | 354    | 1  | CKR5_MOUSE  |
| 18         | 74    | 77.1        | 354    | 1  | CKR5_RAT    |
| 19         | 47    | 49.0        | 355    | 1  | CKR1_MOUSE  |
| 20         | 46    | 47.9        | 373    | 1  | CKR2_MOUSE  |
| 21         | 45    | 46.9        | 355    | 1  | CKR1_MACMU  |
| 22         | 45    | 46.9        | 634    | 1  | YX3_EUGGR   |
| 23         | 45    | 46.9        | 4523   | 1  | DYHE HUMAN  |
| 24         | 44    | 45.8        | 616    | 1  | SECD_HAEIN  |
| 25         | 43    | 44.8        | 300    | 1  | PYRB_MYCPE  |
| 26         | 43    | 44.8        | 355    | 1  | CKR3_CERAE  |
| 27         | 43    | 44.8        | 355    | 1  | CKR3_MACMU  |
| 28         | 43    | 44.8        | 373    | 1  | VIOD_CHRVO  |
| 29         | 43    | 44.8        | 3587   | 1  | SRF2_BACSV  |
| 30         | 42    | 43.8        | 241    | 1  | UTR4_YEAST  |
| 31         | 41.5  | 43.2        | 334    | 1  | FEPD_ECOLI  |
| 32         | 41    | 42.7        | 244    | 1  | Y28K_SSVI   |
| 33         | 41    | 42.7        | 303    | 1  | APP_CACSV   |

|     |      |      |      |   |             |
|-----|------|------|------|---|-------------|
| 34  | 41   | 42.7 | 318  | 1 | NULM_HYLLA  |
| 35  | 41   | 42.7 | 358  | 1 | CKR3_CANPO  |
| 36  | 41   | 42.7 | 373  | 1 | CKR2_RAT    |
| 37  | 41   | 42.7 | 397  | 1 | O22B_DROME  |
| 38  | 41   | 42.7 | 461  | 1 | FCMD_HUMAN  |
| 39  | 41   | 42.7 | 629  | 1 | PR39_YEAST  |
| 40  | 40   | 41.7 | 284  | 1 | SUHA_HUMAN  |
| 41  | 40   | 41.7 | 309  | 1 | YBCK_HAEIN  |
| 42  | 40   | 41.7 | 355  | 1 | CKR1_HUMAN  |
| 43  | 40   | 41.7 | 371  | 1 | Y1B0_CLOAB  |
| 44  | 40   | 41.7 | 437  | 1 | ARLY_CLOAB  |
| 45  | 40   | 41.7 | 501  | 1 | AMPA_BUCBP  |
| 46  | 40   | 41.7 | 634  | 1 | HTPG_PSEAE  |
| 47  | 40   | 41.7 | 635  | 1 | HTPG_PSRSM  |
| 48  | 40   | 41.7 | 672  | 1 | ACSA_METSO  |
| 49  | 39   | 40.6 | 78   | 1 | Y076_WIGBR  |
| 50  | 39   | 40.6 | 180  | 1 | Y16A_MYCHY  |
| 51  | 39   | 40.6 | 217  | 1 | DEOC_MYCHO  |
| 52  | 39   | 40.6 | 392  | 1 | FTZ2_ARCFU  |
| 53  | 39   | 40.6 | 404  | 1 | ALR_RICPR   |
| 54  | 39   | 40.6 | 411  | 1 | SVY_RICCN   |
| 55  | 39   | 40.6 | 449  | 1 | CPSE_STRAS  |
| 56  | 39   | 40.6 | 449  | 1 | CPSE_STRAS  |
| 57  | 39   | 40.6 | 451  | 1 | MURD_STRMU  |
| 58  | 39   | 40.6 | 452  | 1 | MURD_STRPY  |
| 59  | 39   | 40.6 | 452  | 1 | MURD_STRPY  |
| 60  | 39   | 40.6 | 506  | 1 | MATK_ARAAL  |
| 61  | 39   | 40.6 | 535  | 1 | V550_HSVSA  |
| 62  | 39   | 40.6 | 585  | 1 | YB13_YEAST  |
| 63  | 39   | 40.6 | 642  | 1 | NOSZ_ACHCY  |
| 64  | 39   | 40.6 | 662  | 1 | CYOB_BUCAI  |
| 65  | 39   | 40.6 | 674  | 1 | CAN9_RAT    |
| 66  | 39   | 40.6 | 690  | 1 | CAN9_HUMAN  |
| 67  | 39   | 40.6 | 690  | 1 | CAN9_MOUSE  |
| 68  | 39   | 40.6 | 754  | 1 | R1R1_BPT4   |
| 69  | 39   | 40.6 | 827  | 1 | TRKC_CHICK  |
| 70  | 39   | 40.6 | 852  | 1 | WS14_HUMAN  |
| 71  | 39   | 40.6 | 864  | 1 | WS14_MOUSE  |
| 72  | 38.5 | 40.1 | 324  | 1 | MGPA_MYCPN  |
| 73  | 38.5 | 40.1 | 560  | 1 | GUP1_YEAST  |
| 74  | 38   | 39.6 | 135  | 1 | YOR6_ADEG1  |
| 75  | 38   | 39.6 | 181  | 1 | IPYR_UREPA  |
| 76  | 38   | 39.6 | 226  | 1 | UNG_VIBU    |
| 77  | 38   | 39.6 | 249  | 1 | GPM_A_ECOLI |
| 78  | 38   | 39.6 | 249  | 1 | GPM_A_SALTY |
| 79  | 38   | 39.6 | 258  | 1 | Y535_VIBU   |
| 80  | 38   | 39.6 | 258  | 1 | Y535_VIBU   |
| 81  | 38   | 39.6 | 261  | 1 | YVDC_LACLA  |
| 82  | 38   | 39.6 | 314  | 1 | Y315_MYCPN  |
| 83  | 38   | 39.6 | 389  | 1 | O85C_DROME  |
| 84  | 38   | 39.6 | 427  | 1 | CYB6_CHLIT  |
| 85  | 38   | 39.6 | 427  | 1 | CYB6_CHLIT  |
| 86  | 38   | 39.6 | 443  | 1 | COBB_METJA  |
| 87  | 38   | 39.6 | 459  | 1 | Y226_MYCJE  |
| 88  | 38   | 39.6 | 502  | 1 | MATK_SINAL  |
| 89  | 38   | 39.6 | 503  | 1 | Y226_MYCPN  |
| 90  | 38   | 39.6 | 526  | 1 | ALG8_HUMAN  |
| 91  | 38   | 39.6 | 581  | 1 | FUR4_SCHPO  |
| 92  | 38   | 39.6 | 598  | 1 | Y036_HUMAN  |
| 93  | 38   | 39.6 | 879  | 1 | MANB_BOVIN  |
| 94  | 38   | 39.6 | 879  | 1 | MANB_BOVIN  |
| 95  | 38   | 39.6 | 879  | 1 | MANB_HUMAN  |
| 96  | 38   | 39.6 | 940  | 1 | SVI_BUCAI   |
| 97  | 38   | 39.6 | 965  | 1 | PT03_YEAST  |
| 98  | 38   | 39.6 | 1505 | 1 | CUT2_HUMAN  |
| 99  | 37.5 | 39.1 | 304  | 1 | HEMZ_THEVO  |
| 100 | 37.5 | 39.1 | 308  | 1 | HEMZ_THEAC  |

#### ALIGNMENTS

RESULT 1

CCR5 CERAE  
 ID CCR5 CERAE STANDARD; PRT; 352 AA.  
 AC P56493;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKR5.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Kidney;  
 RX MEDLINE=98001387; PubMed=9343222;  
 RA Kuhlmann S.B., Platt E.J., Kozak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 RT implicate specific amino acids in infections by simian and human  
 RT immunodeficiency viruses.";  
 RL J. Virol. 71:8642-8656(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Murayama Y., Matsunaga S., Inoue-Murayama M.;  
 RT "cDNA sequence of African green monkey CCR-5 chemokine receptor  
 RT gene.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 DR EMBL; U83324; AAC51795.1; -;  
 DR EMBL; U83325; AAC51796.1; -;  
 DR EMBL; AB015944; BAA31328.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP F1 1; 1.  
 DR PROSITE; PS50262; G PROTEIN RECP F1 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 KW Polymorphism.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).

FT VARIANT 14 14 N -> Y.  
 FT VARIANT 352 352 F -> L.  
 SQ SEQUENCE 352 AA; 40561 MW; 7952690C72EC29A CRC64;  
 Query Match 100.0%; Score 96; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKFNQTLKIVILG 18  
 DB 185 SQYQFWKFNQTLKIVILG 202  
 RESULT 2  
 ID CCR5 CERPY STANDARD; PRT; 352 AA.  
 AC Q9TV42;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKR5.  
 OS Cercopithecus pygerythrus (Vervet monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=60710;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=100;  
 RX MEDLINE=99335215; PubMed=10408730;  
 RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,  
 RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomgaard A.;  
 RT "Mutations in CCR5-coding sequences are not associated with SIV  
 RT carrier status in African nonhuman primates.";  
 RL AIDS Res. Hum. Retroviruses 15:931-939(1999).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 DR EMBL; AF035222; AAD44015.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP F1 1; 1.  
 DR PROSITE; PS50262; G PROTEIN RECP F1 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301

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FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKFNQTLKIVILG 18
Db 185 SOYQFWKFNQTLKIVILG 202

RESULT 3
CKR5_CERTO STANDARD; PRT; 352 AA.
AC O62743; O62744; O62745; O62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys
naturally infected in west Africa: a comparison of coreceptor usage
of primary SIVsm, HIV-2, and SIVmac.";
RL Virology 246:113-124 (1998).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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or send an email to license@isb-sib.ch).
CC EMBL; AF051902; AAC39830.1; -
CC EMBL; AF051903; AAC39831.1; -
CC EMBL; AF051904; AAC39832.1; -
CC EMBL; AF051905; AAC39833.1; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).

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FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 087).
FT VARIANT 25 25 Y -> G (IN ISOLATE 079).
FT VARIANT 100 100 M -> K (IN ISOLATE 079).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47B49CA CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKFNQTLKIVILG 18
Db 185 SOYQFWKFNQTLKIVILG 202

RESULT 4
CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=97269687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010 (1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
MIP-1-beta and RANTES and subsequently transduces a signal by
increasing the intracellular calcium ions level. May play a role
in the control of granulocytic lineage proliferation or
differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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or send an email to license@isb-sib.ch).
CC EMBL; AF005659; AAB62553.1; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.

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DR PROSITE; P500237; G PROTEIN RECEPTOR FL 1; 1.  
 DR PROSITE; P50262; G PROTEIN RECEPTOR FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 5 (POTENTIAL).  
 FT TRANSMEM 199 218 6 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 7 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40515 MW; DO66FCB9FE5EAC84 CRC64;  
 Query Match 100.0%; Score 96; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWNQTGLKIVLG 18  
 DB 185 SQYQFWNQTGLKIVLG 202  
 RESULT 5  
 CCR5\_HUMAN  
 ID CCR5\_HUMAN STANDARD; PRT; 352 AA.  
 AC P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;  
 AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;  
 AC O14708; O15538; Q9UPA4;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-5 chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5)  
 DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).  
 GN CCR5 OR CMKBR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96241590; PubMed=8639485;  
 RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;  
 RT "Molecular cloning and functional expression of a new human  
 CC chemokine receptor gene."  
 RL Biochemistry 35:3362-3367(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96291862; PubMed=8663314;  
 RA Raport C.J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;  
 RT "Molecular cloning and functional characterization of a novel human  
 CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha."  
 RL J. Biol. Chem. 271:17161-17166(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96295970; PubMed=8699119;  
 RA Combadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;  
 RT "Cloning and functional expression of CC CR5, a human monocyte CC  
 chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and  
 RANTES."  
 RL J. Leukoc. Biol. 60:147-152(1996).  
 RN [4]

RP SEQUENCE FROM N.A.  
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
 RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
 RA Ghaj L., la Bastide M., Kaplan N., Greco T., Touchman J.,  
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,  
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,  
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,  
 RA Watanabe M., Doggett N., Garcia D., Sacripanti J.L.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98001387; PubMed=9343222;  
 RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 RT implicate specific amino acids in infections by simian and human  
 RT immunodeficiency viruses."  
 RL J. Virol. 71:8642-8656(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A., AND POLYMORPHISMS.  
 RX MEDLINE=98022612; PubMed=9359654;  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."  
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98049523; PubMed=9388201;  
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;  
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts  
 RT with 5'-end heterogeneity, dual promoter usage, and evidence for  
 RT polymorphisms within the regulatory regions and noncoding exons."  
 RL J. Biol. Chem. 272:30662-30671(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.  
 RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,  
 RA Debre P.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
 RX MEDLINE=96260017; PubMed=8649511;  
 RA Deng H., Liu R., Ellmeier W., Choe S., Unutmaz D., Burkhart M.,  
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,  
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;  
 RT "Identification of a major co-receptor for primary isolates of  
 RT HIV-1."  
 RL Nature 381:661-666(1996).  
 RN [11]  
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
 RX MEDLINE=96260018; PubMed=8649512;  
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,  
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,  
 RA Paxton W.A.;  
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor  
 RT CC-CCR-5."  
 RL Nature 381:667-673(1996).  
 RN [12]  
 RP SULFATION.  
 RX MEDLINE=99189752; PubMed=10089882;  
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Gayabab M.,  
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;  
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1  
 RT entry."  
 RL Cell 96:667-676(1999).  
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and rantes and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or

differentiation. Acts as co-receptor with CD4 for primary non-syngium-inducing strains (NSI) (macrophage-tropic) of HIV-1 virus. It promotes Env-mediated fusion of the virus.

-|- SUBCELLULAR LOCATION: Integral membrane protein.

-|- TISSUE SPECIFICITY: Found in promyelocytic cells.

-|- PM: Sulfation contributes to the efficiency of HIV-1 entry.

-|- PTM: Modified by O-linked glycosylation, but not by N-linked glycosylation.

-|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; X91492; CAA62796.1; -  
 DR EMBL; U54994; AAC50598.1; -  
 DR EMBL; U57840; AAB17071.1; -  
 DR EMBL; U95626; AAB57793.1; -  
 DR EMBL; U83326; AAC51797.1; -  
 DR EMBL; AF011500; AAB65700.1; -  
 DR EMBL; AF011501; AAB65701.1; -  
 DR EMBL; AF011502; AAB65702.1; -  
 DR EMBL; AF011503; AAB65703.1; -  
 DR EMBL; AF011504; AAB65704.1; -  
 DR EMBL; AF011505; AAB65705.1; -  
 DR EMBL; AF011506; AAB65706.1; -  
 DR EMBL; AF011507; AAB65707.1; -  
 DR EMBL; AF011508; AAB65708.1; -  
 DR EMBL; AF011509; AAB65709.1; -  
 DR EMBL; AF011510; AAB65710.1; -  
 DR EMBL; AF011511; AAB65711.1; -  
 DR EMBL; AF011512; AAB65712.1; -  
 DR EMBL; AF011513; AAB65713.1; -  
 DR EMBL; AF011514; AAB65714.1; -  
 DR EMBL; AF011515; AAB65715.1; -  
 DR EMBL; AF011516; AAB65716.1; -  
 DR EMBL; AF011517; AAB65717.1; -  
 DR EMBL; AF011518; AAB65718.1; -  
 DR EMBL; AF011519; AAB65719.1; -  
 DR EMBL; AF011520; AAB65720.1; -  
 DR EMBL; AF011521; AAB65721.1; -  
 DR EMBL; AF011522; AAB65722.1; -  
 DR EMBL; AF011523; AAB65723.1; -  
 DR EMBL; AF011524; AAB65724.1; -  
 DR EMBL; AF011525; AAB65725.1; -  
 DR EMBL; AF011526; AAB65726.1; -  
 DR EMBL; AF011527; AAB65727.1; -  
 DR EMBL; AF011528; AAB65728.1; -  
 DR EMBL; AF011529; AAB65729.1; -  
 DR EMBL; AF011530; AAB65730.1; -  
 DR EMBL; AF011531; AAB65731.1; -  
 DR EMBL; AF011532; AAB65732.1; -  
 DR EMBL; AF011533; AAB65733.1; -  
 DR EMBL; AF011534; AAB65734.1; -  
 DR EMBL; AF011535; AAB65735.1; -  
 DR EMBL; AF011536; AAB65736.1; -  
 DR EMBL; AF011537; AAB65737.1; -  
 DR EMBL; AF031237; AAB94735.1; -  
 DR EMBL; AF052539; AAD18131.1; -  
 DR EMBL; AY221093; AAO65971.1; -  
 DR GenBank; HGNC:1606; CCR5.

MIM: 601373; - C-endosome; TAS.  
 DR GO; GO:0005768; C:integral to plasma membrane; TAS.  
 DR GO; GO:0005887; F:C-C chemokine receptor activity; TAS.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; TAS.  
 DR GO; GO:0015026; F:coreceptor activity; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006968; P:cellular defense response; TAS.  
 DR GO; GO:0006935; P:chemotaxis; TAS.  
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR GO; GO:0007125; P:invasive growth; TAS.  
 DR GO; GO:0007203; P:phosphatidylinositol-4,5-bisphosphate hydro. .; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP Fl 1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECP Fl 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 KW Polymorphism.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).

Query Match 100.0%; Score 96; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWNFKVILG 18  
 Db 185 SQYQFWNFKVILG 202

RESULT 6  
 CCR5 HYLL  
 ID CCR5 HYLL STANDARD; PRT; 352 AA.  
 AC 097883;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKR5.  
 OS Hylobates leucogynus (White-cheeked gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=61893;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -|- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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EMBL; AF075451; AAD19863.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP Fl 1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECP Fl 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40445 MW; 4FB84F344CEB7C91 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 7  
 CKR5\_HYLM L STANDARD; PRT; 352 AA.  
 AC Q95NC0;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CKR5 OR CMKBR5.  
 OS Hylobates moloch (Silvery gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=81572;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC

DR EMBL; AF177899; AAK43382.1;  
 DR InterPro; IPR000276; GPCR Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.  
 DR PROSITE; PS00262; G PROTEIN RECP FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT

FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 6.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
 |||||  
 DB 185 SQYQFWKNFQTLKIVILG 202

RESULT 8  
 CKR5\_HYLS Y STANDARD; PRT; 352 AA.  
 AC Q95NC5;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CKR5 OR CMKBR5.  
 OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=9590;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC

DR EMBL; AF177884; AAK43367.1;  
 DR InterPro; IPR000276; GPCR Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.  
 DR PROSITE; PS00262; G PROTEIN RECP FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT

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FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40508 MW; F4F64B3AD5AF658A CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 9
ID CKR5_PANTR STANDARD; PRT; 352 AA.
AC P56440; 002778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Sanson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Feiler S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
RN [2]
RX SEQUENCE FROM N.A.
RA Zimmerman P.A., Buckler-White A., Alkhatib G.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RX SEQUENCE FROM N.A.
RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,
RA Ho D.D.;
RX MEDLINE=98022612; PubMed=9359654;
RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."
RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).
RN [4]
RX SEQUENCE FROM N.A.
RA Zacharova V., Zachar V., Goustin A.S.;
RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural
RT HIV type 1 host."
RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).
RN [5]
RX SEQUENCE FROM N.A.
RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;
RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1."
RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).
RN [6]
RX SEQUENCE FROM N.A.
RA Zhang Y., Ryder O.A., Zhang Y.;

```

```

RT "Sequence comparison of the CCR5 gene in primates and primate
RT phylogeny."
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF005663; AAB62557.1; -
CC EMBL; U94329; AAB58446.1; -
CC EMBL; AF011542; AAB65742.1; -
CC EMBL; U97666; AAC51670.1; -
CC EMBL; AF011540; AAB65740.1; -
CC EMBL; U89797; AAC03717.1; -
CC EMBL; AF177894; AAK43377.1; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm.1.1
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 123 123 T -> S (IN REF. 1).
SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B0FE34C CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 10
ID CKR5_PAPHA STANDARD; PRT; 352 AA.
AC P56441;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

```

GN CCR5 OR CMKRS.  
 OS Papio hamadryas (Hamadryas baboon), and  
 OS Papio anubis (Olive baboon)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Papio.  
 OX NCBI\_TaxID=9557, 9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.hamadryas;  
 RX MEDLINE=9726867; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.hamadryas;  
 RX MEDLINE=99210133; PubMed=10195758;  
 RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;  
 RT "Species-specific changes in the CCR5 gene from African and Asian  
 RT nonhuman primates";  
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P. anubis;  
 RA Benton P.A., Tinasus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC EMBL; AF005658; AAB62552.1; -;  
 CC EMBL; AF105287; AAD20556.1; -;  
 CC EMBL; AF105288; AAD20557.1; -;  
 CC EMBL; AF105289; AAD20558.1; -;  
 CC EMBL; AF105290; AAD20559.1; -;  
 CC EMBL; AF023452; AAC63830.1; -;  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS; PR00237; GPCR\_Rhodopsn.  
 CC PROSITE; PS00237; G PROTEIN RECP F1 1; 1.  
 CC PROSITE; PS0262; G PROTEIN RECP F1 2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 1 30  
 FT TRANSMEM 31 58  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124  
 FT DOMAIN 125 141  
 FT TRANSMEM 142 166  
 FT TRANSMEM 167 198  
 FT TRANSMEM 199 218  
 FT TRANSMEM 219 235  
 FT TRANSMEM 236 260  
 FT TRANSMEM 261 277  
 FT TRANSMEM 278 301  
 FT TRANSMEM 302 352  
 FT CYTOPLASMIC (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 FT CARBOHYD 268 268 N-LINKED (GLCNAc...) (POTENTIAL).  
 SQ SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FEBB2 CRC64;  
 Query Match 100.0%; Score 96; DB 1; Length 352;  
 Best Local Similarity 100.0%; Fred. No. 6.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQWKNFQTLKIVIG 18  
 Db 185 SQYQWKNFQTLKIVIG 202  
 RESULT 11  
 CCR5\_PONY STANDARD; PRT; 352 AA.  
 AC 097881;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKRS.  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.  
 OX NCBI\_TaxID=9600;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates";  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL; AF075446; AAD19858.1; -;  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS; PR00237; GPCR\_Rhodopsn.  
 CC PROSITE; PS00237; G PROTEIN RECP F1 1; 1.  
 CC PROSITE; PS0262; G PROTEIN RECP F1 2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 1 30  
 FT TRANSMEM 31 58  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124  
 FT DOMAIN 125 141  
 FT TRANSMEM 142 166  
 FT TRANSMEM 167 198  
 FT TRANSMEM 199 218  
 FT TRANSMEM 219 235  
 FT TRANSMEM 236 260  
 FT TRANSMEM 261 277  
 FT TRANSMEM 278 301  
 FT TRANSMEM 302 352  
 FT CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40527 MW; F4E2F47135AF659A CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 12
CKR5 PYGBI
ID CKR5 PYGBI STANDARD; PRT; 352 AA.
AC O97880;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075445; AAD19857.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PS00237; GPCRHOODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00242; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40585 MW; 4366F142730F938F CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 13
CKR5 PYGNE
ID CKR5 PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075448; AAD19860.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PS00237; GPCRHOODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).

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FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E861 CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18  
 |||||  
 DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 14  
 CKR5\_TRAFR  
 ID CKR5\_TRAFR STANDARD; PRT; 352 AA.  
 AC O97878;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CKR5 OR CMKBR5.  
 OS Trachypithecus francoisi (Francoisi' langur) (Indochinese langur).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Trachypithecus.  
 OC NCBI\_TaxID=54180;  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 MIP-1-beta and RANTES and subsequently transduces a signal by  
 increasing the intracellular calcium ions level. May play a role  
 in the control of granulocytic lineage proliferation or  
 differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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 CC  
 CC EMBL: AF075442; AAD19854.1;  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7tm.1; 1.  
 CC PRINTS: PR00237; GPCRHOOPS.  
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match 100.0%; Score 96; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18  
 |||||  
 DB 185 SOYQFWKNFQTLKIVILG 202

RESULT 15  
 CKR5\_TRAPH  
 ID CKR5\_TRAPH STANDARD; PRT; 352 AA.  
 AC O97879;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CKR5 OR CMKBR5.  
 OS Trachypithecus phayrei (Phayrei's leaf monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;  
 OC Trachypithecus.  
 OC NCBI\_TaxID=61618;  
 OX [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 MIP-1-beta and RANTES and subsequently transduces a signal by  
 increasing the intracellular calcium ions level. May play a role  
 in the control of granulocytic lineage proliferation or  
 differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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 CC  
 CC EMBL: AF075443; AAD19855.1;  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7tm.1; 1.  
 CC PRINTS: PR00237; GPCRHOOPS.  
 CC PROSITE: PS00237; G-PROTEIN RECEPTOR FL 1; 1.  
 CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;  
 Query Match 100.0%; Score 96; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SOYQFWKFNQTLKIVILG 18  
 Db 185 SOYQFWKFNQTLKIVILG 202  
 RESULT 16  
 CCR5\_MACMU  
 ID\_CCR5\_MACMU STANDARD; PRT; 352 AA.  
 AC P79436; 002746;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKR5.  
 OS Macaca mulatta (Rhesus macaque),  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and  
 OS Macaca nemestrina (Pig-tailed macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544, 9541, 9545;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.mulatta;  
 RX MEDLINE=97184592; PubMed=9032394;  
 RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,  
 RA Newman W., Gerard N., Gerard C., Sodroski J.;  
 RT "Utilization of C-C chemokine receptor 5 by the envelope  
 RT glycoproteins of a pathogenic simian immunodeficiency virus,  
 RT SIVmac239.";  
 RL J. Virol. 71:2522-2527(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.mulatta; STRAIN=Indian macaque;  
 RX MEDLINE=97213934; PubMed=9060623;  
 RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;  
 RA "Genetically divergent strains of simian immunodeficiency virus use  
 RT CCR5 as a coreceptor for entry.";  
 RL J. Virol. 71:2705-2714(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.mulatta;  
 RX MEDLINE=21354176; PubMed=11461684;  
 RA Margulies B.J., Hauer D.A., Clements J.E.;  
 RT "Identification and comparison of eleven rhesus macaque chemokine  
 RT receptors.";  
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;  
 RX MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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 CC  
 CC EMBL; U77672; AAC51109.1; -;  
 CC EMBL; U73739; AAC51158.1; -;  
 CC EMBL; U96762; AAC34132.1; -;  
 CC EMBL; AF005660; AAB62554.1; -;  
 CC EMBL; AF005661; AAB62555.1; -;  
 CC EMBL; AF005662; AAB62556.1; -;  
 CC InterPro; IPR000276; GPCR\_Rhodpsn.  
 CC Pfam; PF00001; 7cm.1; 1.  
 CC PRINTS; PR00237; GPCRHOOPS.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 CC PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT CARBOHYD 268 268 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CONFLICT 241 241 M -> I (IN REF. 3).  
 FT CONFLICT 292 292 I -> M (IN REF. 3).  
 SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;  
 Query Match 96.9%; Score 93; DB 1; Length 352;  
 Best Local Similarity 94.4%; Pred. No. 2e-07;  
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SOYQFWKFNQTLKIVILG 18  
 Db 185 SOYQFWKFNQTLKIVILG 202  
 RESULT 17  
 CCR5\_MOUSE  
 ID\_CCR5\_MOUSE STANDARD; PRT; 354 AA.  
 AC P51682; O35313; O35891; P97308; P97405; Q61867;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR-5) (MIP-1  
 DE alpha receptor).  
 GN CCR5 OR CMKR5.  
 OS Mus musculus (Mouse).



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ; TISSUE=Spleen;  
 RX MEDLINE=96205938; PubMed=8631787;  
 RA Borling L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,  
 RA Charo I.P.;  
 RT "Molecular cloning and functional expression of murine JE (monocyte  
 RT chemottractant protein 1) and murine macrophage inflammatory protein  
 RT 1alpha receptors: evidence for two closely linked C-C chemokine  
 RT receptors on chromosome 9.";  
 RL J. Biol. Chem. 271:7551-7558(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
 RX MEDLINE=96278910; PubMed=8662890;  
 RA Meyer A., Coyle A.J., Proudfoot A.E.I., Wells T.N.C., Power C.A.;  
 RT "Cloning and characterization of a novel murine macrophage  
 RT inflammatory protein-1 alpha receptor.";  
 RL J. Biol. Chem. 271:14445-14451(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Ola;  
 RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;  
 RX MEDLINE=98001387; PubMed=9343222;  
 RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 RT implicate specific amino acids in infections by simian and human  
 RT immunodeficiency viruses.";  
 RL J. Virol. 71:8642-8656(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=97404635; PubMed=9261347;  
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Zhang M., Cen Y.H.,  
 RA Wang Z.X., Guo H.H., Du G.G., Accavitti M.A., Doms R.W., Peiper S.C.;  
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human  
 RT immunodeficiency virus type 1.";  
 RL J. Virol. 71:6305-6314(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC Guo B., Kuno K., Harada A., Matsushima K.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,  
 CC but not in nonhematopoietic cell lines.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL; U47036; AAC52454.1; -  
 CC EMBL; X94151; CAB3867.1; -  
 CC EMBL; U68565; AAB37273.1; -  
 CC EMBL; U83327; AAC53386.1; -  
 CC EMBL; AF022990; AAC53389.1; -  
 CC EMBL; AF019772; AAB71183.1; -  
 CC EMBL; D83648; BAA12024.1; -  
 CC MGD; MGI:107182; Ccr5.

DR GO; GO:0016493; P:C-C chemokine receptor activity; IDA.  
 DR GO; GO:0006952; P:defense response; IMP.  
 DR InterPro; IPR000276; GPCR Rhodopsn.  
 DR Pfam; PF00001; 7tm1.1;  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECP\_F1.1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECP\_F1.2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.  
 FT DOMAIN 1 32  
 FT TRANSMEM 33 60  
 FT DOMAIN 61 70  
 FT TRANSMEM 71 91  
 FT DOMAIN 92 104  
 FT TRANSMEM 105 126  
 FT DOMAIN 127 143  
 FT TRANSMEM 144 168  
 FT DOMAIN 169 200  
 FT TRANSMEM 201 220  
 FT DOMAIN 221 237  
 FT TRANSMEM 238 262  
 FT DOMAIN 263 279  
 FT TRANSMEM 280 303  
 FT DOMAIN 304 354  
 FT DISULFID 103 180  
 FT CARBOHYD 270 270  
 FT VARIANT 11 11  
 FT VARIANT 62 62  
 FT VARIANT 66 66  
 FT VARIANT 97 97  
 FT VARIANT 109 109  
 FT VARIANT 156 156  
 FT VARIANT 160 160  
 FT VARIANT 185 185  
 FT VARIANT 213 213  
 FT VARIANT 318 318  
 FT VARIANT 337 337  
 FT CONFLICT 3 3  
 FT CONFLICT 80 80  
 FT CONFLICT 145 145  
 FT CONFLICT 190 190  
 FT CONFLICT 208 208  
 SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;  
 Query Match 77.1%; Score 74; DB 1; Length 354;  
 Best Local Similarity 76.5%; Pred. No. 0.002; 1; Indels 0; Gaps 0;  
 Matches 13; Conservative 3; Mismatches 1;  
 QY 1 SQYQFWKNSFQTLKIVIL 17  
 DB 187 TOYHFWKNSFQTLKIVIL 203  
 RESULT 18  
 CCR5\_RAT  
 ID CCR5\_RAT STANDARD; PRT; 354 AA.  
 AC O08556;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (MIP-1  
 DE alpha receptor).  
 GN CCR5 OR CCR5R5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Brain;  
 RX MEDLINE=98334064; PubMed=9670989;  
 RA Spleiss O., Gourmaud N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,  
 RA Berger M., Gebicke-Haerter P.J.;  
 RT "Cloning of rat HIV-1-chemokine coreceptor CCR5 from microglia and

RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";  
 RL J. Neurosci. Res. 53:16-28(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=98318173; PubMed=9655467;  
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 RT "Chemokine receptor expression in cultured glia and rat experimental  
 RT allergic encephalomyelitis.";  
 RL J. Neuroimmunol. 86:1-12(1998).  
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
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 CC -----  
 DR EMBL; Y12009; CAA2737.1; -;  
 DR EMBL; U77350; AAC03243.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN  
 DR PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECP\_F2\_1; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 32  
 FT TRANSMEM 33 60  
 FT DOMAIN 61 70  
 FT TRANSMEM 71 91  
 FT DOMAIN 92 104  
 FT TRANSMEM 105 126  
 FT DOMAIN 127 143  
 FT TRANSMEM 144 168  
 FT DOMAIN 169 200  
 FT TRANSMEM 201 220  
 FT DOMAIN 221 237  
 FT TRANSMEM 238 262  
 FT DOMAIN 263 279  
 FT TRANSMEM 280 303  
 FT DOMAIN 304 354  
 FT DISULFID 103 180  
 FT CARBOHYD 270 270  
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;  
 Query Match 77.1%; Score 74; DB 1; Length 354;  
 Best Local Similarity 81.2%; Pred. No. 0.0002;  
 Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QYQFWKHFQTLKQVIL 17  
 DB 188 QYQFWKHFQTLKQVIL 203  
 ||:|||||:|||||  
 ||:|||||:|||||  
 RESULT 19  
 CKR1\_MOUSE  
 ID CKR1\_MOUSE STANDARD; PRT; 355 AA.  
 AC P51675; Q91VP9;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)  
 DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)  
 DE (RANTES-R).  
 DE CC1 OR CMKBR1.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV; TISSUE=Peritoneal macrophage;  
 RX MEDLINE=96072806; PubMed=7594543;  
 RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,  
 RA Gerard C.;  
 RT "Molecular characterization of two murine eosinophil beta chemokine  
 RT receptors.";  
 RL J. Immunol. 155:5299-5305 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=95340546; PubMed=7542241;  
 RA Gao J.-L., Murphy P.M.;  
 RT "Cloning and differential tissue-specific expression of three mouse  
 RT beta chemokine receptor-like genes, including the gene for a  
 RT functional macrophage inflammatory protein-1 alpha receptor.";  
 RL J. Biol. Chem. 270:17494-17501(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -I- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND  
 CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR  
 CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL  
 CC PROLIFERATION.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- TISSUE SPECIFICITY: Detected in the heart, spleen, lung,  
 CC peritoneal exudate cells and leukocytes.  
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 DR EMBL; U29678; AAA86119.1; -;  
 DR EMBL; U28404; AAA89153.1; -;  
 DR EMBL; BC011092; AAH1092.1; -;  
 DR PIR; I49339; I49339.  
 DR MGD; MGI:104618; Ccr1.  
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:0030595; P:immune cell chemotaxis; IDA.  
 DR GO; GO:0006954; P:inflammatory response; IMP.  
 DR GO; GO:0030099; P:myeloid blood cell differentiation; IMP.

DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 60 1 (POTENTIAL).  
 FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 65 91 2 (POTENTIAL).  
 FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 108 129 3 (POTENTIAL).  
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 147 171 4 (POTENTIAL).  
 FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 198 223 5 (POTENTIAL).  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 264 6 (POTENTIAL).  
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 282 305 7 (POTENTIAL).  
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 106 183 BY SIMILARITY.  
 FT CONFLICT 55 55 M -> V (IN REF. 2 AND 3).  
 FT CONFLICT 149 149 L -> F (IN REF. 3).  
 FT CONFLICT 278 278 H -> Q (IN REF. 3).  
 SQ SEQUENCE 355 AA; 40901 MW; FCB9FF70B6F38B1 CRC64;

Query Match 49.8%; Score 47; DB 1; Length 355;

Best Local Similarity 61.5%; Pred. No. 3.9;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18  
 DB 195 WKRFQALINLLG 207

## RESULT 20

ID CKR2\_MOUSE STANDARD; PRT; 373 AA.  
 AC P51683; Q61172;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-CR2) (CCR-2) (CCR2)  
 DE (JE/FIC receptor) (MCP-1 receptor).  
 GN CCR2 OR CCR2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96205938; PubMed=8631787;  
 RA Borling L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,  
 RA Charo I.P.;  
 RT "Molecular cloning and functional expression of murine JE (monocyte  
 RT chemoattractant protein 1) and murine macrophage inflammatory protein  
 RT 1alpha receptors: evidence for two closely linked C-C chemokine  
 RT receptors on chromosome 9.";  
 RL J. Biol. Chem. 271:7551-7558 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c;  
 RX MEDLINE=96216064; PubMed=8662823;  
 RA Kurihara T., Bravo R.;  
 RT "Cloning and functional expression of mCCR2, a murine receptor for  
 RT the C-C chemokines JE and FIC.";  
 RL J. Biol. Chem. 271:11603-11606 (1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97026720; PubMed=8872898;  
 RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R.,  
 RA Post T.W., Gerard C., Dorf M.E.;

\*Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse  
 transcriptase-polymerase chain reaction does not detect mRNA for the  
 KC or new MCP-1 receptor.";  
 RL J. Neurosci. Res. 45:382-391 (1996).  
 CC -I- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (FIC) and MCP-5  
 CC chemokines. Transduces a signal by increasing the intracellular  
 CC calcium ions level.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -I- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,  
 CC but not in nonhematopoietic cell lines.  
 CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; U47035; AAC52453.1; -;  
 EMBL; U51717; AAC52557.1; -;  
 EMBL; U56819; AAC52784.1; -;  
 MGD; MGI:106185; Ccr2.  
 DR GO; GO:0016493; F1-C-C chemokine receptor activity; IDA.  
 DR GO; GO:0019955; F1-cytokine binding; IPI.  
 DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); IMP.  
 DR GO; GO:0030097; P:hemopoiesis; IMP.  
 DR GO; GO:0006959; P:humoral immune response; IMP.  
 DR GO; GO:0006954; P:inflammatory response; IMP.  
 DR GO; GO:0030334; P:regulation of cell migration; IMP.

DR InterPro; IPR000276; GPCR\_Rhodpsn.

DR Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1\_1; 1.

DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1\_2; 1.

KW G-protein coupled receptor; Transmembrane.

FT DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 56 83 1 (POTENTIAL).

FT DOMAIN 84 93 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 94 114 2 (POTENTIAL).

FT DOMAIN 115 127 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 128 149 3 (POTENTIAL).

FT DOMAIN 150 166 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 167 191 4 (POTENTIAL).

FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 220 239 5 (POTENTIAL).

FT DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 257 281 6 (POTENTIAL).

FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 299 322 7 (POTENTIAL).

FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).

FT DISULFID 126 203 BY SIMILARITY.

FT CONFLICT 39 39 Y -> H (IN REF. 1).

FT CONFLICT 184 184 A -> G (IN REF. 1).

FT CONFLICT 264 264 V -> G (IN REF. 1).

SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 47.9%; Score 46; DB 1; Length 373;

Best Local Similarity 64.3%; Pred. No. 5.8;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 QFKNFQTLKIVIL 17

DB 209 QLWKNFQTLKIVIL 222

## RESULT 21

CKR1\_MOUSE  
 ID CKR1\_MOUSE STANDARD; PRT; 355 AA.  
 AC P56482;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)

Hypothetical 78.0 kDa protein in P8BC intron 2 (ORF635).  
Euglena gracilis.  
Chloroplast.  
OC  
Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.  
OX NCBI\_TaxID=3039;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=Z / UTEX 753;  
RX MEDLINE=93347989; PubMed=8346031;  
RA Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A.,  
Orsat B., Spielmann A., Stutz E.;  
RT "Complete sequence of Euglena gracilis chloroplast DNA.";  
RL Nucleic Acids Res. 21:3537-3544(1993).  
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CC ce or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; Z11874; -; NOT ANNOTATED\_CDS.  
DR EMBL; X70810; CAA50080.1; -.  
DR PIR; S34499; S34499.  
DR PIR; S34500; S34500.  
KW Chloroplast; Hypoethetical protein.  
SQ SEQUENCE 634 AA; 78049 MW; D966B8864519E334 CRC64;  
  
Query Match 46.9%; Score 45; DB 1; Length 634;  
Best Local Similarity 55.6%; Pred. No. 14;  
Matches 10; Conservative 2; Mismatches 2; Indels 4; Gaps  
  
QY 4 QFW---KNFOTLKIVIL 17  
DB 60 KPWDSQIKNFWTLKIIKL 77  
: ||| ||||| :  
:  
  
RESULT 23  
DYHB\_HUMAN  
ID DYHB\_HUMAN STANDARD; PRT; 4523 AA.  
AC Q96D75; Q9U92;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ciliary dynein heavy chain 11 (Axonemal beta dynein heavy chain 11).  
DE DNAIL1  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A., VARIANT PCD GLN-3004, AND VARIANTS LEU-34;  
ARG-639; CRS-654; ALA-1023; THR-1038; GLY-1640; ASN-2641; THR-3474;  
VAL-3715; PRO-3765 AND ILE-4177.  
RS TTSUE=Nasal epithelium, and Testis;  
MEDLINE=22155903; PubMed=12142464;  
RA Bartoloni L., Blouin J.L., Pan Y., Gehrig C., Maiti A.K., Scamuffa N.,  
Rossier C., Jorissen M., Armengot M., Meeks M., Mitchison H.M.,  
Chung E.-M., Belizier-Blanchet C.D., Craigen W.J., Antonarakis S.E.;  
RT "Mutations in the DNAIL1 (axonemal heavy chain dynein type 11) gene  
cause one form of situs inversus totalis and most likely primary  
ciliary dyskinesia.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:10282-10286(2002).  
[2]  
SEQUENCE OF 1904-2004 FROM N.A.  
RC TTSUE=Nasal polyps;  
RA Maiti A.K., Mattei M.-G., Jorissen M., Volz A., Ziegler A.,  
Bouvagnet P.;  
RT "Chromosomal localization of human dynein heavy chain genes.";  
Submitted (JAN-1999) to the EMBL/GenBank/DDSI databases.  
-!- FUNCTION: Force generating protein of respiratory cilia. Produces  
force towards the minus ends of microtubules. Dynein has ATPase

activity; the force-producing power stroke is thought to occur on release of ADP.

-!- SUBUNIT: Consists of at least two heavy chains and a number of intermediate and light chains.

-!- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem (which binds cargo and interacts with other dynein components), and the head or motor domain. The motor contains six tandemly-linked AAA domains in the head, which form a ring. A stalk-like structure (formed by two of the coiled coil domains) protrudes between AAA 4 and AAA 5 and terminates in a microtubule-binding site. A seventh domain may also contribute to this ring; it is not clear whether the N-terminus or the C-terminus forms this extra domain. There are four well-conserved and two non-conserved ATPase sites, one per AAA domain. Probably only one of these (within AAA 1) actually hydrolyzes ATP, the others may serve a regulatory function.

-!- DISEASE: Defects in DNAH11 are a cause of primary ciliary dyskinesia (PCD) [MIM:242650]; also known as immotile cilia syndrome 1 (ICS1). The phenotype of this autosomal recessive disease is characterized by axonemal abnormalities of respiratory cilia and sperm tails leading to bronchiectasis and sinusitis, which are sometimes associated with situs inversus (Kartagener syndrome) and male sterility.

-!- SIMILARITY: Belongs to the dynein heavy chain family.

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EMBL; AJ320497; CAC60121.1; -  
EMBL; AJ132087; CAA10560.1; -  
Genew; HGNC:2942; DNAH11.  
MIM; 603339; -  
MIM; 242650; -  
GO; GO:0003858; C:axonemal dynein complex; NAS.  
GO; GO:0003775; F:axonemal motor activity; NAS.  
InterPro; IPR003593; AAA ATPase.  
InterPro; IPR004273; Dynein heavy.  
Pfam; PF03028; Dynein heavy; 1.  
SMART; SM00382; AAA; 4.  
Motor protein; Dynein; Microtubule; ATP-binding; Repeat; Coiled coil;  
KW Polymorphism; Disease mutation.  
FT DOMAIN 1 1861 STEM (BY SIMILARITY).  
FT DOMAIN 1862 2083 AAA 1 (BY SIMILARITY).  
FT DOMAIN 2143 2373 AAA 2 (BY SIMILARITY).  
FT DOMAIN 2479 2726 AAA 3 (BY SIMILARITY).  
FT DOMAIN 2824 3073 AAA 4 (BY SIMILARITY).  
FT DOMAIN 3079 3410 STALK (BY SIMILARITY).  
FT DOMAIN 3466 3693 AAA 5 (BY SIMILARITY).  
FT DOMAIN 3903 4129 AAA 6 (BY SIMILARITY).  
FT DOMAIN 1274 1327 COILED COIL (POTENTIAL).  
FT DOMAIN 3079 3143 COILED COIL (POTENTIAL).  
FT DOMAIN 3319 3410 COILED COIL (POTENTIAL).  
FT DOMAIN 3675 3710 COILED COIL (POTENTIAL).  
FT NP\_BIND 1900 1907 ATP (POTENTIAL).  
FT NP\_BIND 2181 2188 ATP (POTENTIAL).  
FT NP\_BIND 2517 2524 ATP (POTENTIAL).  
FT NP\_BIND 2862 2869 ATP (POTENTIAL).  
FT VARIANT 34 34 E -> L (requires 2 nucleotide substitutions).  
FT /FTID=VAR\_013851.  
FT Q -> R.  
FT /FTID=VAR\_013852.  
FT S -> C.  
FT /FTID=VAR\_013853.  
FT V -> A.  
FT /FTID=VAR\_013854.  
FT A -> T.  
FT /FTID=VAR\_013855.

FT VARIANT 1640 1640 D -> G.  
FT /FTID=VAR\_013856.  
FT VARIANT 2641 2641 S -> N.  
FT /FTID=VAR\_013857.  
FT VARIANT 2682 2682 I -> V.  
FT /FTID=VAR\_013858.  
FT VARIANT 3004 3004 R -> Q (in PCD; not proven to be pathogenic).  
FT /FTID=VAR\_013859.  
FT VARIANT 3474 3474 A -> T.  
FT /FTID=VAR\_013860.  
FT VARIANT 3715 3715 L -> V.  
FT /FTID=VAR\_013861.  
FT VARIANT 3765 3765 S -> P.  
FT /FTID=VAR\_013862.  
FT VARIANT 4177 4177 T -> I.  
FT /FTID=VAR\_013863.  
SQ SEQUENCE 4523 AA; 520969 MW; 7C9A71C95E296B89 CRC64;  
Query Match 46.9%; Score 45; DB 1; Length 4523;  
Best Local Similarity 50.0%; Pred. No. 97;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 5 FWKQFOTLKIVILG 18  
Db 648 FWSNFASLYLFLG 661  
RESULT 24  
SECD\_HAEN  
ID SECD\_HAEN STANDARD; PRT; 616 AA.  
AC P44591;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Protein-export membrane protein secd.  
GN SECD OR H10240.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Haemophilus.  
OX NCBI\_TaxID=727;  
RN [1]\_TaxID=727;  
RP SEQUENCE FROM N.A.  
RC STRAIN=RD / KM20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., McKenney K., Sutton G., Tomb J.-F., Dougherty B.A., Merrick J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";  
RL Science 269:496-512 (1995).  
CC -!- FUNCTION: Involved in protein export (By similarity).  
CC -!- SUBUNIT: Part of the prokaryotic protein translocation apparatus which comprise secd, secdB, secdC, secdE, secdF, secdG and secdH (By similarity).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane (By similarity).  
CC -!- SIMILARITY: Belongs to the secd/secdF family. SecD family.  
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DR EMBL; U32710; AAC21908.1; -;  
 DR PIR; I64056; I64056.  
 DR TIGR; H10240; -;  
 DR InterPro; IPR005791; SecD.  
 DR InterPro; IPR003335; SecD\_SecF.  
 DR Pfam; PF02355; SecD\_SecF\_1.  
 DR PRINTS; PR01755; SECFTNLCASE.  
 DR TIGRFAMS; TIGR00916; 2A0604801; 1.  
 DR TIGRFAMS; TIGR01129; secD; 1.  
 DR Protein transport; Translocation; Transmembrane; Inner membrane;  
 KW Complete proteome.  
 FT TRANSMEM 11 31 POTENTIAL.  
 FT TRANSMEM 453 473 POTENTIAL.  
 FT TRANSMEM 475 495 POTENTIAL.  
 FT TRANSMEM 497 517 POTENTIAL.  
 FT TRANSMEM 562 582 POTENTIAL.  
 FT TRANSMEM 595 605 POTENTIAL.  
 SQ SEQUENCE 616 AA; 66986 MW; 7DE1E4B085065F8F CRC64;  
 Query Match 45.8%; Score 44; DB 1; Length 616;  
 Best Local Similarity 38.9%; Pred. No. 20;  
 Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 SQYQFWKQFQTLKIVLG 18  
 Db 3 NRYPLWKNLWYFIVAIG 20  
 RESULT 25  
 PYRB MYCPE STANDARD; PRT; 300 AA.  
 AC QBELK9;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate  
 transcarbamylase) (ATCase).  
 GN PYRB OR MYPE7890.  
 OS Mycoplasma penetrans.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=28227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HF-2;  
 RX MEDLINE=22354719; PubMed=12466555;  
 RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,  
 RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;  
 RT "The complete genomic sequence of Mycoplasma penetrans, an  
 intracellular bacterial pathogen in humans.";  
 RL Nucleic Acids Res. 30:5293-5300(2002).  
 CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate  
 + N-carbamoyl-L-aspartate.  
 CC -!- PATHWAY: Pyrimidine biosynthesis; second step.  
 CC -!- SIMILARITY: Belongs to the ATCase/OTCase family.  
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 CC -----  
 CC EMBL; AF004173; BAC44582.1; -;  
 DR HAMAP; MF 00001; -; 1.  
 DR InterPro; IPR006130; Asp/Orn Cotransf.  
 DR InterPro; IPR002082; Asp carbamyltransf.  
 DR InterPro; IPR006131; OTCace O.  
 DR InterPro; IPR006132; OTCace P.  
 DR Pfam; PF00185; OTCace; 1.  
 DR PRINTS; PR00100; OTCace N; 1.  
 DR TIGRFAMS; TIGR00670; asp\_carb\_tr; 1.

DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.  
 KW Pyrimidine biosynthesis; Transferase; Complete proteome.  
 SQ SEQUENCE 300 AA; 34532 MW; 9F9200EEEDB298E2 CRC64;  
 Query Match 44.8%; Score 43; DB 1; Length 300;  
 Best Local Similarity 50.0%; Pred. No. 14;  
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 YQFWKQFQTLKIVLG 18  
 Db 143 YEKFKSFEGLTAIVG 158  
 RESULT 26  
 CKR3 CERAE STANDARD; PRT; 355 AA.  
 AC P56492;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR3)  
 GN CCR3 OR CCKBR3.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sol N., Treboute C., Gomas E., Ferchal P., Alizon M.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to ectaxin,  
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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 CC -----  
 CC EMBL; Y13775; CAA74106.1; -;  
 DR InterPro; IPR000276; GPCR Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECF\_F1\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECF\_F2\_1; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 62 1 (POTENTIAL).  
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 73 93 2 (POTENTIAL).  
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 108 129 3 (POTENTIAL).  
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 147 171 4 (POTENTIAL).  
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 204 223 5 (POTENTIAL).  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 264 6 (POTENTIAL).  
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 282 305 7 (POTENTIAL).  
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 106 183 BY SIMILARITY  
 SQ SEQUENCE 355 AA; 40830 MW; 44F7A5E9FEB978FF CRC64;  
 Query Match 44.8%; Score 43; DB 1; Length 355;  
 Best Local Similarity 58.3%; Pred. No. 17;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17  
|:|:|:|:|:|:|  
Db 195 WRHFHTLKWTIL 206

RESULT 27  
CKR3\_MACMU  
ID CKR3\_MACMU STANDARD; PRT; 355 AA.  
AC P56483;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)  
DE (CCR3).  
GN CCR3 OR CWKBR3.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9544;  
[1] \_  
RN SEQUENCE FROM N.A.  
RX MEDLINE=21354176; PubMed=11461684;  
RA Margulies B.J., Hauer D.A., Clements J.E.;  
RT "Identification and comparison of eleven rhesus macaque chemokine  
receptors.";  
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
[2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=98118446; PubMed=9454694;  
RA Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Allison M.;  
RT "The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor  
for HIV-2, but not for HIV-1.";  
RL Virology 240:213-220(1998).  
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to sotaxin,  
MCP-3, MCP-4 and RANTES and subsequently transduces a signal by  
increasing the intracellular calcium ions level.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC  
CC EMBL; AF017283; AAB70527.1; -;  
CC EMBL; Y13776; CAA74107.1; -;  
CC InterPro; IPR00276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm 1; 1.  
CC PRINTS; PR00237; GPCR\_Rhodopsin.  
CC PROSITE; PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE; PS00262; G-PROTEIN\_RECEP\_F1\_2; 1.  
CC G-protein coupled receptor; Transmembrane.  
CC DOMAIN 1 34  
CC EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 35 62  
FT DOMAIN 63 72  
CC CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 73 93  
CC DOMAIN 94 107  
FT TRANSMEM 108 129  
CC EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 130 146  
CC CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 147 171  
CC EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 172 203  
CC EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 204 223  
CC CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 224 239  
CC EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 240 264  
CC CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 265 281  
CC EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 282 305  
CC CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 306 355  
CC CYTOPLASMIC (POTENTIAL).

FT DISULFID 106 183 BY SIMILARITY.  
FT CONFLICT 180 180 K -> E (IN REF. 2).  
FT CONFLICT 202 202 K -> R (IN REF. 2).  
SQ SEQUENCE 355 AA; 40805 MW; E271F1B694970D9F CRC64;  
Query Match 44.8%; Score 43; DB 1; Length 355;  
Best Local Similarity 58.3%; Pred. No. 17;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVIL 17  
|:|:|:|:|:|:|  
Db 195 WRHFHTLKWTIL 206

RESULT 28  
VIOD\_CHRVO  
ID VIOD\_CHRVO STANDARD; PRT; 373 AA.  
AC Q9S308; Q9SON2;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Probable tryptophan hydroxylase viod (EC 1.-.-.-).  
GN VIOD OR CV3271.  
OS Chromobacterium violaceum.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
OC Neisseriaceae; Chromobacterium.  
OX NCBI\_TaxID=536;  
[1] \_  
RN SEQUENCE FROM N.A.  
RX STRAIN=UQM51;  
RX MEDLINE=20525185; PubMed=11075927;  
RA August P.R., Grossman T.H., Minor C., Draper M.P., MacNeil I.A.,  
Pemberton J.M., Call K.M., Holt D., Osburne M.S.;  
RT "Sequence analysis and functional characterization of the violacein  
biosynthetic pathway from Chromobacterium violaceum.";  
RL J. Mol. Microbiol. Biotechnol. 2:513-519(2000).  
[2]  
RN SEQUENCE FROM N.A.  
RX STRAIN=JCM 1249;  
RX Hoshino T.;  
RT "Biosynthetic gene cluster for violacein pigment.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
[3]  
RN SEQUENCE FROM N.A.  
RX STRAIN=ATCC 12472 / DSM 30191;  
RX MEDLINE=22882880; PubMed=14500782;  
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,  
Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,  
Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,  
Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,  
Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,  
Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,  
Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,  
Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,  
Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,  
Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,  
Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,  
Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,  
Leoi L.C.T., Lima L.P.A., Loureiro M.F., Lyra M.C.C.P.,  
Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,  
di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,  
Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,  
Pajxao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,  
Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,  
Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,  
Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,  
Silva A.B.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,  
Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,  
Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,  
Vettore A., Wassem R., Zaha A., Simpson A.J.G.;  
RT "The complete genome sequence of Chromobacterium violaceum reveals  
remarkable and exploitable bacterial adaptability.";

```

RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
CC -1- CATALYTIC ACTIVITY: Tryptophan + O(2) = 5-hydroxytryptophan.
CC -1- COFACTOR: FAD (Potential).
CC -1- PATHWAY: Violacein biosynthesis; branch 2; first step.
CC -1- INDUCTION: By N-acetylhomoserine lactone (AHL)
CC -1- BIOTECHNOLOGY: Violacein production is used as a biosensor for the
CC detection of quorum-sensing AHL production. Violacein possesses
CC antibacterial, antiviral, antimicrobial, antileishmanial,
CC trypanocidal and potential antitumoral activities.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; A212851; AA051811.1; -
DR EMBL; AB032799; BA84785.1; -
DR EMBL; AB016921; AA060935.1; -
DR InterPro; IPR000733; Flav monooxygenase.
DR Pfam; PF01360; Monooxygenase; 1.
DR PRINTS; PR00420; RGMNOXGNASE.
KW Oxidoreductase; Flavoprotein; FAD; Antibiotic biosynthesis;
KW Complete proteome.
FT NP BIND 2 20 FAD (POTENTIAL).
FT CONFLICT 31 31 V -> I (IN REF. 1).
FT CONFLICT 153 153 V -> A (IN REF. 1).
SQ SEQUENCE 373 AA; 41622 MW; 64205F8BCED4BC25 CRC64;

Query Match 44.8%; Score 43; DB 1; Length 373;
Best Local Similarity 42.9%; Pred. No. 17;
Matches 9; Conservative 3; Mismatches 1; Indels 8; Gaps 1;

Qy 6 WNFMTLSHDCRCHDGLVLLG 18
Dy 248 WNFMTLSHDCRCHDGLVLLG 268

RESULT 29
SRF2_BACSU STANDARD; PRT; 3587 AA.
AC Q04747;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Surfactin synthetase subunit 2.
GN SRFAB OR SRFAB2 OR COML OR BSU03490.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
[1]
RN SEQUENCE OF 1-3077 FROM N.A.
RC STRAIN=168;
RX MEDLINE=93181186; PubMed=8441623;
RA Fuma S., Fujishima Y., Corbell N., D'Souza C., Nakano M.M.,
RA Zuber P., Yamane K.;
RT "Nucleotide sequence of 5' portion of srfA that contains the region
RT required for competence establishment in Bacillus subtilis.";
RN Nucleic Acids Res. 21:93-97(1993).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=93360813; PubMed=8355609;
RA Cosmina P., Rodriguez F., de Ferra F., Grandi G., Perego M.,
RA Venema G., van Sinderen D.;
RT "Sequence and analysis of the genetic locus responsible for surfactin
RT synthesis in Bacillus subtilis.";
RN Mol. Microbiol. 8:821-831(1993).
[3]
RN SEQUENCE FROM N.A.

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RC STRAIN=168;
RX MEDLINE=97124189; PubMed=8969502;
RA Yamane K., Kumano M., Kurita K.;
RT "The 25 degrees-36 degrees region of the Bacillus subtilis
RT chromosome: determination of the sequence of a 146 kb segment and
RT identification of 113 genes.";
RL Microbiology 142:3047-3056(1996).
[4]
RN SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruchsi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dutertre A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Evington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Kiselev N., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Fujic P., Furnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivoita C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Saanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
[5]
RN SEQUENCE OF 514-800 FROM N.A.
RC STRAIN=ATCC 21332;
RX MEDLINE=92290255; PubMed=1601288;
RA Borchert S., Patil S.S., Marahiel M.A.;
RT "Identification of putative multifunctional peptide synthetase genes
RT using highly conserved oligonucleotide sequences derived from known
RT synthetases.";
RL FEMS Microbiol. Lett. 71:175-180(1992).
CC -1- FUNCTION: THIS PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO
CC ACTIVATE AND POLYMERIZE THE AMINO ACIDS LEU, GLU, ASP AND VAL.
CC ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS.
CC -1- COFACTOR: Contains 3 covalently bound phosphopantetheines.
CC -1- PATHWAY: Cyclic peptide antibiotic surfactin biosynthesis.
CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC family.
CC -1- SIMILARITY: Contains 3 acyl carrier domains.
CC -----
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CC -----
DR EMBL; D13262; BAA02523.1; -
DR EMBL; X70356; CAA49817.1; -
DR EMBL; D50453; BAA08983.1; -
DR EMBL; Z99105; CAB12143.1; -
DR EMBL; X65835; CAA46678.1; -

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DR PIR; I40486; I40486.  
DR HGSP; PI4687; LAMU.  
DR Subtilist; BG10169; srFAB.  
DR InterPro; IPR000873; AMP-bind.  
DR InterPro; IPR001242; Condensatin.  
DR InterPro; IPR006163; Fp bind.  
DR InterPro; IPR006162; Pfantne S.  
DR Pfam; PF00501; AMP-binding; 3.  
DR Pfam; PF00668; Condensation; 4.  
DR Pfam; PF00550; PP-binding; 3.  
DR PRINTS; PR00154; AMPBINDING.  
DR PROSITE; PS00012; PHOSPHOPANTHEINE; 3.  
DR PROSITE; PS00455; AMP BINDING; 3.  
DR PROSITE; PS00075; ACP DOMAIN; 3.  
KW Ligase; Antibiotic biogenesis; Phosphopantetheine; Sporulation;  
KW Multifunctional enzyme; Repeat; Complete. proteome.  
FT REPEAT ? 1040 DOMAIN 1 (VAL-ACTIVATING).  
FT REPEAT ? 2096 DOMAIN 2 (ASP-ACTIVATING).  
FT REPEAT ? 3114 DOMAIN 3 (D-LEU-ACTIVATING).  
FT DOMAIN 970 1036 ACYL CARRIER (ACP) 1.  
FT DOMAIN 2015 2082 ACYL CARRIER (ACP) 2.  
FT DOMAIN 3043 3109 ACYL CARRIER (ACP) 3.  
FT BINDING 999 999 PHOSPHOPANTHEINE (POTENTIAL).  
FT BINDING 2045 2045 PHOSPHOPANTHEINE (POTENTIAL).  
FT BINDING 3073 3073 PHOSPHOPANTHEINE (POTENTIAL).  
FT CONFLICT 33 33 S -> F (IN REF. 1).  
FT CONFLICT 42 42 A -> G (IN REF. 1).  
FT CONFLICT 110 110 Q -> D (IN REF. 1).  
FT CONFLICT 113 115 RQA -> AOG (IN REF. 1).  
FT CONFLICT 139 139 A -> V (IN REF. 1).  
FT CONFLICT 259 259 L -> W (IN REF. 1).  
FT CONFLICT 309 309 R -> A (IN REF. 1).  
FT CONFLICT 478 480 TPA -> SRP (IN REF. 1).  
FT CONFLICT 596 596 MISSING (IN REF. 5).  
FT CONFLICT 648 648 A -> R (IN REF. 1).  
FT CONFLICT 680 682 RHV -> ETL (IN REF. 1).  
FT CONFLICT 694 698 EOSIT -> DKRIS (IN REF. 5).  
FT CONFLICT 788 788 M -> L (IN REF. 5).  
FT CONFLICT 939 940 PL -> LV (IN REF. 1).  
FT CONFLICT 1038 1038 N -> I (IN REF. 1).  
FT CONFLICT 1133 1133 H -> Q (IN REF. 1).  
FT CONFLICT 1310 1310 V -> C (IN REF. 1).  
FT CONFLICT 1333 1333 G -> V (IN REF. 1).  
FT CONFLICT 1384 1384 P -> R (IN REF. 1).  
FT CONFLICT 1582 1582 G -> E (IN REF. 1).  
FT CONFLICT 1677 1682 KRRADG -> E (IN REF. 1).  
FT CONFLICT 1700 1700 C -> S (IN REF. 1).  
FT CONFLICT 1755 1755 F -> K (IN REF. 1).  
FT CONFLICT 1787 1787 T -> S (IN REF. 1).  
FT CONFLICT 1801 1822 GAIARVDLYEPDAFAKPTTG -> APSPGGLICMGRIC  
ETPDNR (IN REF. 1).  
FT CONFLICT 1915 1916 LG -> PK (IN REF. 1).  
FT CONFLICT 2075 2075 R -> C (IN REF. 1).  
FT CONFLICT 2079 2079 A -> V (IN REF. 1).  
FT CONFLICT 2141 2145 ARLTP -> LRSLN (IN REF. 1).  
FT CONFLICT 2445 2445 E -> Q (IN REF. 1).  
FT CONFLICT 2485 2489 ATDLF -> RQICS (IN REF. 1).  
FT CONFLICT 2546 2566 TVHOLFETVQRKHDPATV -> DGCISYSKRLLSATKT  
ARLSHT (IN REF. 1).  
FT CONFLICT 2615 2615 MSAVLGV -> KCPGRSAS (IN REF. 1).  
FT CONFLICT 2644 2645 KL -> NV (IN REF. 1).  
FT CONFLICT 2713 2713 D -> H (IN REF. 1).  
FT CONFLICT 2723 2723 D -> H (IN REF. 1).  
FT CONFLICT 2876 2881 GELCVA -> RALRG (IN REF. 1).  
FT CONFLICT 2899 2900 RF -> L (IN REF. 1).  
FT CONFLICT 2958 2960 EDR -> QDA (IN REF. 1).  
FT CONFLICT 2964 2964 R -> A (IN REF. 1).  
SQ SEQUENCE 3587 AA; 401248 MW; 680505A9FF32054D CRC64;

Query Match 44.8%; Score 43; DB 1; Length 3587;  
Best Local Similarity 33.3%; Pred. No. 1.6e+02;  
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 SOYQFWKFNQTLKIVLIG 18  
Db 1751 ASFAFDANFESLRILVIG 1768  
RESULT 30  
UTR4 YEAST STANDARD; PRT; 241 AA.  
AC P32626;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DE 10-OCT-2003 (Rel. 42, Last annotation update)  
DE UTR4 protein (Unknown transcript 4 protein).  
UTR4 OR YEL038W OR SYGP-ORF20.  
GN Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S288C / AB972;  
RX MEDLINE=97313264; PubMed=9169868;  
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,  
Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,  
Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,  
Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,  
Lin D., Moesdale D., Nakahara K., Namath A., Norgren R., Oefner P.,  
Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,  
Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;  
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V";  
RL Nature 387:78-81 (1997).  
RN [2]  
RP SEQUENCE OF 1-158 FROM N.A.  
RC STRAIN=B-6441;  
RX MEDLINE=94016558; PubMed=8411151;  
RA Melnick L., Sherman F.;  
RT "The gene clusters ARC and COR on chromosomes 5 and 10, respectively,  
of Saccharomyces cerevisiae share a common ancestry.";  
J. Mol. Biol. 233:372-388 (1993).  
CC -----  
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CC -----  
DR EMBL; L22173; AAA34939.1; -;  
DR EMBL; S65964; AAD13973.1; -;  
DR EMBL; S66121; AAB28443.1; -;  
DR EMBL; U18779; AAB65004.1; -;  
DR PIR; S30843; S30843.  
DR Geronline; 139042; -;  
DR SGD; S0000764; UTR4.  
DR InterPro; IPR005834; Hydrolase.  
DR Pfam; PF00702; Hydrolase; 1.  
FT CONFLICT 70 71 ID -> MH (IN REF. 2).  
FT CONFLICT 153 158 AHDSLD -> GMIRMI (IN REF. 2).  
SQ SEQUENCE 241 AA; 26735 MW; BF6FBBC7FB14B5AD CRC64;  
Query Match 43.8%; Score 42; DB 1; Length 241;  
Best Local Similarity 63.6%; Pred. No. 16;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 2 QYQFWKFNQTL 12  
Db 231 KYQVKNFETL 241  
Search completed: March 4, 2004, 18:00:06  
Job time : 9.07755 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:53:42 ; Search time 29.0204 Seconds  
(without alignments)  
195.701 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQQFWKNFQTLKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_todent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 96    | 100.0       | 52     | 4     | Q9PIT5      |
| 2          | 96    | 100.0       | 60     | 4     | Q9PIT4      |
| 3          | 96    | 100.0       | 333    | 4     | O14694      |
| 4          | 96    | 100.0       | 334    | 6     | Q9TUQ7      |
| 5          | 96    | 100.0       | 339    | 4     | Q9UN24      |
| 6          | 96    | 100.0       | 339    | 4     | Q9UN26      |
| 7          | 96    | 100.0       | 339    | 4     | Q9UN23      |
| 8          | 96    | 100.0       | 339    | 4     | Q9UBJ7      |
| 9          | 96    | 100.0       | 339    | 4     | Q9UN25      |
| 10         | 96    | 100.0       | 339    | 4     | Q9UN27      |
| 11         | 96    | 100.0       | 339    | 4     | Q9UBT9      |
| 12         | 96    | 100.0       | 339    | 4     | Q9UN28      |
| 13         | 96    | 100.0       | 339    | 6     | Q9TQW0      |
| 14         | 96    | 100.0       | 339    | 6     | Q9TUX1      |
| 15         | 96    | 100.0       | 339    | 6     | Q9TUX9      |
| 16         | 96    | 100.0       | 339    | 6     | Q9TUX9      |

|    |    |       |     |   |        |
|----|----|-------|-----|---|--------|
| 17 | 96 | 100.0 | 339 | 6 | Q9TS01 |
| 18 | 96 | 100.0 | 339 | 6 | Q9TUX8 |
| 19 | 96 | 100.0 | 339 | 6 | Q9TQW4 |
| 20 | 96 | 100.0 | 339 | 6 | Q9TUX4 |
| 21 | 96 | 100.0 | 339 | 6 | Q9TUX7 |
| 22 | 96 | 100.0 | 339 | 6 | Q9TUX6 |
| 23 | 96 | 100.0 | 339 | 6 | Q9TQV6 |
| 24 | 96 | 100.0 | 339 | 6 | Q9TQW6 |
| 25 | 96 | 100.0 | 339 | 6 | Q9TUX9 |
| 26 | 96 | 100.0 | 339 | 6 | Q9TUX2 |
| 27 | 96 | 100.0 | 339 | 6 | Q9TQV0 |
| 28 | 96 | 100.0 | 339 | 6 | Q9TUX5 |
| 29 | 96 | 100.0 | 339 | 6 | Q9TUX7 |
| 30 | 96 | 100.0 | 339 | 6 | Q9TUX3 |
| 31 | 96 | 100.0 | 339 | 6 | Q9TUX5 |
| 32 | 96 | 100.0 | 339 | 6 | Q9TQV2 |
| 33 | 96 | 100.0 | 339 | 6 | Q9TQV3 |
| 34 | 96 | 100.0 | 339 | 6 | Q9TUX8 |
| 35 | 96 | 100.0 | 339 | 6 | Q9TUX3 |
| 36 | 96 | 100.0 | 339 | 6 | Q9TQW2 |
| 37 | 96 | 100.0 | 339 | 6 | Q9TQX2 |
| 38 | 96 | 100.0 | 339 | 6 | Q9TQX4 |
| 39 | 96 | 100.0 | 339 | 6 | Q9TQX2 |
| 40 | 96 | 100.0 | 339 | 6 | Q9TQX2 |
| 41 | 96 | 100.0 | 339 | 6 | Q9TQX3 |
| 42 | 96 | 100.0 | 339 | 6 | Q9TUX5 |
| 43 | 96 | 100.0 | 339 | 6 | Q9TUX4 |
| 44 | 96 | 100.0 | 339 | 6 | Q9TUX6 |
| 45 | 96 | 100.0 | 339 | 6 | Q9TUX8 |
| 46 | 96 | 100.0 | 339 | 6 | Q9TUX6 |
| 47 | 96 | 100.0 | 339 | 6 | Q9TUX7 |
| 48 | 96 | 100.0 | 339 | 6 | Q9TUX4 |
| 49 | 96 | 100.0 | 339 | 6 | Q9TUX6 |
| 50 | 96 | 100.0 | 339 | 6 | Q9TUX0 |
| 51 | 96 | 100.0 | 339 | 6 | Q9TUX8 |
| 52 | 96 | 100.0 | 339 | 6 | Q9TUX1 |
| 53 | 96 | 100.0 | 339 | 6 | Q9TUX9 |
| 54 | 96 | 100.0 | 344 | 6 | Q9TQX8 |
| 55 | 96 | 100.0 | 344 | 6 | O77833 |
| 56 | 96 | 100.0 | 352 | 6 | Q9TSK1 |
| 57 | 96 | 100.0 | 352 | 6 | Q9SNC5 |
| 58 | 96 | 100.0 | 352 | 6 | Q9TUX9 |
| 59 | 96 | 100.0 | 352 | 6 | Q9XT14 |
| 60 | 96 | 100.0 | 352 | 6 | Q9XT76 |
| 61 | 96 | 100.0 | 352 | 6 | Q9SNC3 |
| 62 | 96 | 100.0 | 352 | 6 | O18771 |
| 63 | 96 | 100.0 | 352 | 6 | Q9TUX4 |
| 64 | 96 | 100.0 | 352 | 6 | Q9SNC1 |
| 65 | 96 | 100.0 | 352 | 6 | O18772 |
| 66 | 96 | 100.0 | 352 | 6 | Q9SNC6 |
| 67 | 96 | 100.0 | 352 | 6 | Q9SNC8 |
| 68 | 96 | 100.0 | 352 | 6 | Q9SNC7 |
| 69 | 96 | 100.0 | 352 | 6 | Q9SNC0 |
| 70 | 96 | 100.0 | 352 | 6 | Q9SNC5 |
| 71 | 96 | 100.0 | 352 | 6 | Q9TUX2 |
| 72 | 96 | 100.0 | 352 | 6 | Q9XT13 |
| 73 | 96 | 100.0 | 352 | 6 | O77776 |
| 74 | 96 | 100.0 | 352 | 6 | Q9MZA3 |
| 75 | 96 | 100.0 | 352 | 6 | Q9TSQ7 |
| 76 | 96 | 100.0 | 352 | 6 | Q9MZA2 |
| 77 | 96 | 100.0 | 352 | 6 | Q9TUX0 |
| 78 | 96 | 100.0 | 352 | 6 | Q9XS99 |
| 79 | 96 | 100.0 | 352 | 6 | Q9TUX5 |
| 80 | 96 | 100.0 | 352 | 6 | Q9SNE1 |
| 81 | 96 | 100.0 | 352 | 6 | Q9SNE6 |
| 82 | 96 | 100.0 | 352 | 6 | Q9SND0 |
| 83 | 96 | 100.0 | 352 | 6 | O97962 |
| 84 | 96 | 100.0 | 352 | 6 | Q9TV43 |
| 85 | 96 | 100.0 | 352 | 6 | Q9SNE8 |
| 86 | 93 | 96.9  | 339 | 6 | Q9TUX4 |
| 87 | 93 | 96.9  | 339 | 6 | Q9TUX3 |
| 88 | 93 | 96.9  | 339 | 6 | Q9TUX9 |
| 89 | 93 | 96.9  | 339 | 6 | Q9TQW0 |

|        |             |
|--------|-------------|
| Q9tsq1 | cercopithec |
| Q9tux8 | cercopithec |
| Q9tqW4 | pan troglod |
| Q9tux4 | pan troglod |
| Q9tqU7 | cercopithec |
| Q9tur6 | cercopithec |
| Q9tqV6 | colobus gue |
| Q9tux6 | pan troglod |
| Q9tuq9 | cercopithec |
| Q9tur2 | erythrocebu |
| Q9tqV0 | papio papio |
| Q9tqU5 | cercopithec |
| Q9tus7 | papio papio |
| Q9tux3 | pango pygma |
| Q9tus5 | papio papio |
| Q9tqV2 | papio papio |
| Q9tqV3 | cercopithec |
| Q9tux8 | cercopithec |
| Q9tqW2 | pango pygma |
| Q9tqX2 | erythrocebu |
| Q9tsq4 | cercopithec |
| Q9tqR2 | gorilla gor |
| Q9tsq3 | cercopithec |
| Q9tur0 | cercopithec |
| Q9tux5 | pan troglod |
| Q9tux4 | erythrocebu |
| Q9tuq6 | erythrocebu |
| Q9tus8 | papio papio |
| Q9tus6 | papio papio |
| Q9tur7 | cercopithec |
| Q9tux4 | cercopithec |
| Q9tux6 | cercopithec |
| Q9tux0 | hylobates c |
| Q9tur8 | cercopithec |
| Q9tus9 | papio papio |
| Q9tur1 | cercopithec |
| Q9tqR8 | cercocobus  |
| Q9tqR3 | cercocobus  |
| Q9tqK1 | cercopithec |
| Q9snc5 | hylobates s |
| Q9tv49 | cercocobus  |
| Q9xt14 | colobus gue |
| Q9xt76 | cercopithec |
| Q9snc3 | miopithecus |
| O18771 | pan troglod |
| Q9tv47 | cercopithec |
| Q9snc1 | theropithec |
| O18772 | pan troglod |
| Q9snc6 | trachypithe |
| Q9snc8 | colobus pol |
| Q9snc7 | nasalis lar |
| Q9snc0 | hylobates m |
| Q9snc5 | cercopithec |
| Q9tv42 | cercopithec |
| Q9xt13 | papio ambi  |
| O77776 | cercocobus  |
| Q9mza3 | hylobates a |
| Q9tsq7 | cercopithec |
| Q9mza2 | cercopithec |
| Q9tv50 | pan troglod |
| Q9xs99 | gorilla gor |
| Q9tv45 | cercopithec |
| Q9sne1 | cercocobus  |
| Q9sne6 | cercopithec |
| Q9snd0 | erythrocebu |
| Q97962 | pygathrix a |
| Q9tv43 | cercopithec |
| Q9sne8 | cercopithec |
| Q9cut4 | macaca neme |
| Q9tux3 | macaca mula |
| Q9tur9 | baguinus sp |
| Q9tqT0 | macaca fasc |

90 93 96.9 339 6 Q9TUT9  
 91 93 96.9 339 6 Q9TSN2  
 92 93 96.9 339 6 Q9TSN3  
 93 93 96.9 339 6 Q9TUT7  
 94 93 96.9 339 6 Q9TUT6  
 95 93 96.9 339 6 Q9TUT6  
 96 93 96.9 339 6 Q9TUT6  
 97 93 96.9 339 6 Q9TUT6  
 98 93 96.9 339 6 Q9TUT6  
 99 93 96.9 339 6 Q9TUT6  
 100 93 96.9 339 6 Q9TUT6

## ALIGNMENTS

RESULT 1  
 Q9PIT5 PRELIMINARY; PRT; 52 AA.  
 ID Q9PIT5  
 AC Q9PIT5  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Mutant chemokine receptor CCR5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99392755; PubMed=10465086;  
 RA Aikhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,  
 RA Bond V.C.;  
 RT "Characterization of a third CCR5 amplicon from CCR5-delta32-  
 heterozygous HIV-1-infected individuals."  
 RL AIDS 13:1585-1586(1999).  
 DR EMBL; AF056019; AAF65578.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON TER 1 1  
 FT VARIANT 41 41  
 SQ SEQUENCE 52 AA; 5962 MW; DAEB2A5A9529C3A9 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQFWKNFQTLKIVILG 18  
 DB 11 SQYQFWKNFQTLKIVILG 28

RESULT 2  
 Q9PIT4 PRELIMINARY; PRT; 60 AA.  
 ID Q9PIT4  
 AC Q9PIT4  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Chemokine receptor CCR5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99392755; PubMed=10465086;  
 RA Aikhionbare F.O., Newman C., Womack C., Roth W.W., Stringer H.G. Jr.,  
 RA Bond V.C.;  
 RT "Characterization of a third CCR5 amplicon from CCR5-delta32-  
 heterozygous HIV-1-infected individuals."

RL AIDS 13:1585-1586(1999).  
 DR EMBL; AF056020; AAF65579.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON TER 1 1  
 FT NON TER 60 60  
 SQ SEQUENCE 60 AA; 7156 MW; AFF4B9CAF6B80AFB CRC64;

Query Match 100.0%; Score 96; DB 4; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
 DB 11 SQYQFWKNFQTLKIVILG 28

RESULT 3  
 O14694 PRELIMINARY; PRT; 333 AA.  
 ID O14694  
 AC O14694  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE CCR5 receptor (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism."  
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).  
 DR EMBL; AF011504; AAB65704.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON TER 333 333  
 SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 100.0%; Score 96; DB 4; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
 DB 166 SQYQFWKNFQTLKIVILG 183

RESULT 4  
 Q9TUQ7 PRELIMINARY; PRT; 334 AA.  
 ID Q9TUQ7  
 AC Q9TUQ7  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).

CCRS.  
 OS Erythrocebus patas (Red guenon) (Hussar).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Erythrocebus.  
 OX NCBI\_TaxID=9538;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF162049; AAD47804.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 334 334  
 SQ SEQUENCE 334 AA; 38460 MW; B19D0C6C67B69F0 CRC64;  
 Query Match 100.0%; Score 96; DB 6; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQYQFWKNFQTLKIVILG 18  
 Db 173 SQYQFWKNFQTLKIVILG 190  
 RESULT 5  
 Q9UN24 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN24;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF161919; AAD47676.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;  
 Query Match 100.0%; Score 96; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQYQFWKNFQTLKIVILG 18  
 Db 178 SQYQFWKNFQTLKIVILG 195  
 RESULT 6  
 Q9UN26 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN26;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF161916; AAD47673.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4B CRC64;  
 Query Match 100.0%; Score 96; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SQYQFWKNFQTLKIVILG 18  
 Db 178 SQYQFWKNFQTLKIVILG 195  
 RESULT 7  
 Q9UN23 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN23;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; AF161920; AAD47677.1; -.  
 Query Match 100.0%; Score 96; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR GO: 0016021; C: integral to membrane; IEA.  
 DR GO: 0004872; F: receptor activity; IEA.  
 DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39115 MW; 3C6369F922C91AA7 CRC64;  
 Query Match 100.0%; Score 96; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQWKNFQTLKIVILG 18  
 DB 178 SQYQWKNFQTLKIVILG 195  
 RESULT 8  
 Q9UBJ7  
 ID Q9UBJ7 PRELIMINARY; PRT; 339 AA.  
 AC Q9UBJ7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161918; AAD47675.1; -.  
 DR GO: 0016021; C: integral to membrane; IEA.  
 DR GO: 0004872; F: receptor activity; IEA.  
 DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;  
 Query Match 100.0%; Score 96; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQWKNFQTLKIVILG 18  
 DB 178 SQYQWKNFQTLKIVILG 195  
 RESULT 9  
 Q9UN25  
 ID Q9UN25 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN25;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161918; AAD47675.1; -.  
 DR GO: 0016021; C: integral to membrane; IEA.  
 DR GO: 0004872; F: receptor activity; IEA.  
 DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFF1E2P27A CRC64;  
 Query Match 100.0%; Score 96; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQWKNFQTLKIVILG 18  
 DB 178 SQYQWKNFQTLKIVILG 195  
 RESULT 9  
 Q9UN25  
 ID Q9UN25 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN25;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161918; AAD47675.1; -.  
 DR GO: 0016021; C: integral to membrane; IEA.  
 DR GO: 0004872; F: receptor activity; IEA.  
 DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;  
 Query Match 100.0%; Score 96; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SQYQWKNFQTLKIVILG 18  
 DB 178 SQYQWKNFQTLKIVILG 195  
 RESULT 10  
 Q9UN27  
 ID Q9UN27 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN27;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161918; AAD47675.1; -.  
 DR GO: 0016021; C: integral to membrane; IEA.  
 DR GO: 0004872; F: receptor activity; IEA.  
 DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.  
 DR GO: 0007186; P: G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

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Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 11
Q9UN28
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 12
Q9UN28
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

RESULT 13
Q9UN28
ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

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RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECF_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECF_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6D81A6 CRC64;

Query Match 100.0%; Score 96; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

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Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

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DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVILG 18
DB 178 SQYQFWKFNQTLKIVILG 195

RESULT 16
Q9TUW9 PRELIMINARY; PRT; 339 AA.
AC Q9TUW9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVILG 18
DB 178 SQYQFWKFNQTLKIVILG 195

RESULT 15
Q9TUW9 PRELIMINARY; PRT; 339 AA.
AC Q9TUW9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161948; AAD47704.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1.1; 1.

DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEBF107E CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNQTLKIVILG 18
DB 178 SQYQFWKFNQTLKIVILG 195

RESULT 17
Q9TSQ1 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

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OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162023; AAD47778.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 33216 MW; 847E935FA03B52D CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 18
Q9TUW8 PRELIMINARY; PRT; 339 AA.
ID Q9TUW8
AC Q9TUW8
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 33049 MW; 6D1A93F66270F3ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 19
Q9TQW4 PRELIMINARY; PRT; 339 AA.
ID Q9TQW4
AC Q9TQW4
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
FT NON_TER 339
SQ SEQUENCE 339 AA; 39129 MW; 4A98F8B601D46A4 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
DB 178 SQYQFWKNFQTLKIVILG 195

RESULT 20
Q9TUM4 PRELIMINARY; PRT; 339 AA.
ID Q9TUM4
AC Q9TUM4
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
CN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.

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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 8E699882BAC0E84 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
DB 178 SQYQWKNFQTLKIVILG 195

RESULT 21
Q9TUR6
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
DE CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162042; AAD47802.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 847D5F92BB03E652 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
DB 178 SQYQWKNFQTLKIVILG 195

RESULT 22
Q9TUR6
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
```

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Q9TUR6;
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
DE CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 9DF2A6F446C5A8D CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
DB 178 SQYQWKNFQTLKIVILG 195

RESULT 23
Q9TUR6
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
DE CCR5.
OS Colobus guereza (black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47760.1; -.
DR EMBL; AF162000; AAD47755.1; -.
DR EMBL; AF162001; AAD47756.1; -.
DR EMBL; AF162002; AAD47757.1; -.
DR EMBL; AF162003; AAD47758.1; -.
DR EMBL; AF162004; AAD47759.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
```

DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72FEBFF566F CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18  
 |||||  
 DB 178 SOYQFWKNFQTLKIVILG 195

## RESULT 24

Q9TUW6 PRELIMINARY; PRT; 339 AA.  
 AC Q9TUW6;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.

OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161900; AAD47657.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39103 MW; 4038C132D024C5M4 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18  
 |||||  
 DB 178 SOYQFWKNFQTLKIVILG 195

## RESULT 25

Q9TUQ9 PRELIMINARY; PRT; 339 AA.  
 AC Q9TUQ9;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.

OS Cercopithecus mona.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=36226;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF162041; AAD47796.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39019 MW; 7176F940AF11F3ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKNFQTLKIVILG 18  
 |||||  
 DB 178 SOYQFWKNFQTLKIVILG 195

## RESULT 26

Q9TUR2 PRELIMINARY; PRT; 339 AA.  
 AC Q9TUR2;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.

OS Erythrocebus patas (Red quonon) (Husar).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Erythrocebus.  
 OX NCBI\_TaxID=9538;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF162034; AAD47789.1; -  
 DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39138 MW; AD31455EBBC69499 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNQTLKIVILG 18  
Db 178 SQYQFWKFNQTLKIVILG 195

## RESULT 27

Q9TQV0 ID Q9TQV0 PRELIMINARY; PRT; 339 AA.  
AC Q9TQV0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5 (Fragment).  
GN CCR5.  
OS Papio papio (Guinea baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Papio.  
OX NCBI\_TaxID=100937;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,  
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
RT "Sequences of the CCR5 genes from diverse simian and prosimian  
species.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF161989; AAD47744.1; -;  
DR EMBL; AF161988; AAD47743.1; -;  
DR GO; GO:0006021; C: integral to membrane; IEA.  
DR GO; GO:0004872; F: receptor activity; IEA.  
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P: G-protein coupled receptor activity; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
FT NON\_TER 1 339  
FT SEQUENCE 339 AA; 39113 MW; 7F9803EAOE0AF9ED CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;  
Best Local Similarity 100.0%; Pred. No. 2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNQTLKIVILG 18  
Db 178 SQYQFWKFNQTLKIVILG 195

## RESULT 28

Q9TQV0 ID Q9TQV0 PRELIMINARY; PRT; 339 AA.  
AC Q9TQV0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5 (Fragment).  
GN CCR5.  
OS Cercopithecus nictitans (white-nosed guenon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Cercopithecus.  
OX NCBI\_TaxID=36228;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,  
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
RT "Sequences of the CCR5 genes from diverse simian and prosimian  
species.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF162046; AAD47801.1; -;  
DR EMBL; AF162043; AAD47798.1; -;  
DR GO; GO:0006021; C: integral to membrane; IEA.  
DR GO; GO:0004872; F: receptor activity; IEA.  
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P: G-protein coupled receptor activity; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
FT NON\_TER 1 339  
FT SEQUENCE 339 AA; 39178 MW; 847F8F936B00B6E2 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;  
Best Local Similarity 100.0%; Pred. No. 2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNQTLKIVILG 18  
Db 178 SQYQFWKFNQTLKIVILG 195

## RESULT 29

Q9TUS7 ID Q9TUS7 PRELIMINARY; PRT; 339 AA.  
AC Q9TUS7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5 (Fragment).  
GN CCR5.  
OS Papio papio (Guinea baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Papio.  
OX NCBI\_TaxID=100937;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstan K., Chen Z., Korber B., Oprende J., Stanton J., Agy M.,  
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
RT "Sequences of the CCR5 genes from diverse simian and prosimian  
species.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF161995; AAD47750.1; -;  
DR GO; GO:0006021; C: integral to membrane; IEA.  
DR GO; GO:0004872; F: receptor activity; IEA.  
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P: G-protein coupled receptor activity; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
FT NON\_TER 1 339  
FT SEQUENCE 339 AA; 39068 MW; 84EB018085DC0A62 CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;  
Best Local Similarity 100.0%; Pred. No. 2e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNQTLKIVILG 18  
Db 178 SQYQFWKFNQTLKIVILG 195

## RESULT 30

Q9TUS7 ID Q9TUS7 PRELIMINARY; PRT; 339 AA.

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AC 09TUM3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161908; AAD47665.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39103 MW; 4350C4625FB0657C CRC64;

Query Match 100.0%; Score 96; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SQYQFWKNFQTLKIVILG 18
Db 178 SQYQFWKNFQTLKIVILG 195

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Search completed: March 4, 2004, 18:02:55  
 Job time : 29.0204 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:55:22 ; Search time 11.5714 Seconds  
(without alignments)  
80.307 Million cell updates/sec

Title: US-10-084-813-13  
Perfect score: 96  
Sequence: 1 SQYFWXNFQTLKIVILG 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues  
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A COMB.pgp.\*  
2: /cgn2\_6/ptodata/2/iaa/5B COMB.pgp.\*  
3: /cgn2\_6/ptodata/2/iaa/6A COMB.pgp.\*  
4: /cgn2\_6/ptodata/2/iaa/6B COMB.pgp.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pgp.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pgp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description          |
|------------|-------|---------------|--------|----|----------------------|
| 1          | 96    | 100.0         | 54     | 4  | US-08-833-752-11     |
| 2          | 96    | 100.0         | 352    | 3  | US-08-466-343D-2     |
| 3          | 96    | 100.0         | 352    | 3  | US-08-087-232A-13    |
| 4          | 96    | 100.0         | 352    | 3  | US-08-861-105-14     |
| 5          | 96    | 100.0         | 352    | 3  | US-08-575-967A-2     |
| 6          | 96    | 100.0         | 352    | 3  | US-09-045-583-52     |
| 7          | 96    | 100.0         | 352    | 4  | US-09-517-605-5      |
| 8          | 96    | 100.0         | 352    | 4  | US-09-534-185-52     |
| 9          | 96    | 100.0         | 352    | 4  | US-08-833-752-5      |
| 10         | 96    | 100.0         | 352    | 4  | US-09-502-783A-2     |
| 11         | 96    | 100.0         | 352    | 4  | US-09-796-202-1      |
| 12         | 82    | 85.4          | 21     | 3  | US-08-907-468-11     |
| 13         | 74    | 77.1          | 354    | 4  | US-08-724-984A-2     |
| 14         | 47    | 49.0          | 355    | 4  | US-08-886-319A-13    |
| 15         | 45    | 46.9          | 355    | 3  | US-09-045-583-53     |
| 16         | 45    | 46.9          | 355    | 4  | US-09-534-185-53     |
| 17         | 43.5  | 45.3          | 352    | 4  | US-09-489-039A-13500 |
| 18         | 43    | 44.8          | 172    | 4  | US-09-621-976-4131   |
| 19         | 43    | 44.8          | 344    | 3  | US-08-681-192-2      |
| 20         | 42    | 43.8          | 460    | 4  | US-08-935-263-4      |
| 21         | 42    | 43.8          | 460    | 4  | US-09-594-185-4      |
| 22         | 42    | 43.8          | 727    | 4  | US-09-540-236-3023   |
| 23         | 41    | 42.7          | 160    | 4  | US-09-328-352-6593   |
| 24         | 41    | 42.7          | 255    | 4  | US-09-491-577-2      |
| 25         | 41    | 42.7          | 363    | 4  | US-09-252-991A-25052 |
| 26         | 40    | 41.7          | 254    | 4  | US-09-134-001C-4582  |
| 27         | 40    | 41.7          | 311    | 4  | US-09-134-001C-5171  |

|     |    |      |      |   |                      |                    |
|-----|----|------|------|---|----------------------|--------------------|
| 28  | 40 | 41.7 | 316  | 4 | US-09-489-039A-8904  | Sequence 8904, Ap  |
| 29  | 40 | 41.7 | 355  | 1 | US-08-012-988A-2     | Sequence 2, Appli  |
| 30  | 40 | 41.7 | 355  | 1 | US-08-450-393A-5     | Sequence 5, Appli  |
| 31  | 40 | 41.7 | 355  | 3 | US-08-446-669-5      | Sequence 5, Appli  |
| 32  | 40 | 41.7 | 355  | 4 | US-09-239-938-1      | Sequence 1, Appli  |
| 33  | 40 | 41.7 | 355  | 4 | US-08-833-752-9      | Sequence 9, Appli  |
| 34  | 40 | 41.7 | 355  | 4 | US-09-886-319A-14    | Sequence 14, Appli |
| 35  | 40 | 41.7 | 355  | 5 | PCT-US95-00476-5     | Sequence 5, Appli  |
| 36  | 40 | 41.7 | 371  | 3 | US/08/622            | INFORMATION FOR    |
| 37  | 40 | 41.7 | 371  | 4 | US-09-165-922A-10    | Sequence 10, Appl  |
| 38  | 40 | 41.7 | 659  | 4 | US-09-252-991A-26013 | Sequence 26013, A  |
| 39  | 40 | 41.7 | 2037 | 4 | US-09-543-681A-5538  | Sequence 5538, Ap  |
| 40  | 39 | 40.6 | 92   | 4 | US-09-328-352-5171   | Sequence 5171, Ap  |
| 41  | 39 | 40.6 | 448  | 4 | US-09-134-000C-3794  | Sequence 3794, Ap  |
| 42  | 39 | 40.6 | 452  | 4 | US-09-530-836-6      | Sequence 6, Appli  |
| 43  | 39 | 40.6 | 485  | 4 | US-09-134-000C-6031  | Sequence 6031, Ap  |
| 44  | 39 | 40.6 | 598  | 2 | US-08-853-659A-53    | Sequence 53, Appl  |
| 45  | 39 | 40.6 | 664  | 4 | US-09-377-497-70     | Sequence 70, Appl  |
| 46  | 39 | 40.6 | 690  | 3 | US-09-422-869-28     | Sequence 28, Appl  |
| 47  | 38 | 39.6 | 87   | 4 | US-09-134-000C-6145  | Sequence 6145, Ap  |
| 48  | 38 | 39.6 | 135  | 4 | US-09-171-461-24     | Sequence 24, Appl  |
| 49  | 38 | 39.6 | 212  | 4 | US-09-489-039A-9275  | Sequence 9275, Ap  |
| 50  | 38 | 39.6 | 243  | 4 | US-09-107-532A-4908  | Sequence 4908, Ap  |
| 51  | 38 | 39.6 | 277  | 4 | US-09-134-000C-4158  | Sequence 4158, Ap  |
| 52  | 38 | 39.6 | 320  | 4 | US-09-252-991A-30676 | Sequence 30676, A  |
| 53  | 38 | 39.6 | 389  | 4 | US-09-491-577-52     | Sequence 52, Appl  |
| 54  | 38 | 39.6 | 576  | 4 | US-09-543-681A-4990  | Sequence 4990, Ap  |
| 55  | 38 | 39.6 | 879  | 1 | US-08-306-546C-2     | Sequence 2, Appli  |
| 56  | 38 | 39.6 | 879  | 2 | US-08-530-524A-2     | Sequence 2, Appli  |
| 57  | 37 | 38.5 | 74   | 4 | US-09-328-352-4234   | Sequence 4234, Ap  |
| 58  | 37 | 38.5 | 105  | 4 | US-09-732-210-130    | Sequence 130, App  |
| 59  | 37 | 38.5 | 118  | 1 | US-08-226-264-23     | Sequence 23, Appl  |
| 60  | 37 | 38.5 | 138  | 4 | US-09-134-001C-4441  | Sequence 4441, Ap  |
| 61  | 37 | 38.5 | 182  | 1 | US-08-226-264-28     | Sequence 28, Appl  |
| 62  | 37 | 38.5 | 216  | 3 | US-08-924-747-12     | Sequence 12, Appl  |
| 63  | 37 | 38.5 | 216  | 3 | US-09-247-373B-12    | Sequence 12, Appl  |
| 64  | 37 | 38.5 | 216  | 3 | US-09-296-715-12     | Sequence 20, Appl  |
| 65  | 37 | 38.5 | 219  | 3 | US-08-924-747-20     | Sequence 20, Appl  |
| 66  | 37 | 38.5 | 219  | 3 | US-09-247-373B-20    | Sequence 20, Appl  |
| 67  | 37 | 38.5 | 219  | 3 | US-09-296-715-20     | Sequence 20, Appl  |
| 68  | 37 | 38.5 | 283  | 6 | 5169835-15           | Patent No. 5169835 |
| 69  | 37 | 38.5 | 283  | 4 | US-09-134-000C-6045  | Sequence 6045, Ap  |
| 70  | 37 | 38.5 | 289  | 4 | US-09-328-352-6027   | Sequence 6027, Ap  |
| 71  | 37 | 38.5 | 329  | 4 | US-09-502-783A-9     | Sequence 9, Appli  |
| 72  | 37 | 38.5 | 344  | 3 | US-08-466-343D-9     | Sequence 9, Appli  |
| 73  | 37 | 38.5 | 347  | 1 | US-08-461-244-3      | Sequence 3, Appli  |
| 74  | 37 | 38.5 | 360  | 1 | US-08-450-393A-4     | Sequence 4, Appli  |
| 75  | 37 | 38.5 | 360  | 3 | US-08-446-669-4      | Sequence 4, Appli  |
| 76  | 37 | 38.5 | 360  | 3 | US-09-045-583-50     | Sequence 50, Appl  |
| 77  | 37 | 38.5 | 360  | 3 | US-09-045-583-51     | Sequence 51, Appl  |
| 78  | 37 | 38.5 | 360  | 4 | US-09-534-185-50     | Sequence 50, Appl  |
| 79  | 37 | 38.5 | 360  | 4 | US-09-534-185-51     | Sequence 51, Appl  |
| 80  | 37 | 38.5 | 360  | 4 | US-08-833-752-7      | Sequence 7, Appli  |
| 81  | 37 | 38.5 | 360  | 4 | US-09-131-827A-2     | Sequence 2, Appli  |
| 82  | 37 | 38.5 | 360  | 4 | US-09-131-827A-20    | Sequence 20, Appl  |
| 83  | 37 | 38.5 | 360  | 5 | PCT-US95-00476-4     | Sequence 4, Appli  |
| 84  | 37 | 38.5 | 374  | 1 | US-08-450-393A-2     | Sequence 2, Appli  |
| 85  | 37 | 38.5 | 374  | 3 | US-08-446-669-2      | Sequence 2, Appli  |
| 86  | 37 | 38.5 | 374  | 5 | PCT-US95-00476-2     | Sequence 2, Appli  |
| 87  | 37 | 38.5 | 380  | 4 | US-09-489-039A-13215 | Sequence 13215, A  |
| 88  | 37 | 38.5 | 454  | 4 | US-09-134-001C-3547  | Sequence 3547, Ap  |
| 89  | 37 | 38.5 | 615  | 3 | US-09-462-844-3      | Sequence 3, Appli  |
| 90  | 37 | 38.5 | 615  | 4 | US-09-899-482-3      | Sequence 3, Appli  |
| 91  | 37 | 38.5 | 731  | 1 | US-09-014-897-2      | Sequence 2, Appli  |
| 92  | 37 | 38.5 | 731  | 1 | US-08-731-716-2      | Sequence 2, Appli  |
| 93  | 37 | 38.5 | 2233 | 2 | US-08-569-853-1      | Sequence 1, Appli  |
| 94  | 37 | 38.5 | 2233 | 2 | US-08-569-853-2      | Sequence 2, Appli  |
| 95  | 37 | 38.5 | 2233 | 3 | US-08-967-439-1      | Sequence 1, Appli  |
| 96  | 36 | 37.5 | 69   | 4 | US-09-673-395A-358   | Sequence 358, App  |
| 97  | 36 | 37.5 | 96   | 4 | US-09-107-532A-5808  | Sequence 5808, Ap  |
| 98  | 36 | 37.5 | 108  | 4 | US-09-107-532A-7196  | Sequence 7196, Ap  |
| 99  | 36 | 37.5 | 113  | 4 | US-09-543-681A-8228  | Sequence 8228, Ap  |
| 100 | 36 | 37.5 | 139  | 4 | US-09-540-236-3184   | Sequence 3184, Ap  |

ALIGNMENTS

```

RESULT 1
US-08-833-752-11
; Sequence 11, Application US/08833752
; Patent No. 6448375
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,752
; FILING DATE: 9-APR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-833-752-11
Query Match 100.0%; Score 96; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 9 SQYQFWKNFQTLKIVILG 26

RESULT 2
US-08-466-343D-2
; Sequence 2, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-466-343D-2
Query Match 100.0%; Score 96; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18
| | | | | | | | | | | | | | | | | |
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 3
US-09-087-232A-13
; Sequence 13, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Quillent et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-087-232A-13

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Query Match 100.0%; Score 96; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNFTLKIVILG 18  
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 4  
US-08-861-105-14  
; Sequence 14, Application US/08861105  
; Patent No. 6258527  
; GENERAL INFORMATION:  
; APPLICANT: LITTMAN, DAN R.  
; APPLICANT: DENG, HONGKUI  
; APPLICANT: ELLMEIER, WILFRIED  
; APPLICANT: LANDAU, NATHANIEL R.  
; APPLICANT: LIU, RONG  
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH  
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
; TITLE OF INVENTION: USES THEREOF  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,105  
; FILING DATE:  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/666,020  
; FILING DATE: 19-JUN-1996  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,319  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-08-861-105-14  
Query Match 100.0%; Score 96; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNFTLKIVILG 18  
Db 185 SQYQFWKFNFTLKIVILG 202

Query Match 100.0%; Score 96; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNFTLKIVILG 18  
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 5  
US-08-575-967A-2  
; Sequence 2, Application US/08575967A  
; Patent No. 6265184  
; GENERAL INFORMATION:  
; APPLICANT: Gray et al.  
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/575,967A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6265184 and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32918  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-485-1900  
; TELEFAX: 206-485-1662  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: /= "88C amino acid sequence"  
US-08-575-967A-2  
Query Match 100.0%; Score 96; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKFNFTLKIVILG 18  
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 6  
US-09-045-583-52  
; Sequence 52, Application US/09045583  
; Patent No. 6287805  
; GENERAL INFORMATION:  
; APPLICANT: Graham, Gerard J. et al.  
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/045,583  
;; FILING DATE: 20-MAR-98  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mandragouras, Amy E.  
;; REGISTRATION NUMBER: 36,207  
;; REFERENCE/DOCKET NUMBER: MNI-044  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617)227-7400  
;; TELEFAX: (617)742-4214  
;; INFORMATION FOR SEQ ID NO: 52:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 352 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
;; US-09-045-583-52

Query Match 100.0%; Score 96; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
DB 185 SQYQFWKNFQTLKIVILG 202

## RESULT 7

US-09-517-605-5  
; Sequence 5, Application US/09517605  
; Patent No. 6391567  
; GENERAL INFORMATION:  
; APPLICANT: Littman, Dan R.  
; APPLICANT: Kwon, Douglas S.  
; APPLICANT: van Kooyk, Yvette  
; APPLICANT: Geijzenbeck, Ineo  
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 1049-1-017  
; CURRENT APPLICATION NUMBER: US/09/517,605  
; CURRENT FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-517-605-5

Query Match 100.0%; Score 96; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
DB 185 SQYQFWKNFQTLKIVILG 202

## RESULT 8

US-09-534-185-52  
; Sequence 52, Application US/09534185  
; Patent No. 6403767  
; GENERAL INFORMATION:  
; APPLICANT: Graham, Gerard J. et al.  
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
; Heptahelical Receptor Superfamily and Uses  
; Therefor  
; NUMBER OF SEQUENCES: 56

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
;; STREET: 28 State Street  
;; CITY: Boston  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02109  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/534,185  
;; FILING DATE: 24-Mar-2000  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/045,583  
;; FILING DATE: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mandragouras, Amy E.  
;; REGISTRATION NUMBER: 36,207  
;; REFERENCE/DOCKET NUMBER: MNI-044  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617)227-7400  
;; TELEFAX: (617)742-4214  
;; INFORMATION FOR SEQ ID NO: 52:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 352 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-09-534-185-52

Query Match 100.0%; Score 96; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
DB 185 SQYQFWKNFQTLKIVILG 202

## RESULT 9

US-08-833-752-5  
; Sequence 5, Application US/08833752  
; Patent No. 6448375  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; APPLICANT: PARMENTIER, MARC  
; APPLICANT: VASSART, GILBERT  
; APPLICANT: LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
; TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/833,752  
; FILING DATE: 9-APR-1997  
; CLASSIFICATION: 536



ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-833-752-5

Query Match 100.0%; Score 96; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKIVILG 18  
DB 185 SQYQFWKFNFTLKIVILG 202

RESULT 10  
US-09-502-783A-2  
Sequence 2, Application US/09502783A  
Patent No. 6511826  
GENERAL INFORMATION:  
APPLICANT: Li, Yi  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS)

FILE REFERENCE: 1488.1150006  
CURRENT APPLICATION NUMBER: US/09/502,783A  
CURRENT FILING DATE: 2001-08-23  
PRIOR FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-502-783A-2

Query Match 100.0%; Score 96; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKIVILG 18  
DB 185 SQYQFWKFNFTLKIVILG 202

RESULT 11  
US-09-796-202-1  
Sequence 1, Application US/09796202  
Patent No. 6548636  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 2048/61010/JPM/SHS  
CURRENT APPLICATION NUMBER: US/09/796,202  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 352  
TYPE: PRT  
ORGANISM: human  
US-09-796-202-1

Query Match 100.0%; Score 96; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.8e-08;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKIVILG 18  
DB 185 SQYQFWKFNFTLKIVILG 202

RESULT 12  
US-08-907-468-11  
Sequence 11, Application US/08907468  
Patent No. 6057102  
GENERAL INFORMATION:  
APPLICANT: Landau, Nathaniel R.  
APPLICANT: Koup, Richard A.  
APPLICANT: Liu, Rong  
APPLICANT: Paxton, William  
TITLE OF INVENTION: HIV CORECEPTOR MUTANTS  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
STREET: Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/907,468  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1049-1-005 N  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
US-08-907-468-11

Query Match 85.4%; Score 82; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.7e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKIV 15  
DB 7 SQYQFWKFNFTLKIV 21

RESULT 13  
US-08-724-984A-2  
Sequence 2, Application US/08724984A  
Patent No. 638055  
GENERAL INFORMATION:  
APPLICANT: Derk Bergsma, Mary Brawner, and Uman Shabon  
TITLE OF INVENTION: No. 638055el Mouse Genomic Clone of the CC-  
TITLE OF INVENTION: CCR5 Receptor  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road, P.O. Box 1539  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: MICROSOFT WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,984A  
FILING DATE: October 3, 1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: William T. Han  
REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: ATG50023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610 270 5024  
TELEFAX: 610 270 5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 354  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-724-984A-2

Query Match 77.1%; Score 74; DB 4; Length 354;  
Best Local Similarity 76.5%; Pred. No. 0.00017;  
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SQYQFWKNTQTLKIVIL 17  
DB 187 TOYHFWKSFQTLKIVIL 203

RESULT 14  
US-09-886-319A-13  
Sequence 13, Application US/09886319A  
Patent No. 6586185  
GENERAL INFORMATION:  
APPLICANT: Wolf, Eckard  
APPLICANT: Werner, Sabine  
APPLICANT: Halle, Joern-Peter  
APPLICANT: Regenbogen, Johannes  
APPLICANT: Goppelt, Andreas  
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for  
the Diagnosis or Treatment of Skin Disorders and Wound  
TITLE OF INVENTION: the Diagnosis and for the Identification of Pharmacologically  
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically  
TITLE OF INVENTION: Active Substances  
FILE REFERENCE: 50125/014002  
CURRENT APPLICATION NUMBER: US/09/886,319A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: US 60/222,081  
PRIOR FILING DATE: 2000-08-01  
PRIOR APPLICATION NUMBER: DE 10030149.5  
PRIOR FILING DATE: 2000-06-20  
NUMBER OF SEQ ID NOS: 84  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 355  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-886-319A-13

Query Match 49.0%; Score 47; DB 4; Length 355;  
Best Local Similarity 61.5%; Pred. No. 5;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18  
DB 195 WKRFOALKNLILG 207

RESULT 15  
US-09-045-583-53  
Sequence 53, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-045-583-53

Query Match 46.9%; Score 45; DB 3; Length 355;  
Best Local Similarity 50.0%; Pred. No. 11;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 YQFWKNTQTLKIVILG 18  
DB 192 FQWKLFOALKNLILG 207

RESULT 16  
US-09-534-185-53  
Sequence 53, Application US/09534185  
Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Heptahelical Receptor Superfamily and Uses  
Therefor  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA

```

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4131
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -30..-1
; US-09-621-976-4131

Query Match 44.8%; Score 43; DB 4; Length 172;
Best Local Similarity 57.1%; Pred. No. 11;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 4 QPWNFQTLKIVIL 17
DB 74 BFRXNFETLRIDVL 87

RESULT 19
US-08-681-192-2
; Sequence 2, Application US/08681192
; Patent No. 6287801
; GENERAL INFORMATION:
; APPLICANT: BERGSMÄ, DERK
; APPLICANT: ELSHOURBAGY, NABIL
; APPLICANT: SARAU, HENRY
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFD578
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/681,192
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO

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; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-681-192-2

Query Match 44.8%; Score 43; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FWNKFNQTLKIVI 16
 |||:| |||:|
Db 195 FKHFTLTKWNI 206

RESULT 20
US-08-935-263-4
; Sequence 4, Application US/08935263A
; Patent No. 6117669
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuva
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/08/935,263A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: EP 96115540.5
; EARLIER FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Kurthia sp.
US-08-935-263-4

Query Match 43.8%; Score 42; DB 3; Length 460;
Best Local Similarity 54.5%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YQFWKNFQTLK 13
 |||:| |||:|
Db 127 YQWKNIDPVK 137

RESULT 21
US-09-594-185-4
; Sequence 4, Application US/09594185
; Patent No. 6365388
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuva
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/09/594,185
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 08/935,263
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: EP 96115540.5
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Kurthia sp.
US-09-594-185-4

Query Match 44.8%; Score 43; DB 3; Length 344;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 FWNKFNQTLKIVI 16
 |||:| |||:|
Db 195 FKHFTLTKWNI 206

RESULT 20
US-08-935-263-4
; Sequence 4, Application US/08935263A
; Patent No. 6117669
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuva
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/08/935,263A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: EP 96115540.5
; EARLIER FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Kurthia sp.
US-08-935-263-4

Query Match 43.8%; Score 42; DB 3; Length 460;
Best Local Similarity 54.5%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 YQFWKNFQTLK 13
 |||:| |||:|
Db 127 YQWKNIDPVK 137

RESULT 21
US-09-594-185-4
; Sequence 4, Application US/09594185
; Patent No. 6365388
; GENERAL INFORMATION:
; APPLICANT: Furuichi, Yasuhiro
; APPLICANT: Hoshino, Tatsuo
; APPLICANT: Kimura, Hitoshi
; APPLICANT: Kiyasu, Tatsuva
; APPLICANT: Nagahashi, Yoshie
; TITLE OF INVENTION: BIOTIN BIOSYNTHETIC GENES
; FILE REFERENCE: Biotin Genes
; CURRENT APPLICATION NUMBER: US/09/594,185
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 08/935,263
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: EP 96115540.5
; PRIOR FILING DATE: 1996-09-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Kurthia sp.
US-09-594-185-4

Query Match 43.8%; Score 42; DB 4; Length 727;
Best Local Similarity 37.5%; Pred. No. 74;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 QYQFWKNFQTLKIVIL 17
 |||:| |||:|
Db 167 QLEYWKNQTLISLITI 182

RESULT 22
US-09-540-236-3023
; Sequence 3023, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATENA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3023
; LENGTH: 727
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-3023

Query Match 43.8%; Score 42; DB 4; Length 727;
Best Local Similarity 37.5%; Pred. No. 74;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 QYQFWKNFQTLKIVIL 17
 |||:| |||:|
Db 167 QLEYWKNQTLISLITI 182

RESULT 23
US-09-328-352-6593
; Sequence 6593, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6593
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6593

Query Match 42.7%; Score 41; DB 4; Length 160;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YQFWKNFQ 10
 |||:| |||:|
Db 146 YVFWKFNQ 153

RESULT 24
US-09-491-577-2
; Sequence 2, Application US/09491577
; Patent No. 6610511
; GENERAL INFORMATION:
; APPLICANT: Yale University
; APPLICANT: Carlson, John R.
; APPLICANT: Kim, Hunhyong
; APPLICANT: Clyne, Peter J.
; APPLICANT: Marr, Coral G.
```

; TITLE OF INVENTION: No. 6610511el Family of Odorant Receptor Genes in Drosophila  
 ; FILE REFERENCE: 44574-5061-US  
 ; CURRENT APPLICATION NUMBER: US/09/491,577  
 ; CURRENT FILING DATE: 2000-01-25  
 ; EARLIER APPLICATION NUMBER: US 60/117,132  
 ; EARLIER FILING DATE: 1999-01-25  
 ; NUMBER OF SEQ ID NOS: 112  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 255  
 ; TYPE: PRT  
 ; ORGANISM: Drosophila melanogaster  
 US-09-491-577-2

Query Match 42.7%; Score 41; DB 4; Length 255;  
 Best Local Similarity 53.3%; Pred. No. 35;  
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 YQWKNFQTLKIVIL 17  
 Db 48 YKLWSTFTLLIFIL 62

## RESULT 25

US-09-252-991A-25052  
 ; Sequence 25052, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 25052  
 ; LENGTH: 363  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-25052

Query Match 42.7%; Score 41; DB 4; Length 363;  
 Best Local Similarity 60.0%; Pred. No. 51;  
 Matches 9; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 4 QFWKNFQTLKIVILG 18  
 Db 237 KFWKHQ---VILG 247

## RESULT 26

US-09-134-001C-4582  
 ; Sequence 4582, Application US/09134001C  
 ; Patent No. 6380370  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
 ; FILE REFERENCE: GTC-007  
 ; CURRENT APPLICATION NUMBER: US/09/134,001C  
 ; CURRENT FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/064,964  
 ; PRIOR FILING DATE: 1997-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/055,779  
 ; PRIOR FILING DATE: 1997-08-14  
 ; NUMBER OF SEQ ID NOS: 5674  
 ; SEQ ID NO 4582  
 ; LENGTH: 254  
 ; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis  
 US-09-134-001C-4582

Query Match 41.7%; Score 40; DB 4; Length 254;  
 Best Local Similarity 53.8%; Pred. No. 51;  
 Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLK 13  
 Db 9 SQYPLWNLQTLK 21

## RESULT 27

US-09-134-001C-5171  
 ; Sequence 5171, Application US/09134001C  
 ; Patent No. 6380370  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lynn Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
 ; FILE REFERENCE: GTC-007  
 ; CURRENT APPLICATION NUMBER: US/09/134,001C  
 ; CURRENT FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/064,964  
 ; PRIOR FILING DATE: 1997-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/055,779  
 ; PRIOR FILING DATE: 1997-08-14  
 ; NUMBER OF SEQ ID NOS: 5674  
 ; SEQ ID NO 5171  
 ; LENGTH: 311  
 ; TYPE: PRT  
 ; ORGANISM: Staphylococcus epidermidis  
 US-09-134-001C-5171

Query Match 41.7%; Score 40; DB 4; Length 311;  
 Best Local Similarity 38.5%; Pred. No. 63;  
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18  
 Db 271 WPNFATILWVVG 283

## RESULT 28

US-09-489-039A-8904  
 ; Sequence 8904, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489,039A  
 ; CURRENT FILING DATE: 2000-01-27  
 ; PRIOR APPLICATION NUMBER: US 60/117,747  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 8904  
 ; LENGTH: 316  
 ; TYPE: PRT  
 ; ORGANISM: Klebsiella pneumoniae  
 US-09-489-039A-8904

Query Match 41.7%; Score 40; DB 4; Length 316;  
 Best Local Similarity 61.5%; Pred. No. 64;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 WKNFQTLKIVILG 18  
 Db 226 WINVQGLKVEILG 238

## RESULT 29

```

US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; TITLE OF INVENTION: alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-012-988A-2

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Query Match 41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 6 WKNFQTLKIVILG 18
Db 195 WKLFQALKNLFG 207

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RESULT 30
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; Sequence 5, Application US/08450393A
; Patent No. 5707815
; GENERAL INFORMATION:
; APPLICANT: Charo, Israel
; APPLICANT: Coughlin, Shaun
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
; TITLE OF INVENTION: PROTEIN RECEPTORS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,393A

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; FILING DATE: May 25, 1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Czeiz, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: UCAL-237/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5165
; TELEFAX: 415-8857-0663
; TELEX: 380816CooleyPA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-450-393A-5
Query Match 41.7%; Score 40; DB 1; Length 355;
Best Local Similarity 53.8%; Pred. No. 73;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 6 WKNFQTLKIVILG 18
Db 195 WKLFQALKNLFG 207
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 18:03:03 ; Search time 24.0612 Seconds  
(without alignments)  
157.962 Million cell updates/sec

Title: US-10-084-813-13

Perfect score: 96

Sequence: 1 SQYQFWKFNQTLKIVILG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Match | Length | ID | Description       |
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| 1          | 96    | 100.0 | 18     | 14 | US-10-084-813-13  |
| 2          | 96    | 100.0 | 18     | 14 | US-10-084-813-77  |
| 3          | 96    | 100.0 | 54     | 9  | US-09-938-719-11  |
| 4          | 96    | 100.0 | 54     | 9  | US-09-938-719-11  |
| 5          | 96    | 100.0 | 54     | 9  | US-09-938-719-11  |
| 6          | 96    | 100.0 | 352    | 9  | US-09-938-719-11  |
| 7          | 96    | 100.0 | 352    | 9  | US-09-759-841-2   |
| 8          | 96    | 100.0 | 352    | 9  | US-09-779-879A-2  |
| 9          | 96    | 100.0 | 352    | 9  | US-09-779-879A-22 |
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| 32 | 96 | 100.0 | 352 | 14 | US-10-164-643-52    |
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| 40 | 93 | 96.9  | 352 | 13 | US-10-106-623-20    |
| 41 | 82 | 85.4  | 22  | 14 | US-10-239-423-43    |
| 42 | 78 | 81.2  | 18  | 14 | US-10-084-813-76    |
| 43 | 78 | 81.2  | 32  | 14 | US-10-057-890A-13   |
| 44 | 78 | 81.2  | 32  | 14 | US-10-072-301-9     |
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| 46 | 78 | 81.2  | 32  | 14 | US-10-239-423-42    |
| 47 | 78 | 81.2  | 32  | 15 | US-10-360-828-3     |
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| 51 | 75 | 77.1  | 18  | 14 | US-10-084-813-78    |
| 52 | 74 | 77.1  | 14  | 14 | US-10-225-567A-1492 |
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| 56 | 47 | 49.0  | 355 | 14 | US-10-376-564-13    |
| 57 | 45 | 46.9  | 355 | 14 | US-10-164-649-53    |
| 58 | 45 | 46.9  | 398 | 15 | US-10-369-493-10241 |
| 59 | 44 | 45.8  | 332 | 14 | US-10-095-876A-2    |
| 60 | 44 | 45.8  | 616 | 14 | US-10-260-877-120   |
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| 66 | 43 | 44.8  | 237 | 10 | US-09-769-744A-70   |
| 67 | 43 | 44.8  | 275 | 9  | US-09-925-300-1292  |
| 68 | 43 | 44.8  | 275 | 14 | US-10-106-698-6216  |
| 69 | 43 | 44.8  | 344 | 9  | US-09-912-025-2     |
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| 82 | 43 | 44.8  | 438 | 10 | US-09-769-787-48    |
| 83 | 43 | 44.8  | 957 | 16 | US-10-389-566-1990  |
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| 85 | 42 | 43.8  | 460 | 13 | US-10-033-078-4     |
| 86 | 41 | 42.7  | 397 | 10 | US-09-932-227-10    |
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# ALIGNMENTS

RESULT 1  
US-10-084-813-13  
; Sequence 13, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-13

Query Match 100.0%; Score 96; DB 14; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKFNFTLKIVILG 18  
Db 1 SOYQFWKFNFTLKIVILG 18

RESULT 2  
US-10-084-813-77  
; Sequence 77, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; PRIOR FILING DATE: 2002-02-27  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 77  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-77

Query Match 100.0%; Score 96; DB 9; Length 54;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKFNFTLKIVILG 18  
Db 9 SOYQFWKFNFTLKIVILG 25

RESULT 4  
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; Sequence 11, Application US/09938719  
; Patent No. US20020106742A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; PARMENTIER, MARC  
; VASSART, GILBERT  
; LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CO-CHEMOKINES RECEPTOR  
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/938,719  
; FILING DATE: 24-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/626,939  
; FILING DATE: 27-JULY-2000  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: <Unknown>  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 54 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-938-719-11

OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-77

Query Match 100.0%; Score 96; DB 14; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKFNFTLKIVILG 18  
Db 1 SOYQFWKFNFTLKIVILG 18

RESULT 3  
US-09-938-719-11  
; Sequence 11, Application US/09938719  
; Patent No. US20020106742A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; PARMENTIER, MARC  
; VASSART, GILBERT  
; LIBERT, FREDERICK  
; TITLE OF INVENTION: ACTIVE AND INACTIVE CO-CHEMOKINES RECEPTOR  
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/938,719  
; FILING DATE: 24-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/626,939  
; FILING DATE: 27-JULY-2000  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: <Unknown>  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 54 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-938-719-11

Query Match 100.0%; Score 96; DB 9; Length 54;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKFNFTLKIVILG 18  
Db 9 SOYQFWKFNFTLKIVILG 25



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; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,226
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-939-226-11

Query Match 100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKNFQTLKIVILG 18
Db 9 SOYQFWKNFQTLKIVILG 26

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; Sequence 11, Application US/09938703
; Patent No. US20020110870A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, FREDERICK
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,703
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939
; FILING DATE: 2000-07-27
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: <Unknown>
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 54 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-938-703-11

Query Match 100.0%; Score 96; DB 9; Length 54;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKNFQTLKIVILG 18
Db 9 SOYQFWKNFQTLKIVILG 26

RESULT 6
US-09-725-285-2
; Sequence 2, Application US/09725285
; Patent No. US20010000241A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/725,285
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-725-285-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOYQFWKNFQTLKIVILG 18
Db 185 SOYQFWKNFQTLKIVILG 202

RESULT 7
US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Ferros, Mancoscos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC1034BPME
; CURRENT APPLICATION NUMBER: US/09/759,841
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; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: GB 0000661.9  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000663.5  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000659.3  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-759-841-2

Query Match 100.0%; Score 96; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
|||  
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 8  
US-09-779-879A-2  
; Sequence 2, Application US/09779879A  
; Patent No. US20020048786A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.115000A  
; CURRENT APPLICATION NUMBER: US/09/779,879A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-879A-2

Query Match 100.0%; Score 96; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
|||  
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 9  
US-09-779-879A-22  
; Sequence 22, Application US/09779879A  
; Patent No. US20020048786A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.115000A  
; CURRENT APPLICATION NUMBER: US/09/779,879A  
; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-879A-22

Query Match 100.0%; Score 96; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
|||  
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 10  
US-09-779-880A-2  
; Sequence 2, Application US/09779880A  
; Patent No. US20020061834A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.115000C  
; CURRENT APPLICATION NUMBER: US/09/779,880A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-880A-2

Query Match 100.0%; Score 96; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
|||  
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 11  
US-09-779-880A-22  
; Sequence 22, Application US/09779880A  
; Patent No. US20020061834A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.115000C  
; CURRENT APPLICATION NUMBER: US/09/779,880A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258

; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-880A-22

Query Match 100.0%; Score 96; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
| | | | | | | | | | | | | | | | | |  
DB 185 SQYQFWKNFQTLKIVILG 202

## RESULT 12

US-09-813-653-15  
; Sequence 15, Application US/09813653  
; Patent No. US2002006470A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, John  
; APPLICANT: Wilson, Carol  
; APPLICANT: See, Raymond  
; APPLICANT: Tan Hehit, Christina  
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds  
; FILE REFERENCE: CNS-005  
; CURRENT APPLICATION NUMBER: US/09/813,653  
; CURRENT FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 60/190,946  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/190,996  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,299  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-813-653-15

Query Match 100.0%; Score 96; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
| | | | | | | | | | | | | | | | | |  
DB 185 SQYQFWKNFQTLKIVILG 202

## RESULT 13

US-09-813-653-17  
; Sequence 17, Application US/09813653  
; Patent No. US2002006470A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, John  
; APPLICANT: Wilson, Carol  
; APPLICANT: See, Raymond  
; APPLICANT: Tan Hehit, Christina  
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds  
; FILE REFERENCE: CNS-005  
; CURRENT APPLICATION NUMBER: US/09/813,653  
; CURRENT FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 60/190,946  
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/190,996  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,299  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-813-653-17

Query Match 100.0%; Score 96; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
| | | | | | | | | | | | | | | | | |  
DB 185 SQYQFWKNFQTLKIVILG 202

## RESULT 14

US-09-796-202-1  
; Sequence 1, Application US/09796202  
; Patent No. US20020068813A1  
; GENERAL INFORMATION:  
; APPLICANT: Dragic, Tatjana  
; APPLICANT: Olson, William  
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
; FILE REFERENCE: 2048/61010/JPM/SHS  
; CURRENT APPLICATION NUMBER: US/09/796,202  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: human  
US-09-796-202-1

Query Match 100.0%; Score 96; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKNFQTLKIVILG 18  
| | | | | | | | | | | | | | | | | |  
DB 185 SQYQFWKNFQTLKIVILG 202

## RESULT 15

US-09-195-662A-2  
; Sequence 2, Application US/09195662A  
; Patent No. US20020076745A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGMR10 (CCR5 Receptor)  
; FILE REFERENCE: 1488.1150002  
; CURRENT APPLICATION NUMBER: US/09/195,662A  
; CURRENT FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/466,343  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Artificial Sequence: Genomic  
; FEATURE:  
; OTHER INFORMATION: Deduced Amino Acid Sequence  
US-09-195-662A-2

Query Match 100.0%; Score 96; DB 9; Length 352;

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Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
Db 185 SQYQWKNFQTLKIVILG 202

RESULT 16
US-09-339-912A-2
; Sequence 2, Application US/09339912A
; Patent No. US20020099176A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNE10
; TITLE OF INVENTION: (CCR5 Receptor)
; FILE REFERENCE: 1488.1150003
; CURRENT APPLICATION NUMBER: US/09/339,912A
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Artificial Sequence: Genomic
; FEATURE:
; OTHER INFORMATION: Deduced Amino Acid Sequence
US-09-339-912A-2

Query Match 100.0%; Score 96; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18
Db 185 SQYQWKNFQTLKIVILG 202

RESULT 17
US-09-938-719-5
; Sequence 5, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; APPLICANT: PARMENTIER, MARC
; APPLICANT: VASSART, GILBERT
; APPLICANT: LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/938,719
; FILING DATE: 24-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/626,939

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Db 185 SOYQFWKMFQTLKIVILG 202

## RESULT 19

US-09-938-703-5  
; Sequence 5, Application US/09938703  
; Patent No. US20020110870A1  
; GENERAL INFORMATION:  
; APPLICANT: SAMSON, MICHEL  
; PARNENTIER, MARC  
; VASSART, GILBERT  
; LIBERT, FREDERICK

TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/938,703

FILING DATE: 24-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/626,939

FILING DATE: 2000-07-27

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-938-703-5

Query Match 100.0%; Score 96; DB 9; Length 352;

Best Local Similarity 100.0%; Pred. No. 3.6e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKMFQTLKIVILG 18

Db 185 SOYQFWKMFQTLKIVILG 202

## RESULT 20

US-09-502-783A-2

; Sequence 2, Application US/09502783A

; Patent No. US20020132269A1

; GENERAL INFORMATION:

; APPLICANT: Li, Yi

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRE

; FILE OF INVENTION: HDGR10

; FILE REFERENCE: 1488.1150006

; CURRENT APPLICATION NUMBER: US/09/502,783A

; CURRENT FILING DATE: 2001-08-23

; PRIOR APPLICATION NUMBER: 08/466,343

; PRIOR FILING DATE: 1995-06-06

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-502-783A-2

Query Match 100.0%; Score 96; DB 9; Length 352;

Best Local Similarity 100.0%; Pred. No. 3.6e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SOYQFWKMFQTLKIVILG 18

Db 185 SOYQFWKMFQTLKIVILG 202

## RESULT 21

US-09-734-221A-14

; Sequence 14, Application US/09734221A

; Publication No. US20030096221A1

; GENERAL INFORMATION:

; APPLICANT: LITTMAN, DAN R.

; DENG, HONGKUI

; ELLMEIER, WILFRIED

; LANDAU, NATHANIEL R.

; LIU, RONG

TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH

MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th

Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/734,221A

FILING DATE: 11-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/666,020

FILING DATE: 19-JUN-1996

APPLICATION NUMBER: US 08/227,319

FILING DATE: 13-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1049-1-004 N2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-734-221A-14

Query Match

100.0%; Score 96; DB 10; Length 352;

Best Local Similarity 100.0%; Pred. No. 3.6e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 SQYQFWKFNFTLKIVILG 18
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 22
US-09-826-509-477
; Sequence 477, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 477
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-477

Query Match 100.0%; Score 96; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKIVILG 18
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 23
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US2002015088A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marehall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US2002015088A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
US-10-106-623-2

Query Match 100.0%; Score 96; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKIVILG 18
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 24
US-10-232-686-2
; Sequence 2, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
; FILE REFERENCE: 1488.115000N
; CURRENT APPLICATION NUMBER: US/10/232,686
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 09/339,912
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/195,662
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-232-686-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQFWKFNFTLKIVILG 18
Db 185 SQYQFWKFNFTLKIVILG 202

RESULT 25
US-10-086-814-1
; Sequence 1, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-086-814-1

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 26
US-10-067-800-2
; Sequence 2, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/328,447
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/341,725
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 27
US-10-067-800-2
; Sequence 22, Application US/10067800
; Publication No. US20030100058A1
; GENERAL INFORMATION:
; APPLICANT: Roschke, Viktor
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10
; FILE REFERENCE: 1488.1150001
; CURRENT APPLICATION NUMBER: US/10/067,800
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/US01/04153
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/779,880
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/297,257
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/310,458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-800-2

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 28
US-10-290-058A-6
; Sequence 6, Application US/10290058A
; Publication No. US20030104455A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and Compositions for Treating
; FILE REFERENCE: MPI01-289P1RM
; CURRENT APPLICATION NUMBER: US/10/290,058A
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/344,552
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-290-058A-6

Query Match 100.0%; Score 96; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SQYQFWKNFQTLKIVILG 18
Db 185 SQYQFWKNFQTLKIVILG 202

RESULT 29
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenma C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352
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US-10-225-567A-352

Query Match 100.0%; Score 96; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 185 SQYQWKNFQTLKIVILG 202

RESULT 30

US-10-323-314-1  
; Sequence 1, Application US/10323314  
; Publication No. US20030139571A1  
; GENERAL INFORMATION:  
; APPLICANT: Dragic, Tatjana  
; APPLICANT: Olson, William  
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
; FILE REFERENCE: 2048/61010-1/JPW/MAP/DJK  
; CURRENT APPLICATION NUMBER: US/10/323,314  
; CURRENT FILING DATE: 2002-12-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: human  
US-10-323-314-1

Query Match 100.0%; Score 96; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.6e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SQYQWKNFQTLKIVILG 18  
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Db 185 SQYQWKNFQTLKIVILG 202

Search completed: March 4, 2004, 18:22:52  
Job time : 25.0612 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 52.3061 Seconds  
(without alignments)  
118.840 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APYNIIVLLNTFQEPFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_29Jan04.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003s.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description        |
|------------|-------|-------------|--------|------------|--------------------|
| 1          | 118   | 100.0       | 22     | 4 AAB88996 | AAB88996 HIV gp120 |
| 2          | 118   | 100.0       | 268    | 7 ADC10142 | ADC10142 Human NOV |
| 3          | 118   | 100.0       | 268    | 7 ADC10144 | ADC10144 Human NOV |
| 4          | 118   | 100.0       | 332    | 2 AAW26766 | AAW26766 Human che |
| 5          | 118   | 100.0       | 352    | 2 AAW27407 | AAW27407 Human CCR |
| 6          | 118   | 100.0       | 352    | 2 AAW27123 | AAW27123 Human che |
| 7          | 118   | 100.0       | 352    | 2 AAW27125 | AAW27125 Macaque c |
| 8          | 118   | 100.0       | 352    | 2 AAW07602 | AAW07602 Human G-p |
| 9          | 118   | 100.0       | 352    | 2 AAW23835 | AAW23835 Human CC  |
| 10         | 118   | 100.0       | 352    | 2 AAW8232  | AAW8232 HIV-1 co-  |
| 11         | 118   | 100.0       | 352    | 3 AAY80128 | AAY80128 Human G-p |
| 12         | 118   | 100.0       | 352    | 4 AAG97089 | AAG97089 Amino aci |
| 13         | 118   | 100.0       | 352    | 4 AAG07046 | AAG07046 Human G-p |
| 14         | 118   | 100.0       | 352    | 4 AAG07048 | AAG07048 Human G-p |
| 15         | 118   | 100.0       | 352    | 4 AAG80111 | AAG80111 Human CCR |
| 16         | 118   | 100.0       | 352    | 4 AAE04321 | AAE04321 Human che |
| 17         | 118   | 100.0       | 352    | 4 AAE07037 | AAE07037 Human G-p |
| 18         | 118   | 100.0       | 352    | 4 AAE07039 | AAE07039 Human G-p |
| 19         | 118   | 100.0       | 352    | 4 AAB46858 | AAB46858 Human HDG |
| 20         | 118   | 100.0       | 352    | 4 AAB56342 | AAB56342 Non-endog |
| 21         | 118   | 100.0       | 352    | 4 AAB83354 | AAB83354 Human CCR |
| 22         | 118   | 100.0       | 352    | 4 AAB82948 | AAB82948 Human HIV |
| 23         | 118   | 100.0       | 352    | 5 AAU97150 | AAU97150 Human G-p |
| 24         | 118   | 100.0       | 352    | 5 AAU97152 | AAU97152 Human G-p |
| 25         | 118   | 100.0       | 352    | 5 AAM52829 | AAM52829 Human CCR |

|    |     |       |     |             |                     |
|----|-----|-------|-----|-------------|---------------------|
| 26 | 118 | 100.0 | 352 | 5 AAM52828  | AAM52828 Human CC   |
| 27 | 118 | 100.0 | 352 | 5 ABG70597  | ABG70597 Human G-p  |
| 28 | 118 | 100.0 | 352 | 5 ABG92883  | ABG92883 Human imm  |
| 29 | 118 | 100.0 | 352 | 5 ABG92880  | ABG92880 Human G-p  |
| 30 | 118 | 100.0 | 352 | 5 AAE25808  | AAE25808 Human G-p  |
| 31 | 118 | 100.0 | 352 | 5 AAE25811  | AAE25811 Human G-p  |
| 32 | 118 | 100.0 | 352 | 5 ABB81054  | ABB81054 G-protein  |
| 33 | 118 | 100.0 | 352 | 5 ABB808343 | ABB808343 Human che |
| 34 | 118 | 100.0 | 352 | 5 ABG75540  | ABG75540 Human G-p  |
| 35 | 118 | 100.0 | 352 | 6 ABR58602  | ABR58602 Human can  |
| 36 | 118 | 100.0 | 352 | 6 AAO29514  | AAO29514 Human C-C  |
| 37 | 118 | 100.0 | 352 | 6 ABU61654  | ABU61654 Human G-p  |
| 38 | 118 | 100.0 | 352 | 6 ABP97728  | ABP97728 Amino aci  |
| 39 | 118 | 100.0 | 352 | 6 ABP81933  | ABP81933 Human C-C  |
| 40 | 118 | 100.0 | 352 | 6 ADC03341  | ADC03341 Human che  |
| 41 | 118 | 100.0 | 352 | 7 ADC03359  | ADC03359 Macaque c  |
| 42 | 118 | 100.0 | 371 | 2 AAW23834  | AAW23834 Human CC   |
| 43 | 118 | 100.0 | 439 | 2 AAY41280  | AAY41280 Fusion pr  |
| 44 | 108 | 91.5  | 354 | 2 AAW54037  | AAW54037 Mouse CC-  |
| 45 | 105 | 89.0  | 354 | 7 ADD44859  | ADD44859 Rat Prote  |
| 46 | 105 | 89.0  | 354 | 7 ADD44863  | ADD44863 Rat Prote  |
| 47 | 103 | 87.3  | 329 | 4 AAB46859  | AAB46859 Human MCP  |
| 48 | 103 | 87.3  | 329 | 5 ABB81055  | ABB81055 Human MCP  |
| 49 | 103 | 87.3  | 344 | 5 ABG92881  | ABG92881 Class I r  |
| 50 | 103 | 87.3  | 344 | 6 ABU61655  | ABU61655 Human mon  |
| 51 | 103 | 87.3  | 360 | 2 AAR79166  | AAR79166 Human mon  |
| 52 | 103 | 87.3  | 360 | 2 AAW35833  | AAW35833 Human mon  |
| 53 | 103 | 87.3  | 360 | 4 AAG80108  | AAG80108 Human CCR  |
| 54 | 103 | 87.3  | 360 | 4 AAU07613  | AAU07613 Human CCR  |
| 55 | 103 | 87.3  | 360 | 4 AAB07614  | AAB07614 Human wil  |
| 56 | 103 | 87.3  | 360 | 4 ABB56340  | ABB56340 Non-endog  |
| 57 | 103 | 87.3  | 360 | 6 ABP97725  | ABP97725 Amino aci  |
| 58 | 103 | 87.3  | 360 | 6 ABP81987  | ABP81987 Human C-C  |
| 59 | 103 | 87.3  | 374 | 2 AAR79165  | AAR79165 Human mon  |
| 60 | 103 | 87.3  | 374 | 4 AAG80107  | AAG80107 Human CCR  |
| 61 | 103 | 87.3  | 374 | 6 ABU09083  | ABU09083 Human che  |
| 62 | 103 | 87.3  | 374 | 7 ADD44861  | ADD44861 Human Pro  |
| 63 | 103 | 87.3  | 374 | 7 ADD44865  | ADD44865 Human Pro  |
| 64 | 94  | 79.7  | 18  | 4 AAB88971  | AAB88971 HIV gp120  |
| 65 | 93  | 78.8  | 18  | 4 AAB88970  | AAB88970 HIV gp120  |
| 66 | 78  | 66.1  | 18  | 4 AAB88972  | AAB88972 HIV gp120  |
| 67 | 74  | 62.7  | 20  | 4 AAB83317  | AAB83317 CCR5 immu  |
| 68 | 71  | 60.2  | 18  | 4 AAB88969  | AAB88969 HIV gp120  |
| 69 | 71  | 60.2  | 28  | 2 AAY39247  | AAY39247 G-protein  |
| 70 | 70  | 59.3  | 344 | 2 AAW26767  | AAW26767 Human che  |
| 71 | 70  | 59.3  | 344 | 2 AAW23957  | AAW23957 Amino aci  |
| 72 | 70  | 59.3  | 344 | 5 ABB84824  | ABB84824 Human PRO  |
| 73 | 70  | 59.3  | 344 | 5 AAU11155  | AAU11155 Human G p  |
| 74 | 70  | 59.3  | 344 | 5 AAE26111  | AAE26111 Human G p  |
| 75 | 70  | 59.3  | 344 | 6 ABB95430  | ABB95430 Human ang  |
| 76 | 70  | 59.3  | 344 | 6 ABP81934  | ABP81934 Human che  |
| 77 | 70  | 59.3  | 344 | 7 ADD10305  | ADD10305 Human sec  |
| 78 | 70  | 59.3  | 344 | 7 ADD11265  | ADD11265 Human sec  |
| 79 | 70  | 59.3  | 344 | 7 ADD37058  | ADD37058 Human sec  |
| 80 | 70  | 59.3  | 344 | 8 ADE41266  | ADE41266 Human sec  |
| 81 | 70  | 59.3  | 356 | 2 AAW48087  | AAW48087 Human mac  |
| 82 | 70  | 59.3  | 356 | 6 ABU09081  | ABU09081 Human mon  |
| 83 | 66  | 55.9  | 26  | 2 AAW40028  | AAW40028 Peptide e  |
| 84 | 65  | 55.1  | 28  | 2 AAY39252  | AAY39252 G-protein  |
| 85 | 63  | 53.4  | 15  | 7 AAE38757  | AAE38757 CCR5 chem  |
| 86 | 61  | 51.7  | 25  | 2 AAW33966  | AAW33966 CCR5 rece  |
| 87 | 61  | 51.7  | 25  | 2 AAW33999  | AAW33999 CCR5 rece  |
| 88 | 57  | 48.3  | 16  | 2 AAW23838  | AAW23838 Human CC   |
| 89 | 57  | 48.3  | 17  | 2 AAW43019  | AAW43019 Synthetic  |
| 90 | 57  | 48.3  | 17  | 2 AAW39913  | AAW39913 Peptide r  |
| 91 | 57  | 48.3  | 17  | 2 AAW46994  | AAW46994 Alanine s  |
| 92 | 57  | 48.3  | 17  | 2 AAW46993  | AAW46993 Alanine s  |
| 93 | 57  | 48.3  | 17  | 2 AAW46995  | AAW46995 Alanine s  |
| 94 | 57  | 48.3  | 17  | 6 ABG75974  | ABG75974 CC-chemok  |
| 95 | 57  | 48.3  | 17  | 6 ABU09551  | ABU09551 Human CC-  |
| 96 | 57  | 48.3  | 18  | 4 AAB88973  | AAB88973 HIV gp120  |
| 97 | 57  | 48.3  | 138 | 5 ABG32539  | ABG32539 Human CCR  |
| 98 | 57  | 48.3  | 157 | 5 ABG32540  | ABG32540 Human CCR  |

99 56 47.5 209 3 AAB58414 Lung canc  
100 56 47.5 295 4 AAG80106 Human CCR

## ALIGNMENTS

## RESULT 1

AAB88996  
ID AAB88996 standard; peptide; 22 AA.  
XX  
AC AAB88996;  
XX  
DT 23-MAY-2001 (first entry)  
XX  
DE HIV gp120 protein binding peptide #89.  
XX  
KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
KW replication; CCR5; CXCR4; CD4; STRL33.  
XX  
OS Homo sapiens.  
XX  
PN WO200116182-A2.  
XX  
PD 08-MAR-2001.  
XX  
PF 25-AUG-2000; 2000WO-US023505.  
XX  
PR 27-AUG-1999; 99US-0151270P.  
XX  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Saxinger C;  
XX  
DR WPI; 2001-244398/25.  
XX

Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.

Claim 21; Page 38; 114pp; English.

The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention

Sequence 22 AA;

Query Match 100.0%; Score 118; DB 4; Length 22;

Best Local Similarity 100.0%; Pred. No. 1.1e-12;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLINTFOFFGLNCS 22

DB 1 APYIVLLINTFOFFGLNCS 22

## RESULT 2

ADCL0142  
ID ADCL0142 standard; protein; 268 AA.

XX AC ADCL0142;

XX DT 18-DEC-2003 (first entry)

XX DE Human NOVX polypeptide SEQ ID NO: 162.

XX cytostatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;  
KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;  
KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;  
KW inflammatory disorder; chromosome mapping; tissue typing;

KW predictive medicine.

OS Homo sapiens.

XX WO2003000842-A2.

XX 03-JAN-2003.

XX 04-JUN-2002; 2002WO-US017443.

XX 04-JUN-2001; 2001US-0295607P.

PR 04-JUN-2001; 2001US-0295661P.

PR 06-JUN-2001; 2001US-0296404P.

PR 06-JUN-2001; 2001US-0296418P.

PR 07-JUN-2001; 2001US-0296575P.

PR 11-JUN-2001; 2001US-0297414P.

PR 12-JUN-2001; 2001US-0295573P.

PR 12-JUN-2001; 2001US-0297567P.

PR 14-JUN-2001; 2001US-0298285P.

PR 15-JUN-2001; 2001US-0298528P.

PR 18-JUN-2001; 2001US-0299133P.

PR 19-JUN-2001; 2001US-0299230P.

PR 21-JUN-2001; 2001US-0299949P.

PR 22-JUN-2001; 2001US-0300177P.

PR 26-JUN-2001; 2001US-0300883P.

PR 28-JUN-2001; 2001US-0301530P.

PR 28-JUN-2001; 2001US-0301550P.

PR 03-JUL-2001; 2001US-0302951P.

PR 31-JUL-2001; 2001US-030890P.

PR 14-SEP-2001; 2001US-032237P.

PR 25-SEP-2001; 2001US-0324669P.

PR 03-DEC-2001; 2001US-0337477P.

PR 14-DEC-2001; 2001US-0341562P.

PR 21-FEB-2002; 2002US-0358656P.

PR 21-FEB-2002; 2002US-0359122P.

PR 22-FEB-2002; 2002US-035978P.

PR 22-FEB-2002; 2002US-0359034P.

PR 22-FEB-2002; 2002US-0359035P.

PR 22-FEB-2002; 2002US-0359121P.

PR 27-FEB-2002; 2002US-0359964P.

PR 01-MAR-2002; 2002US-0360858P.

PR 12-MAR-2002; 2002US-0363430P.

PR 12-MAR-2002; 2002US-0363676P.

PR 10-APR-2002; 2002US-0371346P.

PR 10-MAY-2002; 2002US-0379444P.

PR 04-JUN-2002; 2002US-00379444.

(CURA-) CURAGEN CORP.

Agee M, Anderson DM, Berghs C, Casman SJ, Catterton E;  
Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;  
Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalte T, Ji W, Kekuda R;  
Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet L;  
Ott T, Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieger DK;  
Rothenberg ME, Shency SG, Shinkels RA, Smithson G, Spaderna SK;  
Spytek KA, Stone DJ, Vernet CM, Zhong H, Zhong M, Alsobrook JP;  
Burgess CE, Lepley DM;

WPI; 2003-210149/20.

N-PSDB; ADC10141.

New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory or CNS diseases.

Claim 1; SEQ ID NO 162; 772pp; English.

The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide comprising one or more conservative substitutions. The NOVX polypeptide is useful for treating or preventing a pathology associated with the polypeptide e.g. disorders associated with aberrant expression

CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
 CC endocrine, CNS and inflammatory disorders. They can also be used in  
 CC various detection and screening assays, chromosome mapping, tissue typing  
 CC and predictive medicine. This sequence corresponds to one of the  
 CC polypeptides of the invention.

XX SQ Sequence 268 AA;  
 Query Match 100.0%; Score 118; DB 7; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYIVILLNTFOFFGLNCS 22  
 Db 165 APYIVILLNTFOFFGLNCS 186

RESULT 3  
 ID ADC10144  
 XX ADC10144 standard; protein; 268 AA.  
 AC ADC10144;  
 XX 18-DEC-2003 (first entry)  
 DT Human NOVX polypeptide SEQ ID NO: 164.  
 DE  
 DE cytotatic; antidiabetic; anorectic; cerebroprotective; neuroprotective;  
 KW antinflammatory; gene therapy; antisense therapy; chryomimetic; NOVX;  
 KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;  
 KW inflammatory disorder; chromosome mapping; tissue typing;  
 KW predictive medicine.

OS Homo sapiens.  
 XX WO2003000842-A2.  
 FN 03-JAN-2003.  
 PD  
 XX 04-JUN-2002; 2002WO-US017443.

PR 04-JUN-2001; 2001US-0295607P.  
 PR 04-JUN-2001; 2001US-0295661P.  
 PR 06-JUN-2001; 2001US-0296404P.  
 PR 06-JUN-2001; 2001US-0296418P.  
 PR 07-JUN-2001; 2001US-0296575P.  
 PR 11-JUN-2001; 2001US-0297414P.  
 PR 12-JUN-2001; 2001US-0295573P.  
 PR 12-JUN-2001; 2001US-0297567P.  
 PR 14-JUN-2001; 2001US-0298285P.  
 PR 15-JUN-2001; 2001US-0298528P.  
 PR 18-JUN-2001; 2001US-0298133P.  
 PR 13-JUN-2001; 2001US-0299230P.  
 PR 21-JUN-2001; 2001US-029949P.  
 PR 22-JUN-2001; 2001US-0300177P.  
 PR 26-JUN-2001; 2001US-0300883P.  
 PR 28-JUN-2001; 2001US-0301530P.  
 PR 28-JUN-2001; 2001US-0301550P.  
 PR 03-JUL-2001; 2001US-0302951P.  
 PR 31-JUL-2001; 2001US-030890P.  
 PR 14-SEP-2001; 2001US-0322297P.  
 PR 25-SEP-2001; 2001US-0324669P.  
 PR 03-DEC-2001; 2001US-0337477P.  
 PR 14-DEC-2001; 2001US-0341562P.  
 PR 21-FEB-2002; 2002US-0358656P.  
 PR 21-FEB-2002; 2002US-0359122P.  
 PR 22-FEB-2002; 2002US-0358978P.  
 PR 22-FEB-2002; 2002US-0359034P.  
 PR 22-FEB-2002; 2002US-0359035P.  
 PR 22-FEB-2002; 2002US-0359121P.  
 PR 27-FEB-2002; 2002US-0359964P.  
 PR 01-MAR-2002; 2002US-0360858P.  
 PR 12-MAR-2002; 2002US-0363430P.

PR 12-MAR-2002; 2002US-0363676P.  
 PR 10-APR-2002; 2002US-0371346P.  
 PR 10-MAY-2002; 2002US-0379444P.  
 PR 04-JUN-2002; 2002US-0037944P.

XX (CURA-) CURAGEN CORP.  
 PA Agee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;  
 XX DiPippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;  
 PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;  
 PI Khramsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;  
 PI Ort T, Padigaru M, Patturajan M, Pena CE, Rastelli L, Rieger DK;  
 PI Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;  
 PI Spytek JA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;  
 PI Burgess CE, Lepley DM;  
 XX WPI; 2003-210149/20.  
 DR N-ESDE; ADC10143.

XX New isolated NOVX polypeptides and nucleic acid molecules useful for  
 PT treating, preventing and diagnosing pathological conditions with NOVX-  
 PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
 PT or CNS diseases.

XX Claim 1; SEQ ID NO 164; 772pp; English.  
 XX The invention relates to novel isolated polypeptides, mature form of the  
 CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
 CC polypeptide comprising one or more conservative substitutions. The NOVX  
 CC polypeptide is useful for treating or preventing a pathology associated  
 CC with the polypeptide e.g. disorders associated with aberrant expression  
 CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
 CC endocrine, CNS and inflammatory disorders. They can also be used in  
 CC various detection and screening assays, chromosome mapping, tissue typing  
 CC and predictive medicine. This sequence corresponds to one of the  
 CC polypeptides of the invention.  
 XX SQ Sequence 268 AA;

Query Match 100.0%; Score 118; DB 7; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYIVILLNTFOFFGLNCS 22  
 Db 165 APYIVILLNTFOFFGLNCS 186

RESULT 4  
 AAW26766  
 ID AAW26766 standard; protein; 332 AA.  
 XX AAW26766;  
 AC  
 XX 21-MAY-1998 (first entry)  
 DT Human chemokine receptor MMLR-CCR.  
 DE  
 XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;  
 KW monocyte; macrophage; chemotaxis; haematopoiesis; infection;  
 KW inflammation; proliferative disease; cardiovascular disease; tumour;  
 KW rheumatoid arthritis; alveolitis; atherosclerosis;  
 KW chronic granulomatous disease; asthma; myasthenia gravis; diabetes;  
 KW inflammatory bowel disease; toxic shock syndrome; septic shock;  
 KW Chediak-Higashi syndrome; therapy; diagnosis.

OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Peptide 107..128  
 FT /note= "conserved peptide"  
 FT Misc-difference 121  
 FT /note= "a claimed polypeptide has isoleucine at residue

FT XX 121"

PN WO9741225-A2.

XX 06-NOV-1997.

PD 25-APR-1997; 97WO-US006993.

XX 26-APR-1996; 96US-00638081.

XX (INCY-) INCYTE PHARM INC.

PA Au-Young J, Bandman O, Coleman R, Wilde CG;

XX WPI; 1997-549729/50.

XX N-PSDB; AAT99542.

XX Polynucleotide encoding MMLR-CCR or MPHG-CCR chemokine receptor - useful to study, diagnose and treat, e.g. infection, inflammation, solid tumour and proliferative and cardiovascular disease.

XX Claim 8; Page 37-38; 59pp; English.

XX This protein comprises human MMLR-CCR, a novel C-C chemokine receptor associated with monocyte/macrophage infiltration and chemotaxis and haematopoiesis. The amino acid sequence was deduced from a cDNA clone (see AAT99542) obtained from a cDNA library made from mononuclear cells collected on day 2 of a mixed lymphocyte culture, i.e. cells associated with inflammation and immunomodulation. Another novel chemokine receptor, MPHG-CCR (see AAW36767), is also claimed. MMLR-CCR contains 7 transmembrane spanning segments connected by a series of intracellular and extracellular loops. MMLR-CCR and MPHG-CCR can be used to study, diagnose and treat disease states in which normal leukocyte function is perturbed by normal leukopoiesis or inappropriate activation via chemokine agonists or antagonists, such as infection, inflammation, CC proliferative disease, tumorigenesis, autoimmune disease, abnormal cell proliferation, solid tumours, cardiovascular disease, rheumatoid arthritis, alveolitis, atherosclerosis, chronic granulomatous disease, asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic shock syndrome, septic shock and Chediak-Higashi syndrome

XX SQ Sequence 332 AA;

Query Match 100.0%; Score 118; DB 2; Length 332;

Best Local Similarity 100.0%; Pred. No. 2.7e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22

DB 229 APYNVLLNTFQFFGLNCS 250

RESULT 5

AAW27407

ID AAW27407 standard; protein; 352 AA.

XX AAW27407;

XX 14-APR-1998 (first entry)

XX Human CCR5.

XX Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus; type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;

XX inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;

XX idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;

XX atherosclerosis; autoimmune disorder.

XX Homo sapiens.

XX WO9732019-A2.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-BE000023.

XX 01-MAR-1996; 96EP-00870021.

XX 06-AUG-1996; 96EP-00870102.

XX (EURO-) EUROSREEN SA.

XX Samson M, Parmentier M, Vassart G, Libert F;

XX WPI; 1997-479829/44.

XX N-PSDB; AAT90117.

XX Active and inactive forms of human CC chemokine receptor CCR-5 - useful to diagnose, prevent and/or treat inflammatory disorders, autoimmune disease and viral infection.

XX Claim 4; Fig 1b-c; 94pp; English.

XX The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5), which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, interleukin-8 (IL-8) or growth related gene product alpha (GRO alpha) chemokines. Active CCR-5 is also a receptor of human immunodeficiency virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer, atherosclerosis and autoimmune disorders

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22

DB 249 APYNVLLNTFQFFGLNCS 270

RESULT 6

AAW27123

ID AAW27123 standard; protein; 352 AA.

XX AAW27123;

XX 14-DEC-1997 (first entry)

XX Human chemokine receptor 88C.

XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; ligand; modulator; antibody; human.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..32

FT Domain /label= Extracellular\_domain

FT Domain 56..67

FT Domain /label= Intracellular\_domain

FT Domain 89..112

FT Domain /label= Extracellular\_domain

FT Domain 125..145

FT Domain /label= Intracellular\_domain

FT Domain 166..191

FT Domain /label= Extracellular\_domain

FT Domain 213..235

FT Domain /label= Intracellular\_domain

FT Domain 259..280

FT Domain /label= Extracellular\_domain

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FT Domain 301..352
XX /label= Intracellular_domain
XX WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US020759.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 1997-341689/31.
XX
XX N-PSDB; AAT85163.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 16; Page 47-48; 65pp; English.
XX
XX This polypeptide sequence comprises novel human chemokine receptor 88C, a
XX G protein coupled receptor that is involved in leukocyte trafficking. Its
XX amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
XX macrophage library. It shows 62% identity to CCKBR1. Chemokine receptor
XX 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
XX and their polypeptide fragments can be produced in transformed host
XX cells. The receptors, peptides comprising one or more of the
XX extracellular or intracellular domains, and anti-receptor antibodies can
XX be used to modulate receptor activities, particularly ligand and G
XX protein binding, and are potentially useful in the treatment
XX of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX infection, AIDS, inflammatory conditions, pathological immune response,
XX abnormal haematopoietic processes etc
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 APYNIVLLNTFOEFFGLNCS 22
XX |||||
XX DB 249 APYNIVLLNTFOEFFGLNCS 270
XX
XX RESULT 7
XX AAW27125
XX ID AAW27125 standard; protein; 352 AA.
XX
XX AC AAW27125;
XX
XX DT 14-DEC-1997 (first entry)
XX
XX DE Macaque chemokine receptor 88C.
XX
XX KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
XX asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX modulator; antibody.
XX
XX OS Macaca sp.
XX
XX PN WO9722698-A2.
XX
XX PD 26-JUN-1997.
XX
XX PF 20-DEC-1996; 96WO-US020759.
XX
XX
XX

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PR 20-DEC-1995; 95US-00575967.
PR 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX
XX WPI; 1997-341689/31.
XX
XX N-PSDB; AAT85163.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 36; Page 57-58; 65pp; English.
XX
XX This polypeptide sequence comprises macaque chemokine receptor 88C, a
XX protein coupled receptor that is involved in leukocyte trafficking. Its
XX amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX amplification. It shows 97% identity to human 88C (AAW27123). 88C
XX receptors and their polypeptide fragments can be produced in transformed
XX host cells. The receptors, peptides comprising one or more of the
XX extracellular or intracellular domains, and anti-receptor antibodies can
XX be used to modulate receptor activities, particularly ligand and G
XX protein binding, and are potentially useful in the treatment
XX of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX infection, AIDS, inflammatory conditions, pathological immune response,
XX abnormal haematopoietic processes etc. A hybridoma that produces an
XX antibody that specifically binds to macaque 88C is claimed
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 118; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 2.9e-11;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 APYNIVLLNTFOEFFGLNCS 22
XX |||||
XX DB 249 APYNIVLLNTFOEFFGLNCS 270
XX
XX RESULT 8
XX AAW07602
XX ID AAW07602 standard; protein; 352 AA.
XX
XX AC AAW07602;
XX
XX DT 26-FEB-1997 (first entry)
XX
XX DE Human G-protein chemokine receptor HDGMR10.
XX
XX KW G-protein chemokine receptor; HDGMR10; signal transduction;
XX haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
XX therapy.
XX
XX OS Homo sapiens.
XX
XX PN WO9639437-A1.
XX
XX PD 12-DEC-1996.
XX
XX PF 06-JUN-1995; 95WO-US007173.
XX
XX PR 06-JUN-1995; 95WO-US007173.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX LI Y, Ruben SM;
XX
XX WPI; 1997-043072/04.
XX
XX N-PSDB; AAT44042.
XX
XX Human G-protein chemokine receptor, HDGMR10 - useful to identify
XX

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|          |                                                                                                                       |
|----------|-----------------------------------------------------------------------------------------------------------------------|
| PT       | (ant)agonists, for treatment of haematopoiesis, leukaemia, chronic and acute inflammation, rheumatoid arthritis, etc. |
| XX       | Claim 1; Page 44-46; 61pp: English.                                                                                   |
| XX       | Novel human mature G-protein chemokine receptor HDGMR10 (AAW07602) is a 7                                             |
| CC       | -transmembrane protein involved in signal transduction. Its amino acid                                                |
| CC       | sequence was deduced from a cDNA clone (AA144042) isolated from a human                                               |
| CC       | monocyte library. Isolation of the cDNA allows prodn. of recombinant                                                  |
| CC       | HDGMR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant                                                     |
| CC       | receptor can be used to identify agonists or antagonists of the receptor;                                             |
| CC       | such cpds. can be used to treat conditions related to the under- and over                                             |
| XX       | -expression of G-protein chemokine receptors                                                                          |
| XX       | Sequence 352 AA;                                                                                                      |
| SQL      | Query Match 100.0%; Score 118; DB 2; Length 352;                                                                      |
|          | Best Local Similarity 100.0%; Pred. No. 2.9e-11;                                                                      |
|          | Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                           |
| QY       | 1 APYNIVLLNTFOEFFGLNCS 22                                                                                             |
|          |                                                                                                                       |
| Db       | 249 APYNIVLLNTFOEFFGLNCS 270                                                                                          |
| RESULT 9 |                                                                                                                       |
| AAW23835 |                                                                                                                       |
| ID       | AAW23835 standard; protein; 352 AA.                                                                                   |
| XX       | AC                                                                                                                    |
| AC       | AAW23835;                                                                                                             |
| XX       | XX                                                                                                                    |
| DT       | 08-JUN-1998 (first entry)                                                                                             |
| XX       | XX                                                                                                                    |
| DE       | Human CC chemokine receptor 5 (CCR5).                                                                                 |
| XX       | XX                                                                                                                    |
| KW       | CC chemokine receptor 5; CCR5; G-protein coupled receptor;                                                            |
| KW       | human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.                                             |
| XX       | XX                                                                                                                    |
| OS       | Homo sapiens.                                                                                                         |
| Key      | Location/Qualifiers                                                                                                   |
| FT       | 29..55                                                                                                                |
| FT       | /label= I                                                                                                             |
| FT       | /note= "transmembrane domain"                                                                                         |
| FT       | 104..126                                                                                                              |
| FT       | /label= III                                                                                                           |
| FT       | /note= "transmembrane domain"                                                                                         |
| FT       | 109..120                                                                                                              |
| FT       | /note= "extracellular loop-1 (Claim 19)"                                                                              |
| FT       | 143..171                                                                                                              |
| FT       | /label= IV                                                                                                            |
| FT       | /note= "transmembrane domain"                                                                                         |
| FT       | 187..210                                                                                                              |
| FT       | /note= "extracellular loop-2 (Claim 19)"                                                                              |
| FT       | 194..219                                                                                                              |
| FT       | /label= V                                                                                                             |
| FT       | /note= "transmembrane domain"                                                                                         |
| FT       | 238..258                                                                                                              |
| FT       | /label= VI                                                                                                            |
| FT       | /note= "transmembrane domain"                                                                                         |
| FT       | 261..276                                                                                                              |
| FT       | /note= "extracellular loop-3 (Claim 19)"                                                                              |
| FT       | 277..300                                                                                                              |
| FT       | /label= VII                                                                                                           |
| FT       | /note= "transmembrane domain"                                                                                         |
| XX       | WO9745543-A2.                                                                                                         |
| PN       | XX                                                                                                                    |
| PD       | 04-DEC-1997.                                                                                                          |
| XX       | XX                                                                                                                    |
| XX       | 28-MAY-1997; 97WO-US009586.                                                                                           |
| PR       | 28-MAY-1996; 96US-0018508P.                                                                                           |

XX W09854317-A1.  
 XX 03-DEC-1998.  
 XX 29-MAY-1998; 98WO-EP003437.  
 XX 30-MAY-1997; 97US-0048057P.  
 XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.  
 XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;  
 XX WPI; 1999-059835/05.  
 XX N-PSDB; AAV84126.  
 XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing  
 XX resistance of CCR5-expressing cells to HIV-1 infection.  
 XX Disclosure; Page 34-35; 55pp; English.  
 XX This is the amino acid sequence of wild-type human CCR5, which serves as  
 XX a co-receptor for infection by macrophage-tropic (M-tropic) strains of  
 XX HIV-1. The invention relates to the identification of a CCR5 variant (see  
 XX AAV84231), designated CCR5m303, comprising the first two transmembrane  
 XX domains of wild-type CCR5, but lacking transmembrane domains 3-7. The  
 XX presence of the CCR5m303 variant with the wild type CCR5 allele shows a  
 XX positive correlation with resistance to infection with M-tropic HIV-1  
 XX strains, and may indicate slower progression of the disease. The  
 XX detection of CCR5 variants may be used to identify individuals at lower  
 XX risk of infection relative to the general population who, if infected,  
 XX may exhibit slower progression to AIDS. Probes and primers (see AAV84127-  
 XX 36) are provided for use in diagnostic methods for detecting the presence  
 XX of such variants. A method is provided for inhibiting HIV-1 infection of  
 XX a cell expressing the CCR5 receptor. This involves introducing a nucleic  
 XX acid encoding a CCR5 variant into the cell, thereby reducing the number  
 XX of functional CCR5 molecules present on the cell surface

XX SQ Sequence 352 AA;  
 Query Match 100.0%; Score 118; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22  
 |||||  
 Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 11  
 AAY80128  
 ID AAY80128 standard; protein; 352 AA.  
 AC AAY80128;  
 XX 19-MAY-2000 (first entry)  
 XX Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.  
 XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;  
 XX diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;  
 XX tumour; infection; leukaemia; psoriasis; allergy;  
 XX T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;  
 XX inflammation; allergic reaction; silicosis; sarcoidosis;  
 XX rheumatoid arthritis; hyper-eosinophilia syndrome.  
 XX Homo sapiens.  
 XX US6025154-A.  
 XX 15-FEB-2000.  
 XX 06-JUN-1995; 95US-00466343.

XX 06-JUN-1995; 95US-00466343.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Li Y, Ruben SM;  
 XX WPI; 2000-181807/16.  
 XX N-PSDB; AAZ91481.  
 XX Isolated nucleic acid encoding human G-protein chemokine receptor useful  
 XX for diagnostic assays, scientific research and screening for compounds  
 XX which bind to and activate or inhibit activation of the receptor  
 XX polypeptides.  
 XX Claim 1; Fig 1; 22pp; English.  
 XX The present sequence represents a human G-protein chemokine receptor  
 XX designated HDGNR10. HDGNR10 polynucleotides are useful in methods of  
 XX screening for compounds which bind to and either: (1) activate the  
 XX HDGNR10 polypeptides causing stimulation of haematopoiesis, wound  
 XX healing, coagulation, and angiogenesis; treatment of solid tumours,  
 XX chronic infections, leukaemia, T-cell mediated autoimmune diseases,  
 XX parasitic infections, psoriasis, and to stimulate growth factor activity;  
 XX or (2) inhibit activation of the HDGNR10 polypeptides which is useful for  
 XX preventing and/or treating allergy, atherosclerosis, anaphylaxis,  
 XX E-mediated allergic reactions, prostaglandin-independent fever, bone  
 XX marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and  
 XX hyper-eosinophilia syndrome. The polynucleotides are also useful for  
 XX diagnostic assays for detecting diseases related to mutations in the  
 XX nucleic acid sequences encoding the polypeptides and for detecting an  
 XX altered level of the soluble form of the receptor polypeptides. The  
 XX polynucleotides are also useful for in vitro purposes related to  
 XX scientific research, synthesis of DNA and manufacture of DNA vectors

XX SQ Sequence 352 AA;  
 Query Match 100.0%; Score 118; DB 3; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22  
 |||||  
 Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 12  
 AAG79089  
 ID AAG79089 standard; protein; 352 AA.  
 XX AAG79089;  
 XX 10-DEC-2001 (first entry)  
 XX Amino acid sequence of human CCR5 protein.  
 XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;  
 XX C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.  
 XX Homo sapiens.  
 XX WO200164752-A2.  
 XX 07-SEP-2001.  
 XX 28-FEB-2001; 2001WO-US006322.  
 XX 02-MAR-2000; 2000US-00517605.  
 XX (UZYNY ) UNIV NEW YORK STATE.  
 XX (UTNI-) UNIV NIJMEGEN.

PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;  
 XX WPI; 2001-602565/68.  
 XX  
 PT An antibody for the treatment or prevention of HIV-infection comprises a  
 PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of  
 FT DC-SIGN due to concomitant conformational change.  
 XX  
 PS Disclosure; Page 118-119; 131pp; English.  
 XX  
 CC The specification describes an antibody which is specific for an  
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or  
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant  
 CC conformational change. DC-SIGN is a receptor that is specifically  
 CC expressed on dendritic cells and facilitates infection of T lymphocytes  
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC  
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)  
 CC with high affinity. The antibody of the invention inhibits the trans  
 CC enhancement of HIV entry into a T cell or macrophage facilitated by  
 CC dendritic cells. The antibody is useful to treat or prevent HIV  
 CC infection. The present sequence represents a human CCR5 protein, which is  
 CC a translocation promoting agent that interacts with CD4. This receptor  
 CC functions in HIV-1 entry into cells  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 118; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYIVILLNTFOEFFGLNCS 22  
 DB 249 APYIVILLNTFOEFFGLNCS 270  
 RESULT 13  
 AAE07046  
 ID AAE07046 standard; protein; 352 AA.  
 AC AAE07046;  
 XX  
 XX 16-OCT-2001 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.  
 XX  
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;  
 KW cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..36  
 FT /label= Extracellular\_domain  
 FT 37..305  
 FT /label= Transmembrane\_domain  
 FT 37..58  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 1"  
 FT 59..67  
 FT /label= Intracellular\_loop\_1  
 FT 68..88  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 2"  
 FT 89..102  
 FT /label= Extracellular\_loop\_1  
 FT 103..124

FT /label= Transmembrane\_domain  
 FT 125..141  
 FT /note= "Segment 3"  
 FT /label= Intracellular\_loop\_2  
 FT 142..166  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 4"  
 FT 167..195  
 FT /label= Extracellular\_loop\_2  
 FT 196..223  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 5"  
 FT 224..235  
 FT /label= Intracellular\_loop\_3  
 FT 236..260  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 6"  
 FT 261..274  
 FT /label= Extracellular\_loop\_3  
 FT 287..305  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 7"  
 FT 306..352  
 FT /label= Intracellular\_domain  
 FT XX  
 PN WO200158916-A2.  
 XX  
 XX 16-AUG-2001.  
 PD  
 XX  
 PF 09-FEB-2001; 2001WO-US004153.  
 XX  
 PR 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187939P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX  
 XX WPI; 2001-488966/53.  
 DR N-PSDB; AND13282.  
 DR  
 XX  
 XX  
 FT Isolated nucleic acid encoding a human G-protein chemokine receptor  
 FT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
 FT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 FT neurodegenerative disorders.  
 FT  
 PS Claim 102; Fig 1; 518pp; English.  
 CC The invention relates to human G-protein chemokine receptor (CCR5)  
 CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are  
 CC useful for treating, preventing or ameliorating a disease or disorder  
 CC associated with inflammation, defective or aberrant chemotaxis of immune  
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's  
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell  
 CC interaction. The disease or disorder may also be an infectious disease  
 CC (e.g. a viral infection such as an early stage HIV infection, a  
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune  
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The  
 CC disease or disorder may be associated with aberrant CCR5 expression, lack  
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand  
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative  
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful  
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,  
 CC protein, antibodies, agonists and antagonists are also useful in the  
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal  
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,  
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)  
 CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The  
 CC present sequence is human CCR5 HDGNR10 protein  
 XX



SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQFFGLNCS 22  
|||||  
Db 249 APYNIIVLLNTFQFFGLNCS 270

RESULT 14

AAE07048  
ID AAE07048 standard; protein; 352 AA.

XX  
AC AAE07048;

DT 16-OCT-2001 (first entry)

DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.

XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerability;  
KW cytostatic; immunosuppressive; neutropenic; neuroprotective; gene therapy;  
KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
KW cardiovascular disorder; myocardial ischaemia.

XX Homo sapiens.

XX WO200158916-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004153.

XX 09-FEB-2000; 2000US-0181258P.

XX 09-MAR-2000; 2000US-0187999P.

XX 22-SEP-2000; 2000US-0234336P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Roschke V, Li Y, Ruben SM;

XX WPI; 2001-488966/53.

XX N-PSDB; AAD13299.

XX Isolated nucleic acid encoding a human G-protein chemokine receptor

XX (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune

XX diseases e.g. rheumatoid arthritis, hyperproliferative disorders and

XX neurodegenerative disorders.

XX Example 40; Page 504-505; 518pp; English.

XX The invention relates to human G-protein chemokine receptor (CCR5)  
CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are  
CC useful for treating, preventing or ameliorating a disease or disorder  
CC associated with inflammation, defective or aberrant chemotaxis of immune  
CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's  
CC sarcoma) or defective or aberrant T-cell antigen presenting cell  
CC interaction. The disease or disorder may also be an infectious disease  
CC (e.g. a viral infection such as an early stage HIV infection, a  
CC cytomegalovirus infection, or a poxvirus infection), an autoimmune  
CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The  
CC disease or disorder may be associated with aberrant CCR5 expression, lack  
CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand  
CC function. CCR5 HDGNR10 protein is used as a food additive or preservative  
CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful  
CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA,  
CC protein, antibodies, agonists and antagonists are also useful in the

CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal  
CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,  
CC urogenital); immune disorders (Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)  
CC ; cardiovascular disorders (myocardial ischaemia) and wound healing. The  
CC present sequence is human CCR5 HDGNR10 protein

XX Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQFFGLNCS 22  
|||||

Db 249 APYNIIVLLNTFQFFGLNCS 270

RESULT 15

AAG80111

ID AAG80111 standard; protein; 352 AA.

XX  
AC AAG80111;

DT 17-JAN-2002 (first entry)

DE Human CCR5 protein.

XX Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
KW antirheumatic; antiarthritic.

XX Homo sapiens.

XX WO200172830-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-EP003708.

XX 31-MAR-2000; 2000DE-01016013.

XX (IPEP-) IPF PHARM GMEH.

XX (FORS/) FORSMANN U.

XX Forssmann W, Adermann K, Heitland A, Spotsberg N;

XX WPI; 2001-626256/72.

XX Diagnostic agent containing two or more receptor-specific ligands, useful  
XX for detecting tumors, inflammation etc., also therapeutic use of ligand  
XX inhibitors.

XX Disclosure; Page 10; 26pp; German.

XX This invention describes a novel diagnostic agent (A) comprising at least  
CC two different ligands (I) for receptors (II) that are implicated in  
CC disease. (A) are used for the diagnosis of tumors (especially colorectal  
CC or prostatic), organ rejection, inflammation and autoimmune diseases.  
CC Also inhibitors of (I) are used therapeutically against tumors (and their  
CC metastases), inflammation (particularly bronchial asthma or chronic bowel  
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
CC endocrine, motor or urogenital systems or skin are affected, and bone  
CC marrow diseases. The products of the invention are chemokine derivatives  
CC which have cytostatic, antiinflammatory, antirheumatic, antiarthritic.  
CC immunosuppressive, dermatological, antitumor, antiproliferative  
CC Chemokines act on specific tumor and inflammatory cells through a  
CC constellations of chemokine receptors (CR), which control migration and  
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine

CC fragments used to illustrate the method of the invention

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQEPFFGLNCS 22  
 DB 249 APYNVILLNTQEPFFGLNCS 270

RESULT 16  
 AAE04321  
 ID AAE04321 standard; protein; 352 AA.  
 XX  
 AC AAE04321;  
 XX  
 DT 04-SEP-2001 (first entry)  
 XX  
 DE Human chemokine receptor (CCR), CC-CR-5 related protein #2.  
 XX  
 KW Human; transformed mammalian cell; CD4; reporter gene; translocation;  
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;  
 KW Chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;  
 KW CC-CR-5; envelope glycoprotein; anti-HIV.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6258527-B1.  
 XX  
 PD 10-JUL-2001.  
 XX  
 PF 21-MAY-1997; 97US-00861105.  
 XX  
 PR 20-MAY-1996; 96US-0017157P.  
 PR 19-JUN-1996; 96US-0030043P.  
 PR 19-MAY-1997; 97US-00858660.  
 XX  
 PA (AARO-) AARON DIAMOND AIDS RES CENT.  
 PA (UUNY ) UNIV NEW YORK STATE.  
 XX  
 PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;  
 XX  
 DR WPI; 2001-417127/44.  
 DR N-PSDB; RAD08577.  
 XX  
 PT Transformed mammalian cell (I) that contains a CD4 gene, reporter gene  
 PT and HIV LTR for identification of drugs and antibodies for treatment of  
 PT HIV.  
 XX  
 PS Disclosure; Col 47-50; 37pp; English.  
 XX  
 CC The present invention relates to a transformed mammalian cell that  
 CC contains a gene encoding CD4, a construct encoding a reporter gene under  
 CC the regulation of an human immuno deficiency virus (HIV) long terminal  
 CC repeat (LTR) and that has been transduced with a vector encoding a human  
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the  
 CC cell surface of transformed mammalian cell. The invention is useful for  
 CC identifying drugs or antibodies that interfere with the translocation of  
 CC HIV into transformed mammalian cell or for identifying a human chemokine  
 CC receptor that facilitates the infection of a particular HIV strain into  
 CC the transformed mammalian cell. Compounds identified can be used to treat  
 CC cellular dysfunction and to prevent or combat HIV infection. The present  
 CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.  
 CC CC-CR-5 is the principal cofactor for entry mediated by the envelope  
 CC glycoproteins of primary macrophage-tropic strains of HIV-1  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQEPFFGLNCS 22  
 DB 249 APYNVILLNTQEPFFGLNCS 270

RESULT 17  
 AAE07037  
 ID AAE07037 standard; protein; 352 AA.  
 XX  
 AC AAE07037;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCRS) HDGMR10 protein #1.  
 XX  
 KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnary;  
 KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Domain  
 FT 1. .36  
 FT /label= Extracellular\_domain  
 FT Domain  
 FT 37. .305  
 FT /label= Transmembrane\_domain  
 FT Domain  
 FT 37. .58  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 1"  
 FT Domain  
 FT 59. .67  
 FT /label= Intracellular\_loop\_1  
 FT Domain  
 FT 68. .88  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 2"  
 FT Domain  
 FT 89. .102  
 FT /label= Extracellular\_loop\_1  
 FT Domain  
 FT 103. .124  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 3"  
 FT Domain  
 FT 125. .141  
 FT /label= Intracellular\_loop\_2  
 FT Domain  
 FT 142. .166  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 4"  
 FT Domain  
 FT 167. .195  
 FT /label= Extracellular\_loop\_2  
 FT Domain  
 FT 196. .223  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 5"  
 FT Domain  
 FT 224. .235  
 FT /label= Intracellular\_loop\_3  
 FT Domain  
 FT 236. .260  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 6"  
 FT Domain  
 FT 261. .274  
 FT /label= Extracellular\_loop\_3  
 FT Domain  
 FT 287. .305  
 FT /label= Transmembrane\_domain  
 FT /note= "Segment 7"  
 FT Domain  
 FT 306. .352  
 FT /label= Intracellular\_domain  
 XX  
 PN WO200158915-A2.  
 XX  
 PD 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004152.  
 XX  
 XX 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 PI WPI; 2001-488965/53.  
 XX DR N-PSDB; AAD13181.  
 XX  
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor  
 PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune  
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 PT neurodegenerative disorders.  
 XX  
 XX Claim 102; Fig 1; 495pp; English.  
 PS  
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10  
 CC protein. CCR5 HDGMR10 cDNA is included in ATCC Deposit No: 97183. CCR5  
 CC HDGMR10 antibodies are useful for treating, preventing or ameliorating a  
 CC disease or disorder associated with inflammation, defective or aberrant  
 CC chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii  
 CC pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen  
 CC presenting cell interaction. The disease or disorder may also be an  
 CC infectious disease (e.g. a viral infection such as an early stage HIV  
 CC infection, a cytomegalovirus infection, or a poxvirus infection), an  
 CC autoimmune disease (e.g. rheumatoid arthritis) or a neurodegenerative  
 CC disorder. The disease or disorder may be associated with aberrant CCR5  
 CC expression, lack of CCR5 function, aberrant CCR5 ligand expression, or  
 CC lack of CCR5 ligand function. CCR5 HDGMR10 protein is used as a food  
 CC additive or preservative to increase or decrease storage capabilities.  
 CC CCR5 HDGMR10 DNA are useful for chromosome identification and in gene  
 CC therapy. CCR5 HDGMR10 DNA, protein, antibodies, agonists and antagonists  
 CC are also useful in the diagnosis, treatment and prevention of cancer  
 CC (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,  
 CC liver, lung, urogenital); immune disorders (Addison's disease, allergies,  
 CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
 CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 CC colitis); cardiovascular disorders (myocardial ischaemias) and wound  
 CC healing  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 118; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYNVLLNTFFQFFGLNCS 22  
 |||||  
 DB 249 APYNVLLNTFFQFFGLNCS 270  
 RESULT 18  
 AAEE07039  
 ID AAEE07039 standard; protein; 352 AA.  
 XX  
 AC AAEE07039;  
 XX  
 XX 16-OCT-2001 (first entry)  
 DT  
 XX Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.  
 DE  
 XX Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;  
 KW cytosolic; immunosuppressive; nontropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;

KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.  
 OS Homo sapiens.  
 XX WO200158915-A2.  
 XX  
 XX 16-AUG-2001.  
 XX  
 XX 09-FEB-2001; 2001WO-US004152.  
 PF  
 XX 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 PI WPI; 2001-488965/53.  
 XX DR N-PSDB; AAD13198.  
 XX  
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor  
 PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune  
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 PT neurodegenerative disorders.  
 XX  
 XX Example 40; Page 486-487; 495pp; English.  
 PS  
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGMR10  
 CC protein. CCR5 HDGMR10 antibodies are useful for treating, preventing or  
 CC ameliorating a disease or disorder associated with inflammation,  
 CC defective or aberrant chemotaxis of immune cells, HIV infection (such as  
 CC Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or  
 CC aberrant T-cell antigen presenting cell interaction. The disease or  
 CC disorder may also be an infectious disease (e.g. a viral infection such  
 CC as an early stage HIV infection, a cytomegalovirus infection, or a  
 CC neurodegenerative disorder). The disease or disorder may be associated  
 CC with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5  
 CC ligand expression, or lack of CCR5 ligand function. CCR5 HDGMR10 protein  
 CC is used as a food additive or preservative to increase or decrease  
 CC storage capabilities. CCR5 HDGMR10 DNA are useful for chromosome  
 CC identification and in gene therapy. CCR5 HDGMR10 DNA, protein,  
 CC antibodies, agonists and antagonists are also useful in the diagnosis,  
 CC treatment and prevention of cancer (breast, ovary, adrenal gland, bone,  
 CC bone marrow, gastrointestinal tract, liver, lung, urogenital); immune  
 CC disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,  
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple  
 CC sclerosis, rheumatoid arthritis and ulcerative colitis); cardiovascular  
 CC disorders (myocardial ischaemias) and wound healing  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 118; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYNVLLNTFFQFFGLNCS 22  
 |||||  
 DB 249 APYNVLLNTFFQFFGLNCS 270  
 RESULT 19  
 AAB46858  
 ID AAB46858 standard; protein; 352 AA.  
 XX  
 AC AAB46858;  
 XX  
 XX 16-AUG-2001 (revised)  
 DT 02-AUG-2001 (revised)  
 DT 04-MAY-2001 (first entry)  
 XX

DE XX Human HDGMR10 protein.

KW HDGMR10; human; G-protein chemokine receptor; antiinflammatory;  
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;  
 KW cytosolic; antiparasitic; antipsoriasis; antirheumatic; antiarthritic;  
 KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;  
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;  
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;  
 KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;  
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;  
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;  
 KW hyper-eosinophilic syndrome; vulnery.

XX OS Homo sapiens.

XX PN US200100241-A1.

XX PD 12-APR-2001.

XX PF 29-NOV-2000; 2000US-00725285.

XX PR 06-JUN-1995; 95US-00466343.

XX PR 18-NOV-1998; 98US-00195662.

XX PR 25-JUN-1999; 99US-00339912.

XX PA (LIYY// LI Y.

XX PA (RUBE// RUBEN S M.

XX PI Li Y, Ruben SM;

XX PT WPI; 2001-226317/23.

XX DR N-PSDB; AAF26390.

XX PS New human G-protein chemokine receptor polypeptides and polynucleotides,  
 PT useful for identifying (ant)agonists to the G-protein chemokine receptor.

XX PS Claim 1a; Page 15; 22pp; English.

CC This invention describes a novel receptor polypeptide (I) selected from  
 CC (i) a fully defined 329 amino acid sequence (ii) fully disclosed in the  
 CC specification; and (iii) a polypeptide encoded by the cDNA contained in a  
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The  
 CC products of the invention have antiinflammatory, immunomodulatory,  
 CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytosolic,  
 CC antiparasitic, antipsoriasis, antirheumatic, antiarthritic and vasotropic  
 CC activity and can be used for gene therapy. The G-protein chemokine  
 CC receptors HDGMR10, (I) are useful for screening for compounds which  
 CC activate or inhibit activation of (I). The products of the invention can  
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,  
 CC angiogenesis, treating solid tumours, chronic infections, leukemia, T-  
 CC cell mediated autoimmune diseases, parasitic infections, psoriasis, and  
 CC stimulating growth factor activity. HDGMR10 is useful for treating  
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic  
 CC reactions, prostaglandin-independent fever, bone marrow failure,  
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-  
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct  
 CC errors in the keyword formatting)

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNVILLNTQEFFGLNCS 22  
 |||||

Db 249 APYNVILLNTQEFFGLNCS 270  
 |||||

RESULT 21  
 AAB56342  
 ID AAB56342 standard; protein; 352 AA.

XX AC AAB56342;

XX DT 09-OCT-2001 (first entry)

XX DE Human CCR5 protein sequence.

XX KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;  
 KW human immunodeficiency virus; anti-inflammatory disease; human.

XX OS Homo sapiens.

XX PN EP1118858-A2.

XX PD 25-JUL-2001.

XX PF 03-JAN-2001; 2001EP-00300020.

XX AC ABB56342;

XX DT 18-FEB-2002 (first entry)

XX DE Non-endogenous human GPCR protein, SEQ ID NO: 477.

XX KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;  
 KW constitutively activated GPCR; agonist; disease.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200177172-A2.

XX PD 18-OCT-2001.

XX PF 05-APR-2001; 2001WO-US011098.

XX PR 07-APR-2000; 2000US-0195747P.

XX PA (AREN-) ARENA PHARM INC.

XX PI Lehmann-Bruinsma K, Liaw CW, Lin I;

XX DR WPI; 2001-648759/74.

XX DR N-PSDB; ABI97978.

XX PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in  
 PT disease treatment, comprises contacting candidate compounds with versions  
 PT of GPCRs.

XX PS Claim 1; Page 277-278; 394pp; English.

CC The invention relates to G protein-coupled receptors (GPCRs) for which  
 CC the endogenous ligand has been identified. Non-endogenous constitutively  
 CC activated versions of known GPCRs are used in the invention for the  
 CC direct identification of candidate compounds as receptor agonists,  
 CC inverse agonists or partial agonists. Such agonists are useful as  
 CC therapeutic agents for diseases or disorders associated with GPCRs. The  
 CC present sequence is a non-endogenous version of a known human GPCR

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 118; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. NO. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNVILLNTQEFFGLNCS 22  
 |||||

Db 249 APYNVILLNTQEFFGLNCS 270  
 |||||

RESULT 21  
 AAB56342  
 ID AAB56342 standard; protein; 352 AA.

XX AC AAB56342;

XX DT 09-OCT-2001 (first entry)

XX DE Human CCR5 protein sequence.

XX KW Chemotactic chemokine receptor 5; gp120; CD4; therapy; HIV; CCR5;  
 KW human immunodeficiency virus; anti-inflammatory disease; human.

XX OS Homo sapiens.

XX PN EP1118858-A2.

XX PD 25-JUL-2001.

XX PF 03-JAN-2001; 2001EP-00300020.

XX 12-JAN-2000; 2000GB-00000659.  
 PR 12-JAN-2000; 2000GB-00000661.  
 PR 12-JAN-2000; 2000GB-00000663.  
 XX (PF1Z ) PFIZER LTD.  
 PA (PF1Z ) PFIZER INC.  
 XX Dobbs S, Perros M, Rickett GA;  
 PI WPI; 2001-477088/52.  
 XX N-PSDB; AAF87099.  
 DR  
 DR  
 XX Determining if an agent can modulate CCR5-gp120 interaction, comprises  
 PT incubating the agent with CCR5 and gp120 and determining if the agent  
 PT modulates the interaction.  
 PT  
 XX Claim 1; Page 110; 113pp; English.  
 PS  
 XX This sequence represents the human CCR5 protein sequence. The invention  
 CC relates to a method for determining whether an agent is capable of  
 CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)  
 CC with gp120, comprising incubating the agent with CCR5 and gp120 and  
 CC determining whether the agent modulates the interaction, where gp120 is  
 CC associated with CD4, and where the interaction is a low affinity binding.  
 CC The method is used to identify an agent capable of modulating the  
 CC interaction of CCR5 with gp120. An agent identified by the method is used  
 CC to prepare a pharmaceutical composition for the treatment of a disease or  
 CC with a disease or condition associated with CCR5 and gp120 interaction,  
 CC and for preparing a pharmaceutical for treating human immunodeficiency  
 CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method  
 CC is commercially useful, amenable to high throughput screening, and  
 CC detects interaction of gp120 with cells expressing only CCR5  
 CC  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 118; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYIVLLNTTQFFGLNCS 22  
 DB 249 APYIVLLNTTQFFGLNCS 270  
 RESULT 22  
 AAB82948  
 ID AAB82948 standard; protein; 352 AA.  
 XX AC AAB82948;  
 XX 21-DEC-2001 (first entry)  
 DT  
 DE Human HIV-1 co-receptor CCR5.  
 XX CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;  
 KW infection; therapy; vaccine; anti-HIV-1.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Binding-site 2..18  
 FT /note= "binds to HIV-1 gp120"  
 XX  
 PN WC200164710-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 XX 28-FEB-2001; 2001WO-US006699.  
 PF  
 PF 29-FEB-2000; 2000US-0185667P.  
 PR 19-MAY-2000; 2000US-0205839P.  
 PR

PR 07-FEB-2001; 2001US-0267231P.  
 XX (PROG-) PROGENICS PHARM INC.  
 PA (AARO-) AARON DIAMOND AIDS RES CENT.  
 XX Dragic T, Olson WC;  
 DR WPI; 2001-611273/70.  
 DR N-PSDB; AAH26903.  
 XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-  
 PT receptor) amino terminal domain including negatively charged and two  
 PT sulfated tyrosine residues is useful for treating HIV infection in  
 PT humans.  
 XX  
 PS Claim 1; Page 30; 163pp; English.  
 XX  
 XX The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids  
 CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding  
 CC site that determines the specificity of the interaction between CCR5 and  
 CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the  
 CC CCR5 N-terminus is required for gp120 binding and may critically modulate  
 CC the susceptibility of target cells to HIV-1 infection in vivo. The  
 CC invention provides claimed sulfated peptides (see AAB82947) that are  
 CC based on the CCR5 N-terminal region and which are effective for  
 CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed  
 CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+  
 CC cells from becoming infected with HIV, of treating a subject whose CD4+  
 CC cells are infected with HIV, and of identifying an agent which inhibits  
 CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried  
 CC out in a subject, especially a human, infected (therapeutic method), not  
 CC infected with HIV (prophylactic method), or in a subject who is not  
 CC infected with, but has been exposed to, HIV  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 118; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYIVLLNTTQFFGLNCS 22  
 DB 249 APYIVLLNTTQFFGLNCS 270  
 RESULT 23  
 AAU97150  
 ID AAU97150 standard; protein; 352 AA.  
 XX AC AAU97150;  
 XX 13-AUG-2002 (first entry)  
 DT  
 DE Human G-protein chemokine receptor (CCR5) HDGNR10 #1.  
 XX  
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;  
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;  
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;  
 KW hyperproliferative disease; neurological disease; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2002048786-A1.  
 XX  
 PD 25-APR-2002.  
 XX  
 XX 09-FEB-2001; 2001US-00779879.  
 PF  
 XX 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 PR  
 PA (ROSE/) ROSEN C A.

PA (ROSC/) ROSCHKE V.  
 PA (LIYY/) LI Y.  
 PA (RUBE/) RUBEN S M.  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX WPI; 2002-434754/46.  
 DR N-PSDB; ABK51853.  
 XX  
 XX New nucleic acid encoding an antibody specific for the G-protein  
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.  
 PT inflammation.  
 XX  
 PS Claim 61; Fig 1; 180pp; English.  
 XX  
 CC The present invention relates to the isolation of a novel human G-protein  
 CC chemokine receptor (CCR5) designated HDGMR10, and polynucleotide  
 CC sequences encoding it. The invention also describes antibodies that bind  
 CC human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide  
 CC sequences encoding the antibodies. The antibodies are useful for treating  
 CC or preventing inflammation, defective or aberrant chemotaxis of immune  
 CC cells and T-cell/antigen-presenting cell interactions, infections and  
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral  
 CC infections (especially early-stage human immune deficiency virus (HIV),  
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions  
 CC associated with aberrant or deficient expression of the CCR5 receptor or  
 CC its ligands. The antibodies are also useful to determine CCR5 expression,  
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other  
 CC hyperproliferative diseases. The polynucleotide sequences encoding human  
 CC G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the  
 CC recombinant receptor, and in the treatment of a wide range of diseases  
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.  
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The  
 CC present sequence represents human G-protein chemokine receptor (CCR5)  
 CC HDGMR10 #1  
 CC  
 XX Sequence 352 AA;  
 XX  
 Query Match 100.0%; Score 118; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYNVILLNTFQFFGLNCS 22  
 |||||  
 Db 249 APYNVILLNTFQFFGLNCS 270  
 |||||  
 RESULT 24  
 AAU97152  
 ID AAU97152 standard; protein; 352 AA.  
 XX  
 AC AAU97152;  
 XX  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5) HDGMR10 #2.  
 XX  
 XX Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation;  
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;  
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;  
 KW hyperproliferative disease; neurological disease; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002048786-A1.  
 PN  
 XX  
 XX 25-APR-2002.  
 PD  
 XX  
 XX 09-FEB-2001; 2001US-00779879.  
 PF  
 XX  
 XX 09-FEB-2000; 2000US-0181258P.  
 PR  
 XX 09-MAR-2000; 2000US-0187999P.  
 PR  
 XX 22-SEP-2000; 2000US-0234336P.  
 PR

XX (ROSC/) ROSEN C A.  
 PA (ROSC/) ROSCHKE V.  
 PA (LIYY/) LI Y.  
 PA (RUBE/) RUBEN S M.  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX WPI; 2002-434754/46.  
 DR N-PSDB; ABK51870.  
 XX  
 XX New nucleic acid encoding an antibody specific for the G-protein  
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.  
 PT inflammation.  
 XX  
 PS Disclosure; Page 165-166; 180pp; English.  
 XX  
 CC The present invention relates to the isolation of a novel human G-protein  
 CC chemokine receptor (CCR5) designated HDGMR10, and polynucleotide  
 CC sequences encoding it. The invention also describes antibodies that bind  
 CC human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide  
 CC sequences encoding the antibodies. The antibodies are useful for treating  
 CC or preventing inflammation, defective or aberrant chemotaxis of immune  
 CC cells and T-cell/antigen-presenting cell interactions, infections and  
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral  
 CC infections (especially early-stage human immune deficiency virus (HIV),  
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions  
 CC associated with aberrant or deficient expression of the CCR5 receptor or  
 CC its ligands. The antibodies are also useful to determine CCR5 expression,  
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other  
 CC hyperproliferative diseases. The polynucleotide sequences encoding human  
 CC G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the  
 CC recombinant receptor, and in the treatment of a wide range of diseases  
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.  
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The  
 CC present sequence represents human G-protein chemokine receptor (CCR5)  
 CC HDGMR10 #2  
 CC  
 XX Sequence 352 AA;  
 XX  
 Query Match 100.0%; Score 118; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYNVILLNTFQFFGLNCS 22  
 |||||  
 Db 249 APYNVILLNTFQFFGLNCS 270  
 |||||  
 RESULT 25  
 AAMS2829  
 ID AAMS2829 standard; protein; 352 AA.  
 XX  
 AC AAMS2829;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Human CCR5 Gln 55 variant.  
 XX  
 XX CCR5; CC chemokine receptor 5; human; HIV infection;  
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
 KW drug screening; identification; variant.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 55 /note= "Glu replaces wild-type Leu; encoded by CTG"  
 FT Misc-difference 58 /note= "Encoded by AGC"  
 FT  
 XX WC200171346-A2.  
 XX

PD 27-SEP-2001.  
 XX 21-MAR-2001; 2001WO-US009155.  
 XX 21-MAR-2000; 2000US-0190946P.  
 PR 21-MAR-2000; 2000US-0190996P.  
 PR 21-MAR-2000; 2000US-0191299P.  
 PR 20-MAR-2001; 2001US-00813448.  
 PR 20-MAR-2001; 2001US-00813651.  
 PR 20-MAR-2001; 2001US-00813653.  
 XX (CONS-) CONSENSUS PHARM INC.  
 PA Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;  
 XX WPI; 2002-010610/01.  
 XX N-PSDB; ABA02318.  
 DR Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
 PT comprises binding a molecule from library to a molecule having binding  
 PT property corresponding to CCR5 and identifying bound molecule.  
 XX Example 3; Fig 4B; 50pp; English.  
 PS The invention relates to a method for identifying a binding compound for  
 CC CC chemokine receptor 5 (CCR5). The method involves screening a library  
 CC of test molecules (particularly peptides) with immobilised CCR5, and then  
 CC identifying those molecules which bind. The invention also relates to  
 CC CCR5-binding molecules identified using the method of the invention,  
 CC methods for identifying consensus motifs for CCR5-binding peptides, a  
 CC transfer vector encoding tagged CCR5, a computer-aided methods for  
 CC determining the relative binding affinity of a test molecule to CCR5 and  
 CC a computer aided drug screening assay that utilises the three-dimensional  
 CC structure of CCR5. Compounds identified using the methods of the  
 CC invention are useful for treating or preventing HIV (human  
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency  
 CC syndrome) in a patient. The methods of the invention may also be used to  
 CC identify agonists or antagonists of the interaction of CCR5 with its  
 CC natural ligand, and to determine a binding motif for CCR5. The present  
 CC sequence represents a naturally occurring variant of human CCR5 in which  
 CC there is a glutamine, rather than a leucine, at position 55  
 XX Sequence 352 AA;  
 SQ Query Match 100.0%; Score 118; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYNIVLLNTFOEFFGLNCS 22  
 DB 249 APYNIVLLNTFOEFFGLNCS 270  
 RESULT 26  
 ID AAM52828  
 AC AAM52828 standard; protein; 352 AA.  
 AC AAM52828;  
 XX 22-FEB-2002 (first entry)  
 DE Human CC chemokine receptor 5 (CCR5).  
 XX CCR5; CC chemokine receptor 5; human; HIV infection;  
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
 KW drug screening; identification.  
 XX Homo sapiens.  
 OS WC200171346-A2.  
 PN 27-SEP-2001.  
 PD 27-SEP-2001.  
 XX

PF 21-MAR-2001; 2001WO-US009155.  
 XX 21-MAR-2000; 2000US-0190946P.  
 PR 21-MAR-2000; 2000US-0190996P.  
 PR 21-MAR-2000; 2000US-0191299P.  
 PR 20-MAR-2001; 2001US-00813448.  
 PR 20-MAR-2001; 2001US-00813651.  
 PR 20-MAR-2001; 2001US-00813653.  
 XX (CONS-) CONSENSUS PHARM INC.  
 PA Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;  
 XX WPI; 2002-010610/01.  
 XX N-PSDB; ABA02317.  
 DR Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
 PT comprises binding a molecule from library to a molecule having binding  
 PT property corresponding to CCR5 and identifying bound molecule.  
 XX Example 3; Fig 4A; 50pp; English.  
 PS The invention relates to a method for identifying a binding compound for  
 CC CC chemokine receptor 5 (CCR5). The method involves screening a library  
 CC of test molecules (particularly peptides) with immobilised CCR5, and then  
 CC identifying those molecules which bind. The invention also relates to  
 CC CCR5-binding molecules identified using the method of the invention,  
 CC methods for identifying consensus motifs for CCR5-binding peptides, a  
 CC transfer vector encoding tagged CCR5, a computer-aided methods for  
 CC determining the relative binding affinity of a test molecule to CCR5 and  
 CC a computer aided drug screening assay that utilises the three-dimensional  
 CC structure of CCR5. Compounds identified using the methods of the  
 CC invention are useful for treating or preventing HIV (human  
 CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency  
 CC syndrome) in a patient. The methods of the invention may also be used to  
 CC identify agonists or antagonists of the interaction of CCR5 with its  
 CC natural ligand, and to determine a binding motif for CCR5. The present  
 CC sequence represents human CCR5  
 XX Sequence 352 AA;  
 SQ Query Match 100.0%; Score 118; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYNIVLLNTFOEFFGLNCS 22  
 DB 249 APYNIVLLNTFOEFFGLNCS 270  
 RESULT 27  
 ID ABG70597  
 AC ABG70597 standard; protein; 352 AA.  
 AC ABG70597;  
 XX 03-DEC-2002 (first entry)  
 DE Human G-protein chemokine receptor, HDGNR10.  
 XX Human; G-protein chemokine receptor; HDGNR10; CCR5 receptor;  
 KW haematopoiesis; wound healing; coagulation; angiogenesis; solid tumour;  
 KW chronic infection; leukaemia; T-cell mediated autoimmune disease;  
 KW parasitic infection; psoriasis; growth factor activity; allergy;  
 KW atherogenesis; anaphylaxis; malignancy; inflammation; histamine;  
 KW immunoglobulin E; IgE-mediated allergic reaction; sarcoidosis;  
 KW prostaglandin-independent fever; bone marrow failure; shock;  
 KW rheumatoid arthritis; hyper-eosinophilic syndrome; cytostatic;  
 KW immunosuppressive; antiparasitic; antiseptics; antiallergic;  
 KW antiarteriosclerotic; antiinflammatory; antirheumatic; antiarthritic;  
 KW antipyretic; receptor.  
 XX Homo sapiens.  
 OS

XX US2002099176-A1.  
XX 25-JUL-2002.  
XX 25-JUN-1999; 99US-00339912.  
XX 06-JUN-1995; 95US-00466343.  
XX (LIYY//) LI Y.  
XX (RUEB//) RUBEN S M.  
XX Li Y, Ruben SM;  
XX WPI; 2002-690494/74.  
XX N-PSDB; ABS54272.  
XX Novel human G-protein chemokine receptor polypeptide useful for  
XX identifying modulators for stimulating hematopoiesis, wound healing,  
XX leukemia, for treating allergy, rheumatoid arthritis, shock and as  
XX research agents.  
XX Claim 7; Fig 1; 22pp; English.  
XX The present invention relates to the isolation of human G-protein  
XX chemokine receptor, HDGNR10 (CCR5 receptor), and the polynucleotide  
XX sequence encoding it. HDGNR10 polypeptide and polynucleotide sequences  
XX are useful for diagnosing a disease or a susceptibility to a disease  
XX related to underexpression of HDGNR10. They are useful for identifying  
XX modulators for stimulating hematopoiesis, wound healing, coagulation,  
XX angiogenesis, to treat solid tumors, chronic infections, leukaemia, T-  
XX cell mediated autoimmune diseases, parasitic infections, psoriasis, or  
XX for stimulating growth factor activity. The sequences are also useful for  
XX preventing and/or treating allergy, atherogenesis, anaphylaxis,  
XX malignancy, chronic and acute inflammation, histamine and immunoglobulin  
XX E (IgE)-mediated allergic reactions, prostaglandin-independent fever,  
XX bone marrow failure, sarcoidosis, rheumatoid arthritis, shock and hyper-  
XX eosinophilic syndrome. Polynucleotide sequences encoding HDGNR10 can be  
XX used in gene therapy to treat conditions related to underexpression of  
XX HDGNR10. The present sequence represents human G-protein chemokine  
XX receptor, HDGNR10  
XX Sequence 352 AA;  
Query Match 100.0%; Score 118; DB 5; Length 352;  
Best Local Similarity 100.0%; Pred. NO. 2.9e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYIVILLNTQEFGLNCS 22  
Db 249 APYIVILLNTQEFGLNCS 270  
RESULT 28  
ABG92883  
ID ABG92883 standard; protein; 352 AA.  
XX ABG92883;  
XX 19-NOV-2002 (first entry)  
XX Human immunoglobulin variable heavy domain #1.  
XX Immunoglobulin; variable heavy chain; variable light chain; human;  
XX G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;  
XX immunologic deficiency syndrome; blood protein disorder; nephritis;  
XX ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;  
XX histiocytosis; chemotaxis; infectious disease; autoimmune disease;  
XX Addison's disease; dermatitis; rheumatoid arthritis; allergy;  
XX neurodegenerative disorder; viral infection; poxvirus infection; HIV;  
XX human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;  
XX Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;  
XX lymphocytopenia.

XX Homo sapiens.  
XX OS  
XX WO200264612-A2.  
XX 22-AUG-2002.  
XX 08-FEB-2002; 2002WO-US003634.  
XX 09-FEB-2001; 2001US-00779880.  
XX 09-FEB-2001; 2001WO-US004153.  
XX 12-JUN-2001; 2001US-0297257P.  
XX 08-AUG-2001; 2001US-0310458P.  
XX 12-OCT-2001; 2001US-032847P.  
XX 21-DEC-2001; 2001US-0341725P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Roschke V, Rosen CA, Ruben SM;  
XX N-PSDB; ABS68606.  
XX WPI; 2002-643455/69.  
XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for  
XX treating, preventing, ameliorating or monitoring diseases or disorders  
XX associated with aberrant expression of HDGNR10 e.g. cancer.  
XX Example 55; Fig 4; 562pp; English.  
XX The invention describes an isolated polynucleotide encoding a first  
XX antibody at least 95-100% identical to a second antibody consisting of an  
XX amino acid sequence comprising at least one, two or three CDR regions of  
XX a variable heavy (VH) or variable light (VL) domain of the antibody  
XX expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1B8,  
XX XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9B6, XF27/28.7D5, XF27/28.1B85,  
XX XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody  
XX is useful treating, preventing, ameliorating, prognosing or monitoring  
XX cancers or other diseases or disorders e.g. immunologic deficiency  
XX syndromes such as blood protein disorders and ataxia telangiectasia,  
XX inflammation associated disorders such as endotoxin lethality, nephritis  
XX and inflammatory bowel disease, conditions associated with an increase in  
XX certain haematopoietic cells such as histiocytosis, defective or aberrant  
XX chemotaxis of immune cells or T-cell antigen presenting cell interaction,  
XX an infectious disease, an autoimmune disease such as Addison's disease,  
XX dermatitis and rheumatoid arthritis, allergies, a neurodegenerative  
XX disorder, a viral infection e.g. HIV infection, cytomegalovirus or  
XX poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,  
XX cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a  
XX disease or disorder associated with aberrant expression of novel human G-  
XX protein chemokine receptor (CCR5) HDGNR10. This is the amino acid  
XX sequence of human immunoglobulin sequence associated with the antibodies  
XX against HDGNR10  
XX Sequence 352 AA;  
Query Match 100.0%; Score 118; DB 5; Length 352;  
Best Local Similarity 100.0%; Pred. NO. 2.9e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYIVILLNTQEFGLNCS 22  
Db 249 APYIVILLNTQEFGLNCS 270  
RESULT 29  
ABG92880  
ID ABG92880 standard; protein; 352 AA.  
XX ABG92880;  
XX 19-NOV-2002 (first entry)  
XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.



XX Immunoglobulin; variable heavy chain; variable light chain; human;  
 KW G-protein chemokine receptor; CCR5; HDGNR10; cancer; inflammation;  
 KW immunologic deficiency syndrome; blood protein disorder; nephritis;  
 KW ataxia telangiectasia; endotoxin lethality; inflammatory bowel disease;  
 KW histiocytosis; chemotaxis; infectious disease; autoimmune disease;  
 KW Addison's disease; dermatitis; rheumatoid arthritis; allergies;  
 KW neurodegenerative disorder; viral infection; poxvirus infection; HIV;  
 KW human immunodeficiency virus; cytomegalovirus; Kaposi's sarcoma;  
 KW Pneumocystis carinii infection; cardiovascular disorder; atherosclerosis;  
 KW lymphocytopenia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200264612-A2.  
 XX  
 XX 22-AUG-2002.  
 XX  
 XX 08-FEB-2002; 2002WO-US003634.  
 XX  
 XX 09-FEB-2001; 2001US-00779880.  
 XX  
 XX 09-FEB-2001; 2001WO-US004153.  
 XX  
 XX 12-JUN-2001; 2001US-0297257P.  
 XX  
 XX 08-AUG-2001; 2001US-0310458P.  
 XX  
 XX 12-OCT-2001; 2001US-0310458P.  
 XX  
 XX 21-DEC-2001; 2001US-0341725P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Roschke V, Rosen CA, Ruben SM;  
 XX  
 XX WPI; 2002-643455/69.  
 XX  
 XX N-PSDB; ABS68553.  
 XX  
 XX New human G-protein Chemokine Receptor gene (HDGNR10) useful for  
 PT treating, preventing, ameliorating or monitoring diseases or disorders  
 PT associated with aberrant expression of HDGNR10 e.g. cancer.  
 XX  
 XX Disclosure; Fig 1A-B; 562pp; English.  
 PS  
 XX The invention describes an isolated polynucleotide encoding a first  
 CC antibody at least 95-100% identical to a second antibody consisting of an  
 CC amino acid sequence comprising at least one, two or three CDR regions of  
 CC a variable heavy (VH) or variable light (VL) domain of the antibody  
 CC expressed by a hybridoma cell line consisting of XF3.5F1, XF11.1F8,  
 CC XF3.6A2, XF3.10B8, XF22.3C9.6, XF22.9E6, XF27/28.7D5, XF27/28.18B5,  
 CC XF27/28.25G10, XF27/28.36A12, XF27/28.36F11 or XF27/28.43E2. The antibody  
 CC is useful treating, preventing, ameliorating, prognosing or monitoring  
 CC cancers or other diseases or disorders e.g. immunologic deficiency  
 CC syndromes such as blood protein disorders and ataxia telangiectasia,  
 CC inflammation associated disorders such as endotoxin lethality, nephritis  
 CC and inflammatory bowel disease, conditions associated with an increase in  
 CC certain haematopoietic cells such as histiocytosis, defective or aberrant  
 CC chemotaxis of immune cells or T-cell antigen presenting cell interaction,  
 CC an infectious disease, an autoimmune disease such as Addison's disease,  
 CC dermatitis and rheumatoid arthritis, allergies, a neurodegenerative  
 CC disorder, a viral infection e.g. HIV infection, cytomegalovirus or  
 CC poxvirus infection, a Pneumocystis carinii infection, Kaposi's sarcoma,  
 CC cardiovascular disorders such as atherosclerosis, lymphocytopenias, or a  
 CC disease or disorder associated with aberrant expression of novel human G-  
 CC protein chemokine receptor (CCR5) HDGNR10. This is an amino acid sequence  
 CC of Human G-protein chemokine receptor (CCR5) HDGNR10 #1  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 118; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYNVLLNTFQEFFGLNCS 22  
 DB 249 APYNVLLNTFQEFFGLNCS 270  
 Search completed: March 4, 2004, 17:59:24  
 Job time : 53.3061 secs

RESULT 30  
 AAE25808  
 ID AAE25808 standard; protein; 352 AA.  
 XX  
 AC AAE25808;  
 XX  
 DT 24-FEB-2003 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5), HDGNR10 #1.  
 XX  
 KW Human; G-protein chemokine receptor; CCR5; HDGNR10 protein; cancer;  
 KW inflammation; viral infection; autoimmune disease; neurodegeneration;  
 KW rheumatoid arthritis; Pneumocystis carinii infection; Kaposi's sarcoma;  
 KW hyperproliferative disease; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002061834-A1.  
 XX  
 XX 23-MAY-2002.  
 XX  
 XX 09-FEB-2001; 2001US-00779880.  
 XX  
 XX 09-FEB-2000; 2000US-0181258P.  
 XX  
 XX 09-MAR-2000; 2000US-0187999P.  
 XX  
 XX 22-SEP-2000; 2000US-0234336P.  
 XX  
 XX (ROSE/) ROSEN C A.  
 XX  
 XX (ROSC/) ROSCHKE V.  
 XX  
 XX (LIYY/) LI Y.  
 XX  
 XX (RUBE/) RUBEN S M.  
 XX  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX  
 XX WPI; 2002-499674/53.  
 XX  
 XX N-PSDB; RAD42409.  
 XX  
 XX New nucleic acid encoding antibodies to the human CCR5 receptor HDGNR10,  
 PT useful for treatment, prevention and diagnosis of e.g. cancer, also  
 PT related antibodies.  
 XX  
 XX Claim 61; Page 163-164; 186pp; English.  
 PS  
 CC The invention relates to human G-protein chemokine receptor (CCR5),  
 CC HDGNR10 proteins and nucleic acid molecules encoding such proteins. CCR5  
 CC antibodies are used for the treatment or prevention of inflammation,  
 CC defective or aberrant chemotaxis of immune cells or T cell antigen-  
 CC presenting cell interaction, viral infections (specifically human immune  
 CC deficiency (including its early stages), cytomegalovirus or pox viruses),  
 CC autoimmune disease, rheumatoid arthritis, neurodegeneration, Pneumocystis  
 CC carinii infection, Kaposi's sarcoma or any condition associated with the  
 CC aberrant expression of CCR5 or their ligands. They are also used for the  
 CC detection, diagnosis, prognosis and monitoring of cancers or other  
 CC hyperproliferative diseases. The present sequence is human G-protein  
 CC chemokine receptor (CCR5), HDGNR10 DNA  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 118; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYNVLLNTFQEFFGLNCS 22  
 DB 249 APYNVLLNTFQEFFGLNCS 270  
 Search completed: March 4, 2004, 17:59:24  
 Job time : 53.3061 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 11.2245 Seconds  
(without alignments)  
188.535 Million cell updates/sec

Title: US-10-084-813-14  
Perfect score: 118  
Sequence: 1 APYINVILLNTQFFGLNCS 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 78.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID     | Description         |
|------------|-------|-------------|--------|--------|---------------------|
| 1          | 118   | 100.0       | 352    | A43113 | chemokine (C-C) re  |
| 2          | 103   | 87.3        | 360    | JC2443 | chemokine (C-C) re  |
| 3          | 103   | 87.3        | 374    | I38450 | chemokine (C-C) re  |
| 4          | 70    | 59.3        | 344    | J05942 | chemokine receptor  |
| 5          | 56    | 47.5        | 355    | A45177 | chemokine (C-C) re  |
| 6          | 54.5  | 46.2        | 1075   | T07448 | probable DNA-direc  |
| 7          | 53    | 44.9        | 360    | A57160 | chemokine (C-C) re  |
| 8          | 52    | 44.1        | 355    | G02436 | chemokine (C-C) re  |
| 9          | 52    | 44.1        | 360    | JC4587 | chemokine (C-C) re  |
| 10         | 52    | 44.1        | 383    | S55594 | G protein-coupled   |
| 11         | 52    | 44.1        | 466    | JH0197 | muscarinic acetylch |
| 12         | 52    | 44.1        | 466    | S10126 | muscarinic acetylch |
| 13         | 52    | 44.1        | 466    | S10856 | muscarinic acetylch |
| 14         | 52    | 44.1        | 466    | A27386 | muscarinic acetylch |
| 15         | 51    | 43.2        | 589    | A29476 | muscarinic acetylch |
| 16         | 50    | 42.4        | 490    | A35546 | muscarinic acetylch |
| 17         | 48    | 40.7        | 294    | A29337 | hypothetical prote  |
| 18         | 48    | 40.7        | 300    | H98344 | hypothetical prote  |
| 19         | 48    | 40.7        | 342    | G69502 | histidinol-phospha  |
| 20         | 48    | 40.7        | 359    | I49341 | MIP-1 alpha recept  |
| 21         | 48    | 40.7        | 484    | A48657 | muscarinic acetylch |
| 22         | 48    | 40.7        | 589    | B29514 | muscarinic acetylch |
| 23         | 48    | 40.7        | 590    | S10128 | muscarinic acetylch |
| 24         | 48    | 40.7        | 590    | S01114 | muscarinic acetylch |
| 25         | 48    | 40.7        | 590    | S47572 | muscarinic acetylch |
| 26         | 48    | 40.7        | 639    | A55019 | muscarinic acetylch |
| 27         | 47    | 39.8        | 352    | B69901 | fatty-acid desatur  |
| 28         | 47    | 39.8        | 478    | C29514 | muscarinic acetylch |
| 29         | 47    | 39.8        | 479    | S10127 | muscarinic acetylch |

muscarinic acetylch  
probable sugar tra  
hypothetical prote  
glutamine ABC tran  
macrophage inflam  
G protein-coupled  
G protein-coupled  
hypothetical prote  
DNA-directed RNA p  
hypothetical prote  
probable G protein  
G protein-coupled  
pentamidine resist  
guanylate cyclase-  
guanylate cyclase  
guanylate cyclase-  
hypothetical prote  
NADH dehydrogenase  
muscarinic acetylch  
preprotein translo  
preprotein translo  
histidinol-phospha  
hypothetical prote  
conserved hypotet  
NADH2 dehydrogenas  
MDCR15 protein - h  
G protein-coupled  
neurokinin 2 recep  
neurokinin 2 recep  
CDP-4-keto-6-deoxy  
CDP-4-keto-6-deoxy  
probable CDP-4-ket  
probable dehydrata  
muscarinic acetylch  
muscarinic acetylch  
muscarinic acetylch  
muscarinic acetylch  
muscarinic recepto  
muscarinic acetylch  
muscarinic acetylch  
hypothetical prote  
hypothetical prote  
DNA-directed RNA p  
DNA-directed RNA p  
probable membrane  
YJX protein - Bsc  
hypothetical prote  
hypothetical prote  
sugar transporter-  
lipoxigenase (EC 1  
probable DNA-direc  
probable outer mem  
myosin-2 isoform -  
probable membrane  
gene 9 protein - p  
major facilitator  
hypothetical prote  
hypothetical prote  
protein F17L21.16  
cyclic nucleotide  
hypothetical prote  
cytochrome C oxida  
hypothetical prote  
hypothetical prote  
hypothetical prote  
alcohol dehydrogen  
glutamyl-tRNA redu  
hypothetical prote  
protoporphyrinogen

## ALIGNMENTS

RESULT 1  
A43113  
chemokine (C-C) receptor 5 - human  
N:Alternate names: C-C CKR-5; CCR5  
C:Species: Homo sapiens (man)  
C:Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 20-Jun-2000  
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833  
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
Biochemistry 35, 3362-3367, 1996  
A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
A:Reference number: A43113; MUID:96241590; PMID:8639485  
A:Accession: A43113  
A:Molecule type: mRNA  
A:Residues: 1-352 <SAM1>  
A:Cross-references: GB:X91492; NID:gl262810; PIDN:CAAG2796.1; PID:gl262811  
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liegnard, C.; Farber, C.M.; Saragosti  
M.; Imal, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.  
Nature 382, 722-725, 1996  
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the *CCR5* gene  
A:Reference number: S71808; MUID:96345670; PMID:8751444  
A:Accession: S71808  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 182-206; 207-230 <SAM2>  
A:Accession: A58834  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-184, 'KDSHLCGAPAAACGHHLLGNPKNSASVSK' <SAM3>  
A:Cross-references: GB:X99393; NID:gl524062; PIDN:CAAG67767.1; PID:gl524063  
A>Note: This frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection  
R:Comandeur, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.  
J. Leukoc. Biol. 60, 147-152, 1996  
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor  
A:Reference number: A58832; MUID:96295970; PMID:8699119  
A:Accession: A58832  
A:Molecule type: mRNA  
A:Residues: 1-352 <COM1>  
A:Cross-references: GB:U57840; PIDN:AAAL7071.1; PID:gl502409  
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
R:Comandeur, C.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: H01541  
A:Accession: G02653  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-89, 'L', 91-352 <COM2>  
A:Cross-references: EMBL:U57840  
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
J. Biol. Chem. 271, 17161-17166, 1996  
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor  
A:Reference number: A58833; MUID:96291862; PMID:8663314  
A:Accession: A58833  
A:Molecule type: mRNA  
A:Residues: 1-352 <RAP>  
A:Cross-references: GB:U54994; PIDN:AAAC50598.1; PID:gl457946  
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30574) and dual-tropic strains of HIV-1 bind to a complex of chemokine receptor and MIP-1alpha  
C:Genetics:  
A:Gene: GDB:CMKBR5; CCR5; CC-CKR-5; CCR5; ChemR13  
A:Map position: 3p21-3p21  
C:Function:  
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES  
A>Note: probably acts to control granulocyte proliferation and differentiation  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
F:32-56/Domain: transmembrane #status predicted <TM1>  
F:67-87/Domain: transmembrane #status predicted <TM2>  
F:103-124/Domain: transmembrane #status predicted <TM3>

F:142-166/Domain: transmembrane #status predicted <TM4>  
F:193-218/Domain: transmembrane #status predicted <TM5>  
F:236-257/Domain: transmembrane #status predicted <TM6>  
F:285-300/Domain: transmembrane #status predicted <TM7>  
F:207-226/Domain: transmembrane #status predicted <TM8>  
F:244-268/Domain: transmembrane #status predicted <TM9>  
F:287-309/Domain: transmembrane #status predicted <TM10>  
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:340/343/Binding site: phosphate (Thr) (covalent) #status predicted  
Query Match 100.0%; Score 118; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 APYIVILLNTFOEFFGLNCS 22  
Db 249 APYIVILLNTFOEFFGLNCS 270  
RESULT 2  
JC2443  
chemokine (C-C) receptor 2, splice form B - human  
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1  
C:Species: Homo sapiens (man)  
C:Date: 21-Feb-1995 #sequence revision 05-Apr-1995 #text change 20-Jun-2000  
C:Accession: JC2443; I38463  
R:Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.  
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994  
A:Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1  
A:Reference number: JC2443; MUID:94324942; PMID:8048929  
A:Accession: JC2443  
A:Molecule type: mRNA  
A:Residues: 1-360 <YAM>  
A:Cross-references: DDBJ:D29984; NID:gs31246; PIDN:BAAG6253.1; PID:gs31247  
R:Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2  
A:Reference number: A53477; MUID:94195821; PMID:8146186  
A:Accession: I38463  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-360 <RES>  
A:Cross-references: EMBL:U03905; NID:9472557; PIDN:AAAL9120.1; PID:9472558  
C:Genetics:  
A:Gene: GDB:CMKBR2  
A:Map position: 3p21-3p21  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein  
F:43-70/Domain: transmembrane #status predicted <TM1>  
F:81-100/Domain: transmembrane #status predicted <TM2>  
F:115-136/Domain: transmembrane #status predicted <TM3>  
F:154-178/Domain: transmembrane #status predicted <TM4>  
F:207-226/Domain: transmembrane #status predicted <TM5>  
F:244-268/Domain: transmembrane #status predicted <TM6>  
F:287-309/Domain: transmembrane #status predicted <TM7>  
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:113-190/Disulfide bonds: #status predicted  
Query Match 87.3%; Score 103; DB 2; Length 360;  
Best Local Similarity 90.0%; Pred. No. 9.3e-09;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 PYIVILLNTFOEFFGLNCS 21  
Db 258 PYIVILLNTFOEFFGLNCS 277  
RESULT 3  
I38450  
chemokine (C-C) receptor 2, splice form A - human  
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence revision 16-Feb-1996 #text change 13-Aug-1999

```

Query Match 47.5%; Score 56; DB 2; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.33;
Matches 8; Conservative 6; Mismatches 0; Gaps 0;

QY 2 PYNIVLLNTFOEFGFLNNC 21
 |||:||||:||||:|
DB 254 PYNITILISVFQDFLFTHEC 273

RESULT 6
T07448
probable DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Japanese black pine chlor
C:Species: chloroplast Pinus thunbergiana (Japanese black pine)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 18-Aug-2000
C:Accession: T07448
R:Wakasugi, T.; Taudzuki, J.; Ito, S.; Nakashima, K.; Taudzuki, T.; Sugiura, M.
A:Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genome
A:Reference number: Z16030; MUD:95024047; PMID:17957893
A:Accession: T07448
A:Accession: T07448
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1075 <WAK>
A:Cross-references: EMBL:U17510; NID:g529643; PIDN:BAA04326.1; PID:gl262609
C:Genetics:
A:Gene: rpoB
A:Genome: chloroplast
A:Superfamily: DNA-directed RNA polymerase beta chain
C:Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 46.2%; Score 54.5; DB 2; Length 1075;
Best Local Similarity 63.2%; Pred. No. 1.8;
Matches 12; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

QY 2 PYNIV--LLNTFOEFGG 17
 ||:|:|||:|||||
DB 355 PQNLVSTLLKNTQDFGG 373

RESULT 7
A57160

```

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F:36-60/Domain: transmembrane #status predicted <TM1>  
F:71-91/Domain: transmembrane #status predicted <TM2>  
F:108-129/Domain: transmembrane #status predicted <TM3>  
F:147-171/Domain: transmembrane #status predicted <TM4>  
F:205-223/Domain: transmembrane #status predicted <TM5>  
F:240-261/Domain: transmembrane #status predicted <TM6>  
F:288-305/Domain: transmembrane #status predicted <TM7>  
F:324-273,106-183/disulfide bonds: #status predicted <TM7>  
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 355;  
Best Local Similarity 40.0%; Pred. No. 1.4;  
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNVILLNTFQEFFGLNCC 21  
DB 254 PYNVAILLSYQSLFGNDC 273  
||||:||||:|:|  
|:::|:::|::|

RESULT 9

JC4587  
chemokine (C-C) receptor 4 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000  
C:Accession: JC4587  
R:Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
Biochem. Biophys. Res. Commun. 218, 337-343, 1996  
A:Article: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to  
A:Reference number: JC4587; MUID:96136324; PMID:8573157  
A:Accession: JC4587  
A:Molecule type: mRNA  
A:Residues: 1-360 <HOO>  
A:Cross-references: EMBL:X90862; NID:gl167851; PIDN:CAA62372.1; PID:gl167852  
A:Experimental source: thymus  
C:Genetics:  
A:Gene: cc ckr-4  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus  
F:2,183,194/Binding site: carbohydate (Aam) (covalent) #status predicted  
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
F:145/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 360;  
Best Local Similarity 47.6%; Pred. No. 1.5;  
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNVILLNTFQEFFGLNCC 22  
DB 257 PYNVLFLETLVEVLQDCT 277  
||||:||||:|:|  
|:::|:::|::|

RESULT 10

S55594  
G Protein-coupled receptor E1 - equine herpesvirus 2  
C:Species: equine herpesvirus 2  
C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 13-Aug-1999  
C:Accession: S55594  
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
J. Mol. Biol. 249, 520-528, 1995  
A:Title: The DNA sequence of equine herpesvirus 2.  
A:Reference number: S55594; MUID:9502501; PMID:7783207  
A:Accession: S55594  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-383 <TEL>  
A:Cross-references: GS-U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor

Query Match 44.1%; Score 52; DB 2; Length 383;  
Best Local Similarity 90.9%; Pred. No. 1.6;

Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFF 12  
 |||||:|:|  
 Db 293 PYNIVLLSTF 303

RESULT 11

JH0197  
 muscarinic acetylcholine receptor M2 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 24-Nov-1999  
 C:Accession: JH0197; D37121  
 R:Rial, J.; Bloom, J.W.; Yamamura, H.I.; Roeske, W.R.  
 Life Sci. 47, 1001-1013, 1990  
 A>Title: Amplification of the rat m2 muscarinic receptor gene by the polymerase chain re  
 A:Reference number: JH0197; MUID:91041524; PMID:2172674  
 A:Accession: JH0197  
 A:Molecule type: DNA  
 A:Residues: 1-466 <LAI>  
 R:Kuttenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.  
 J. Biol. Chem. 265, 13702-13708, 1990  
 A>Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invo  
 A:Reference number: A37121; MUID:90337982; PMID:2380182  
 A:Accession: D37121  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 60-122 <KUR>  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme  
 F:23-48/Domain: transmembrane #status predicted <TM1>  
 F:98-119/Domain: transmembrane #status predicted <TM2>  
 F:139-162/Domain: transmembrane #status predicted <TM3>  
 F:184-207/Domain: transmembrane #status predicted <TM4>  
 F:389-409/Domain: transmembrane #status predicted <TM5>  
 F:421-442/Domain: transmembrane #status predicted <TM6>  
 F:421-442/Domain: transmembrane #status predicted <TM7>

Query Match 44.1%; Score 52; DB 2; Length 466;  
 Best Local Similarity 66.7%; Pred. No. 1.9;  
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFF 12  
 |||||:|:|  
 Db 401 APYNVWLINTF 412

RESULT 12

S10126  
 muscarinic acetylcholine receptor M2 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 24-Nov-1999  
 C:Accession: S10126  
 R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
 EMBO J. 6, 3923-3929, 1987  
 A>Title: Distinct primary structures, ligand-binding properties and tissue-specific exp  
 A:Reference number: S04326; MUID:88166632; PMID:3443095  
 A:Accession: S10126  
 A:Molecule type: DNA  
 A:Residues: 1-466 <PER>  
 A:Cross-references: EMBL:X15264; NID:g32319; PIDN:CAA33335.1; PID:g32320  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
 F:23-48/Domain: transmembrane #status predicted <TM1>  
 F:60-89/Domain: transmembrane #status predicted <TM2>  
 F:98-119/Domain: transmembrane #status predicted <TM3>  
 F:139-162/Domain: transmembrane #status predicted <TM4>  
 F:184-207/Domain: transmembrane #status predicted <TM5>  
 F:389-409/Domain: transmembrane #status predicted <TM6>  
 F:421-442/Domain: transmembrane #status predicted <TM7>  
 F:2,6,9/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 44.1%; Score 52; DB 2; Length 466;

Best Local Similarity 66.7%; Pred. No. 1.9;  
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFF 12  
 |||||:|:|  
 Db 401 APYNVWLINTF 412

RESULT 13

S10856  
 muscarinic acetylcholine receptor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 24-Nov-1999  
 C:Accession: S10856  
 R:Gocayne, J.; Robinson, D.A.; FitzGerald, M.G.; Chung, F.Z.; Kerlavage, A.R.; Lenters, R.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 8296-8300, 1987  
 A>Title: Primary structure of rat cardiac beta-adrenergic and muscarinic cholinergic rec  
 A:Reference number: S10855; MUID:88068581; PMID:2825184  
 A:Accession: S10856  
 A:Molecule type: mRNA  
 A:Residues: 1-466 <GOC>  
 A:Cross-references: EMBL:J03025; NID:g203461; PIDN:AAA40926.1; PID:g203462  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
 F:23-48/Domain: transmembrane #status predicted <TM1>  
 F:61-85/Domain: transmembrane #status predicted <TM2>  
 F:98-119/Domain: transmembrane #status predicted <TM3>  
 F:139-162/Domain: transmembrane #status predicted <TM4>  
 F:184-207/Domain: transmembrane #status predicted <TM5>  
 F:389-409/Domain: transmembrane #status predicted <TM6>  
 F:421-442/Domain: transmembrane #status predicted <TM7>

Query Match 44.1%; Score 52; DB 2; Length 466;  
 Best Local Similarity 66.7%; Pred. No. 1.9;  
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFF 12  
 |||||:|:|  
 Db 401 APYNVWLINTF 412

RESULT 14

A27386  
 muscarinic acetylcholine receptor, cardiac - pig  
 N:Alternate names: muscarinic acetylcholine receptor M2  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 31-Dec-2000  
 C:Accession: A27386; A25656  
 R:Peralta, E.G.; Winslow, J.W.; Peterson, G.L.; Smith, D.H.; Ashkenazi, A.; Ramachandran  
 Science 236, 600-605, 1987  
 A>Title: Primary structure and biochemical properties of an M-2 muscarinic receptor.  
 A:Reference number: A27386; MUID:87206169; PMID:3107123  
 A:Accession: A27386  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-466 <PER>  
 A:Cross-references: GB:M16331; NID:g164311; PIDN:AAA30986.1; PID:g164313  
 A:Experimental source: atrial muscle  
 A>Note: the protein sequence derived from the mRNA clones differs from that of the genom  
 R:Castro, J.  
 FEBS Lett. 209, 367-372, 1986  
 A>Title: Primary structure of porcine cardiac muscarinic acetylcholine receptor deduced  
 A:Reference number: A25656; MUID:87080790; PMID:3792556  
 A:Accession: A25656  
 A:Molecule type: mRNA  
 A:Residues: 1-329, K, 331-466 <KUB>  
 A:Cross-references: GB:X04708; NID:g1859; PIDN:CAA28413.1; PID:g1860  
 A:Experimental source: cardiac muscle  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: cardiac muscle; G protein-coupled receptor; glycoprotein; heart; neurotransm  
 F:23-48/Domain: transmembrane #status predicted <TM1>  
 F:61-85/Domain: transmembrane #status predicted <TM2>  
 F:98-119/Domain: transmembrane #status predicted <TM3>  
 F:139-162/Domain: transmembrane #status predicted <TM4>

|                       |        |                |       |             |
|-----------------------|--------|----------------|-------|-------------|
| Query Match           | 42.4%; | Score 50;      | DB 2; | Length 490; |
| Best Local Similarity | 61.5%; | Pred. No. 4.2; |       |             |

histidinol-phosphate aminotransferase (hisC-2) homolog - Archaeoglobus fulgidus  
 C:Species: Archaeoglobus fulgidus  
 C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 29-Sep-1999  
 C:Accession: G69502  
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S.  
 Smith, H.O.; Woose, C.R.; Venter, J.C.  
 A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
 A:Reference number: A69250; MUID:98049343; PMID:9389475  
 A:Accession: G69502  
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-342 <KLE>  
 C:Cross-references: GB:AE000963; GB:AE000782; MID:g2689286; PIDN:AA089229.1; PID:g264851  
 C:Superfamily: probable histidinol-phosphate transaminase

Query Match 40.7%; Score 48; DB 2; Length 342;  
 Best Local Similarity 50.0%; Pred. No. 6.1;  
 Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 YNIVLLNTFOEFFGL 18  
 |||:::|:|:|  
 Db 195 YNNLVLSFSKFGFL 210

## RESULT 20

I49341  
 MIP-1 alpha receptor like-2 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 02-Jul-1998  
 C:Accession: I49341  
 R:Gao, J.L.; Murphy, P.M.  
 J. Biol. Chem. 270, 17494-17501, 1995  
 A>Title: Cloning and differential tissue-specific expression of three mouse beta chemoki  
 A:Reference number: I49339; MUID:95340546; PMID:7542241  
 A:Accession: I49341  
 A>Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-359 <RES>  
 C:Cross-references: EMBL:U28406; MID:9881551; PID:g881552  
 C:Superfamily: vertebrate rhodopsin

Query Match 40.7%; Score 48; DB 2; Length 359;  
 Best Local Similarity 45.0%; Pred. No. 6.4;  
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNMC 21  
 |||:::|:|:|  
 Db 258 PYNVLVLSAFHSTFLETSC 277

## RESULT 21

S48657  
 muscarinic acetylcholine receptor MR - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 15-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
 C:Accession: S48657; S24948  
 R:Herrera, L.; Carvallo, P.; Antonelli, M.; Olate, J.  
 FEBS Lett. 352, 175-179, 1994  
 A>Title: Cloning of a Xenopus laevis muscarinic receptor encoded by an intronless gene.  
 A:Reference number: S48657; MUID:95010703; PMID:7925970  
 A:Accession: S48657  
 A:Molecule type: mRNA  
 A:Residues: 1-484 <HEP>  
 C:Cross-references: GB:X65865; MID:g64900; PIDN:CAA46694.1; PID:g64901  
 R:Olate, J.  
 submitted to the EMBL Data Library, April 1992  
 A:Reference number: S24948  
 A:Accession: S24948  
 A:Molecule type: mRNA

A:Residues: 1-131, 'X', 133-484 <OLA>  
 A:Cross-references: EMBL:X65865; MID:g64900; PID:g64901  
 C:Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme  
 E:33-58/Domain: transmembrane #status predicted <TM1>  
 F:71-95/Domain: transmembrane #status predicted <TM2>  
 F:108-129/Domain: transmembrane #status predicted <TM3>  
 F:149-172/Domain: transmembrane #status predicted <TM4>  
 F:194-217/Domain: transmembrane #status predicted <TM5>  
 F:407-427/Domain: transmembrane #status predicted <TM6>  
 F:439-460/Domain: transmembrane #status predicted <TM7>

Query Match 40.7%; Score 48; DB 2; Length 484;  
 Best Local Similarity 63.6%; Pred. No. 8.7;  
 Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12  
 |||:::|:|:|  
 Db 420 PYNVWLINTF 430

## RESULT 22

B29514  
 muscarinic acetylcholine receptor M3 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 18-Feb-2000  
 C:Accession: B94518; B94293; B37121; B29514  
 R:Bonner, T.I.  
 submitted to GenBank, July 1987  
 A:Reference number: A94518  
 A:Accession: B94518  
 A:Molecule type: mRNA  
 A:Residues: 1-589 <BO1>  
 R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.  
 Science 237, 527-532, 1987  
 A>Title: Identification of a family of muscarinic acetylcholine receptor genes.  
 A:Reference number: A94293; MUID:97263421; PMID:3037705  
 A:Accession: B94293  
 A:Molecule type: mRNA  
 A:Residues: 1-269; 463-589 <BO2>  
 A:Experimental source: cerebral cortex  
 A>Note: only a part of the protein translation is given; none of the nucleotide sequence  
 R:Kurenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.  
 J. Biol. Chem. 265, 13702-13708, 1990  
 A>Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv  
 A:Reference number: A37121; MUID:90337982; PMID:2380182  
 A:Accession: B37121  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 104-166 <KUR>  
 C:Superfamily: vertebrate rhodopsin  
 F:67-90/Domain: transmembrane #status predicted <TM1>  
 F:104-124/Domain: transmembrane #status predicted <TM2>  
 F:142-163/Domain: transmembrane #status predicted <TM3>  
 F:184-206/Domain: transmembrane #status predicted <TM4>  
 F:230-251/Domain: transmembrane #status predicted <TM5>  
 F:492-512/Domain: transmembrane #status predicted <TM6>  
 F:527-545/Domain: transmembrane #status predicted <TM7>  
 F:6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.7%; Score 48; DB 2; Length 589;  
 Best Local Similarity 72.7%; Pred. No. 11;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTF 12  
 |||:::|:|:|  
 Db 505 PYNVWLINTF 515

## RESULT 23

S10128  
 muscarinic acetylcholine receptor M4 - human



C;Species: Homo sapiens (man)  
 C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 18-Feb-2000  
 C;Accession: S10128  
 R;Peralta, B.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.D.  
 EMO J. 6, 3923-3929, 1987  
 A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of two human rhodopsin genes  
 A;Reference number: S04326; MUID:98166632; PMID:3443095  
 A;Accession: S10128  
 A;Molecule type: DNA  
 A;Residues: 1-590 <PER>  
 A;Cross-references: EMBL:X15266; NID:g32323; PIDN:CAA33337.1; PID:g32324  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein  
 F;105-131/Domain: transmembrane #status predicted <TM1>  
 F;143-164/Domain: transmembrane #status predicted <TM2>  
 F;185-207/Domain: transmembrane #status predicted <TM3>  
 F;231-252/Domain: transmembrane #status predicted <TM4>  
 F;293-313/Domain: transmembrane #status predicted <TM5>  
 F;493-513/Domain: transmembrane #status predicted <TM6>  
 F;525-546/Domain: transmembrane #status predicted <TM7>  
 F;5,6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.7%; Score 48; DB 2; Length 590;  
 Best Local Similarity 72.7%; Pred. No. 11;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFF 12  
 |||||:|:|  
 Db 506 PYNIMVLVNTF 516

RESULT 24  
 S01114  
 muscarinic acetylcholine receptor M2, glandular - pig  
 N;Alternate names: muscarinic acetylcholine receptor III  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 18-Feb-2000  
 C;Accession: S01114  
 R;Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.  
 FEBS Lett. 235, 257-261, 1988  
 A;Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonists binding site  
 A;Reference number: S01114; MUID:98296835; PMID:3402600  
 A;Accession: S01114  
 A;Molecule type: DNA  
 A;Residues: 1-590 <AKI>  
 A;Cross-references: EMBL:X12712; NID:g1861; PIDN:CAA31215.1; PID:g1862  
 C;Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein  
 C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein  
 F;143-164/Domain: transmembrane #status predicted <TM1>  
 F;185-207/Domain: transmembrane #status predicted <TM2>  
 F;231-252/Domain: transmembrane #status predicted <TM3>  
 F;293-313/Domain: transmembrane #status predicted <TM4>  
 F;493-513/Domain: transmembrane #status predicted <TM5>  
 F;528-546/Domain: transmembrane #status predicted <TM6>

Query Match 40.7%; Score 48; DB 2; Length 590;  
 Best Local Similarity 72.7%; Pred. No. 11;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFF 12  
 |||||:|:|  
 Db 506 PYNIMVLVNTF 516

RESULT 25  
 S47572  
 muscarinic acetylcholine receptor m3 - bovine  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 18-Feb-2000  
 C;Accession: S47572  
 R;Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.  
 Biochim. Biophys. Acta 1223, 151-154, 1994

A;Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 receptor  
 A;Reference number: S47572; MUID:94339178; PMID:8061048  
 A;Accession: S47572  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-590 <LEE>  
 A;Cross-references: EMBL:U08286; NID:g520465; PIDN:AAA51866.1; PID:g520466  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: neurotransmitter receptor

Query Match 40.7%; Score 48; DB 2; Length 590;  
 Best Local Similarity 72.7%; Pred. No. 11;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFF 12  
 |||||:|:|  
 Db 506 PYNIMVLVNTF 516

RESULT 26  
 A55019  
 muscarinic acetylcholine receptor, M3 isoform - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 21-Jul-2000  
 C;Accession: A55019  
 R;Gadbut, A.P.; Galper, J.B.  
 J. Biol. Chem. 269, 25823-25829, 1994  
 A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and ventricle  
 A;Reference number: A55019; MUID:95014393; PMID:7929287  
 A;Accession: A55019  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-639 <GAD>  
 A;Cross-references: GB:I10617; NID:g530097; PIDN:AAA65961.1; PID:g530098  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: neurotransmitter receptor

Query Match 40.7%; Score 48; DB 2; Length 639;  
 Best Local Similarity 72.7%; Pred. No. 12;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFF 12  
 |||||:|:|  
 Db 556 PYNIMVLVNTF 566

RESULT 27  
 B69901  
 fatty-acid desaturase homolog yocE - Bacillus subtilis  
 C;Species: Bacillus subtilis  
 C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000  
 C;Accession: B69901  
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Eyring, J.; Fabel, C.; Ferrari, E.; Nature 390, 249-256, 1997  
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle, Jech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Fortetelli, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, T.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A;Reference number: A69580; MUID:98044033; PMID:9384377  
 A;Accession: B69901  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-352 <KUN>  
 A;Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13810.1; PID:g2634311



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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 7.18367 Seconds  
(without alignments)  
159.465 Million cell updates/sec

Title: US-10-084-813-14  
Perfect score: 118  
Sequence: 1 APYINVILLNTQFEFFGLNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1          | 118   | 100.0         | 352    | 1     | CKR5 CERAE  |
| 2          | 118   | 100.0         | 352    | 1     | CKR5 CERPY  |
| 3          | 118   | 100.0         | 352    | 1     | CKR5 CERTO  |
| 4          | 118   | 100.0         | 352    | 1     | CKR5 GORGO  |
| 5          | 118   | 100.0         | 352    | 1     | CKR5 HUMAN  |
| 6          | 118   | 100.0         | 352    | 1     | CKR5 HYLL   |
| 7          | 118   | 100.0         | 352    | 1     | CKR5 HYLL   |
| 8          | 118   | 100.0         | 352    | 1     | CKR5 HYLSY  |
| 9          | 118   | 100.0         | 352    | 1     | CKR5 MACMU  |
| 10         | 118   | 100.0         | 352    | 1     | CKR5 PANTR  |
| 11         | 118   | 100.0         | 352    | 1     | CKR5 PAPHA  |
| 12         | 118   | 100.0         | 352    | 1     | CKR5 PONPY  |
| 13         | 118   | 100.0         | 352    | 1     | CKR5 PYGHI  |
| 14         | 118   | 100.0         | 352    | 1     | CKR5 PYGNE  |
| 15         | 118   | 100.0         | 352    | 1     | CKR5 TRAPF  |
| 16         | 118   | 100.0         | 352    | 1     | CKR5 TRAPH  |
| 17         | 108   | 91.5          | 354    | 1     | CKR5 MOUSE  |
| 18         | 105   | 89.0          | 354    | 1     | CKR5 RAT    |
| 19         | 103   | 87.3          | 360    | 1     | CKR2 MACMU  |
| 20         | 103   | 87.3          | 374    | 1     | CKR2 HUMAN  |
| 21         | 87    | 73.7          | 373    | 1     | CKR2 RAT    |
| 22         | 79    | 66.9          | 373    | 1     | CKR2 MOUSE  |
| 23         | 56    | 47.5          | 355    | 1     | CKR1 HUMAN  |
| 24         | 54.5  | 46.2          | 1075   | 1     | RPOB PINTH  |
| 25         | 53    | 44.9          | 360    | 1     | CKR4 HUMAN  |
| 26         | 52    | 44.1          | 355    | 1     | CKR3 HUMAN  |
| 27         | 52    | 44.1          | 359    | 1     | CKR3 RAT    |
| 28         | 52    | 44.1          | 360    | 1     | CKR4 MOUSE  |
| 29         | 52    | 44.1          | 440    | 1     | ACM2 PANTR  |
| 30         | 52    | 44.1          | 466    | 1     | ACM2 HUMAN  |
| 31         | 52    | 44.1          | 466    | 1     | ACM2 MOUSE  |
| 32         | 52    | 44.1          | 466    | 1     | ACM2 PIG    |
| 33         | 52    | 44.1          | 466    | 1     | ACM2 RAT    |

|     |      |      |      |   |            |                     |
|-----|------|------|------|---|------------|---------------------|
| 34  | 51.5 | 43.6 | 355  | 1 | CKR3 CERAE | P56492 cercopithec  |
| 35  | 51.5 | 43.6 | 355  | 1 | CKR3 MACMU | P56483 macaca mula  |
| 36  | 51   | 43.2 | 355  | 1 | CKR1 MACMU | P56482 macaca mula  |
| 37  | 50   | 42.4 | 490  | 1 | ACM4 CHICK | P17200 gallus       |
| 38  | 48   | 40.7 | 342  | 1 | HI82 ARCFU | O28255 archaeoglob  |
| 39  | 48   | 40.7 | 359  | 1 | CKR3 MOUSE | P51678 mus musculus |
| 40  | 48   | 40.7 | 484  | 1 | ACM4 XENLA | P30544 xenopus lae  |
| 41  | 48   | 40.7 | 589  | 1 | ACM3 MOUSE | Q9er23 mus musculus |
| 42  | 48   | 40.7 | 589  | 1 | ACM3 RAT   | P08483 rattus norv  |
| 43  | 48   | 40.7 | 590  | 1 | ACM3 BOVIN | P41984 bos taurus   |
| 44  | 48   | 40.7 | 590  | 1 | ACM3 GORGO | Q9n2a3 gorilla gor  |
| 45  | 48   | 40.7 | 590  | 1 | ACM3 HUMAN | P20309 homo sapien  |
| 46  | 48   | 40.7 | 590  | 1 | ACM3 PANTR | Q9n2a4 pan troglod  |
| 47  | 48   | 40.7 | 590  | 1 | ACM3 PIG   | P11483 sus scrofa   |
| 48  | 48   | 40.7 | 590  | 1 | ACM3 PONPY | Q9n2a2 pongo pygma  |
| 49  | 48   | 40.7 | 639  | 1 | ACM3 CHICK | P49578 gallus gall  |
| 50  | 47   | 39.8 | 478  | 1 | ACM4 RAT   | P08485 rattus norv  |
| 51  | 47   | 39.8 | 479  | 1 | ACM4 HUMAN | P08173 homo sapien  |
| 52  | 47   | 39.8 | 479  | 1 | ACM4 MOUSE | P32211 mus musculus |
| 53  | 46   | 39.0 | 355  | 1 | CKR1 MOUSE | P51675 mus musculus |
| 54  | 46   | 39.0 | 374  | 1 | CCRS MOUSE | Q04683 mus musculus |
| 55  | 46   | 39.0 | 374  | 1 | CCRS RAT   | P34997 rattus norv  |
| 56  | 45.5 | 38.6 | 1070 | 1 | RPOB SPIOL | P11703 spinacia ol  |
| 57  | 45.5 | 38.6 | 1072 | 1 | RPOB OENHO | Q9mtm5 oenothera h  |
| 58  | 45   | 38.1 | 354  | 1 | C3X1 RAT   | P35411 rattus norv  |
| 59  | 45   | 38.1 | 355  | 1 | CKR8 HUMAN | P51685 homo sapien  |
| 60  | 45   | 38.1 | 356  | 1 | CKR8 MACMU | O07650 macaca mula  |
| 61  | 45   | 38.1 | 384  | 1 | CK06 HUMAN | O00590 homo sapien  |
| 62  | 44.5 | 37.7 | 423  | 1 | PNT1 YEAST | P38969 saccharomyc  |
| 63  | 44   | 37.3 | 171  | 1 | YJXJ SALTU | P39432 salmonella   |
| 64  | 44   | 37.3 | 198  | 1 | GCAL CHICK | P79880 gallus gall  |
| 65  | 44   | 37.3 | 200  | 1 | GCAL HUMAN | P43080 homo sapien  |
| 66  | 44   | 37.3 | 201  | 1 | GCAL MOUSE | P43081 mus musculus |
| 67  | 44   | 37.3 | 204  | 1 | GCAL BOVIN | P46065 bos taurus   |
| 68  | 44   | 37.3 | 388  | 1 | MTLD BUCAP | Q8K912 buchnera ap  |
| 69  | 44   | 37.3 | 466  | 1 | ACM2 CHICK | P30372 gallus gall  |
| 70  | 44   | 37.3 | 704  | 1 | NEUL HUMAN | Q9byt8 homo sapien  |
| 71  | 44   | 37.3 | 806  | 1 | SECA MYGGE | P47318 mycoplasma   |
| 72  | 44   | 37.3 | 808  | 1 | SECA MYCPN | P75559 mycoplasma   |
| 73  | 43.5 | 36.9 | 357  | 1 | CKR9 HUMAN | P51686 homo sapien  |
| 74  | 43.5 | 36.9 | 358  | 1 | CKR3 CAVPO | Q92213 cavia porce  |
| 75  | 43.5 | 36.9 | 373  | 1 | HI58 METJA | Q58365 methanococc  |
| 76  | 43   | 36.4 | 196  | 1 | YK59 ARCFU | O28220 archaeoglob  |
| 77  | 43   | 36.4 | 221  | 1 | NUGM PODAN | P15959 podospora a  |
| 78  | 43   | 36.4 | 372  | 1 | CKR5 HUMAN | P32302 homo sapien  |
| 79  | 43   | 36.4 | 382  | 1 | CK06 RAT   | O09027 rattus norv  |
| 80  | 43   | 36.4 | 384  | 1 | NK2R BOVIN | P05363 bos taurus   |
| 81  | 43   | 36.4 | 384  | 1 | NK2R MOUSE | P30549 mus musculus |
| 82  | 43   | 36.4 | 390  | 1 | NK2R RAT   | P16610 rattus norv  |
| 83  | 43   | 36.4 | 437  | 1 | RFBH SALTU | P26398 salmonella   |
| 84  | 43   | 36.4 | 460  | 1 | ACM1 HUMAN | P11229 homo sapien  |
| 85  | 43   | 36.4 | 460  | 1 | ACM1 MACMU | P56489 macaca mula  |
| 86  | 43   | 36.4 | 460  | 1 | ACM1 MOUSE | P12657 mus musculus |
| 87  | 43   | 36.4 | 460  | 1 | ACM1 PIG   | P04761 sus scrofa   |
| 88  | 43   | 36.4 | 460  | 1 | ACM1 RAT   | P08482 rattus norv  |
| 89  | 43   | 36.4 | 531  | 1 | ACM5 RAT   | P08911 rattus norv  |
| 90  | 43   | 36.4 | 532  | 1 | ACM5 HUMAN | P08912 homo sapien  |
| 91  | 43   | 36.4 | 532  | 1 | ACM5 MACMU | P56490 macaca mula  |
| 92  | 43   | 36.4 | 721  | 1 | FRTP HSV7J | P52385 human herpe  |
| 93  | 42.5 | 36.0 | 1070 | 1 | RPOB LOTJA | Q9bb89 lotus japon  |
| 94  | 42.5 | 36.0 | 1070 | 1 | RPOB TOBAC | P06271 nicotiana t  |
| 95  | 42.5 | 36.0 | 1072 | 1 | RPOB ARATH | P05054 arabidopsis  |
| 96  | 42   | 35.6 | 170  | 1 | YJXJ ECOS7 | Q8xb14 escherichia  |
| 97  | 42   | 35.6 | 170  | 1 | YJXJ ECOLI | P39411 escherichia  |
| 98  | 42   | 35.6 | 175  | 1 | YJXJ ECOL6 | Q8fa41 escherichia  |
| 99  | 42   | 35.6 | 354  | 1 | C3X1 MOUSE | Q920d9 mus musculus |
| 100 | 42   | 35.6 | 862  | 1 | LOXA PHAVU | P27480 phaeoculus v |

## ALIGNMENTS

RESULT 1

CKR5 CERAE  
ID CKR5 CERAE STANDARD; PRT; 352 AA.  
AC P56493;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).  
GN CKR5 OR CMKR5.  
OS Cercopithecus aethiops (Green monkey) (Grivet).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=98001387; PubMed=9343222;  
RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
implicate specific amino acids in infections by simian and human  
immunodeficiency viruses.";  
RL J. Virol. 71:8642-8656(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;  
RT "cDNA sequence of African green monkey CCR-5 chemokine receptor  
gene.";  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
CC MIP-1-beta and RANTES and subsequently transduces a signal by  
CC increasing the intracellular calcium ions level. May play a role  
CC in the control of granulocytic lineage proliferation or  
CC differentiation.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC  
CC EMBL; U83324; AAC51795.1; --  
CC EMBL; U83325; AAC51796.1; --  
CC EMBL; AB015944; BRA31328.1; --  
CC InterPro; IPR000276; GPCR\_Rhodopsn.  
CC Pfam; PF00001; 7tm1; 1.  
CC PRINTS; PR00237; GPCR\_Rhodopsn.  
CC PROSITE; PS00237; G PROTEIN RECF FL 1; 1.  
CC PROSITE; PS50262; G PROTEIN RECF FL 2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
CC Polymorphism.  
CC  
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 31 58 1 (POTENTIAL).  
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 69 89 2 (POTENTIAL).  
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 103 124 3 (POTENTIAL).  
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 142 166 4 (POTENTIAL).  
CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 199 218 5 (POTENTIAL).  
CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 236 260 6 (POTENTIAL).  
CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 278 301 7 (POTENTIAL).  
CC DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 353 378 BY SIMILARITY.  
CC FT DISULFID 101 178  
CC FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
CC FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
CC FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).

FT VARIANT 14 14 N -> Y.  
FT VARIANT 352 352 F -> L.  
SQ SEQUENCE 352 AA; 40561 MW; 7F52E690C72EC29A CRC64;  
Query Match 100.0%; Score 118; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.7e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYNIVILLNTFOEPPGLNCS 22  
DB 249 APYNIVILLNTFOEPPGLNCS 270  
RESULT 2  
ID CKR5\_CERP STANDARD; PRT; 352 AA.  
AC Q9TV42;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (CCR5).  
GN CKR5 OR CMKR5.  
OS Cercopithecus pygerythrus (Vervet monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=60710;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=100;  
RX MEDLINE=99335215; PubMed=10408730;  
RA Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,  
RA Diop O., Rigoulet J., Barre-Sinoussi F., Fomsgaard A.;  
RT "Mutations in CCR5-coding sequences are not associated with SIV  
carrier status in African nonhuman primates.";  
RL AIDS Res. Hum. Retroviruses 15:931-939(1999).  
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
CC MIP-1-beta and RANTES and subsequently transduces a signal by  
CC increasing the intracellular calcium ions level. May play a role  
CC in the control of granulocytic lineage proliferation or  
CC differentiation.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC  
CC EMBL; AF035222; AAD44015.1; --  
CC InterPro; IPR000276; GPCR\_Rhodopsn.  
CC Pfam; PF00001; 7tm1; 1.  
CC PRINTS; PR00237; GPCR\_Rhodopsn.  
CC PROSITE; PS00237; G PROTEIN RECF FL 1; 1.  
CC PROSITE; PS50262; G PROTEIN RECF FL 2; 1.  
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
CC  
CC DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 31 58 1 (POTENTIAL).  
CC DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 69 89 2 (POTENTIAL).  
CC DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 103 124 3 (POTENTIAL).  
CC DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 142 166 4 (POTENTIAL).  
CC DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 199 218 5 (POTENTIAL).  
CC DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
CC TRANSSEM 236 260 6 (POTENTIAL).  
CC DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
CC TRANSSEM 278 301 7 (POTENTIAL).

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FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 118; DB 1; Length 352;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFFGLNCS 22
DB 249 APYNVLLNTFOEFFGLNCS 270

RESULT 3
CKR5 CERTO STANDARD; PRT; 352 AA.
AC O62743; O62744; O62745; O62746;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9331;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVM Isolates use the CKR5 coreceptor from sooty mangabeys
RT naturally infected in west Africa: a comparison of coreceptor usage
RT of primary SIVM, HIV-2, and SIVmac.";
RL Virology 246:113-124(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF051902; AAC39830.1; -
CC EMBL; AF051903; AAC39831.1; -
CC EMBL; AF051904; AAC39832.1; -
CC EMBL; AF051905; AAC39833.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; P500237; G PROTEIN RECP Fl 1; 1.
CC PROSITE; P50262; G PROTEIN RECP Fl 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).

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FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
FT VARIANT 25 25 V -> G (IN ISOLATE 087).
FT VARIANT 100 100 M -> K (IN ISOLATE 079).
FT VARIANT 107 107 L -> V (IN ISOLATE 089).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match
Best Local Similarity 100.0%; Score 118; DB 1; Length 352;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFOEFFGLNCS 22
DB 249 APYNVLLNTFOEFFGLNCS 270

RESULT 4
CKR5 GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUN-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominiidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268697; PubMed=9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CKR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc Natl Acad Sci U S A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF005659; AAB62553.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.

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DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40515 MW; D0B6FCB9FE5EACB4 CRC64;  
 Query Match 100.0%; Score 118; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYIVLLNTQFFGLNCS 22  
 DB 249 APYIVLLNTQFFGLNCS 270  
 RESULT 5  
 ID CCR5\_HUMAN STANDARD; PRT; 352 AA.  
 AC P51681; O14692; O14693; O14696; O14697; O14698; O14699;  
 AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;  
 AC O14708; O15538; Q9UPA4;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)  
 DE (HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).  
 GN CCR5 OR CMKBR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96241590; PubMed=8639485;  
 RA Samson M., Labbe O., Mollereau C., Vassart G., Parmentier M.;  
 RT "Molecular cloning and functional expression of a new human  
 CC chemokine receptor gene.";  
 RL Biochemistry 35:3362-3367(1996).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96291862; PubMed=8663314;  
 RA Raport C.J., Gosling J., Schweighart V.L., Gray P.W., Charo I.F.;  
 RT "Molecular cloning and functional characterization of a novel human  
 CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha.";  
 RL J. Biol. Chem. 271:17161-17166(1996).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96295970; PubMed=8699119;  
 RA Comadiere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;  
 RT "Cloning and functional expression of CC CKR5, a human monocyte CC  
 chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and  
 RANTES.";  
 RL J. Leukoc. Biol. 60:147-152(1996).  
 [4]

RP SEQUENCE FROM N.A.  
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
 RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
 RA Gao J.L., la Bastide M., Kaplan M., Greco T., Touchman J.,  
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Fang M.,  
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,  
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,  
 RA Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98001387; PubMed=9343222;  
 RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 implicate specific amino acids in infections by simian and human  
 immunodeficiency viruses.";  
 RL J. Virol. 71:8642-8656(1997).  
 [6]  
 RP SEQUENCE FROM N.A., AND POLYMORPHISMS.  
 RX MEDLINE=98022612; PubMed=9359654;  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";  
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
 [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98049523; PubMed=9388201;  
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;  
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts  
 with 5'-end heterogeneity, dual promoter usage, and evidence for  
 polymorphisms within the regulatory regions and noncoding exons.";  
 RL J. Biol. Chem. 272:30662-30671(1997).  
 [8]  
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.  
 RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,  
 RA Debre P.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 [9]  
 RP SEQUENCE FROM N.A.  
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 [10]  
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
 RX MEDLINE=96260017; PubMed=8649511;  
 RA Deng H., Liu R., Elmeyer W., Choe S., Uutemaz D., Burkhardt M.,  
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,  
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;  
 RT "Identification of a major co-receptor for primary isolates of  
 HIV-1.";  
 RL Nature 381:661-666(1996).  
 [11]  
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
 RX MEDLINE=96260018; PubMed=8649512;  
 RA Draglic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,  
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,  
 RA Paxton W.A.;  
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor  
 CC-CKR-5.";  
 RL Nature 381:667-673(1996).  
 [12]  
 RP SULFATION.  
 RX MEDLINE=99189752; PubMed=10089882;  
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,  
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;  
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1  
 entry.";  
 RL Cell 96:667-676(1999).  
 CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and rantes and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or

CC differentiation. Acts as co-receptor with CD4 for primary non-  
CC syncytium-inducing strains (NSI) (macrophage-tropic) of HIV-1  
CC virus. It promotes Env-mediated fusion of the virus.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Found in promyelocytic cells.  
CC -!- PFM: Sulfation contributes to the efficiency of HIV-1 entry.  
CC -!- PTM: Modified by O-linked glycosylation, but not by N-linked  
CC glycosylation.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X91492; AAC62796.1; -  
CC EMBL; U54994; AAC50598.1; -  
CC EMBL; U57840; AAB17071.1; -  
CC EMBL; U95626; AAB57793.1; -  
CC EMBL; U83326; AAC51797.1; -  
CC EMBL; AF011500; AAB65700.1; -  
CC EMBL; AF011501; AAB65701.1; -  
CC EMBL; AF011502; AAB65702.1; -  
CC EMBL; AF011503; AAB65703.1; -  
CC EMBL; AF011505; AAB65705.1; -  
CC EMBL; AF011506; AAB65706.1; -  
CC EMBL; AF011507; AAB65707.1; -  
CC EMBL; AF011508; AAB65708.1; -  
CC EMBL; AF011509; AAB65709.1; -  
CC EMBL; AF011510; AAB65710.1; -  
CC EMBL; AF011511; AAB65711.1; -  
CC EMBL; AF011512; AAB65712.1; -  
CC EMBL; AF011513; AAB65713.1; -  
CC EMBL; AF011514; AAB65714.1; -  
CC EMBL; AF011515; AAB65715.1; -  
CC EMBL; AF011516; AAB65716.1; -  
CC EMBL; AF011517; AAB65717.1; -  
CC EMBL; AF011518; AAB65718.1; -  
CC EMBL; AF011519; AAB65719.1; -  
CC EMBL; AF011520; AAB65720.1; -  
CC EMBL; AF011521; AAB65721.1; -  
CC EMBL; AF011522; AAB65722.1; -  
CC EMBL; AF011523; AAB65723.1; -  
CC EMBL; AF011524; AAB65724.1; -  
CC EMBL; AF011525; AAB65725.1; -  
CC EMBL; AF011526; AAB65726.1; -  
CC EMBL; AF011527; AAB65727.1; -  
CC EMBL; AF011528; AAB65728.1; -  
CC EMBL; AF011529; AAB65729.1; -  
CC EMBL; AF011530; AAB65730.1; -  
CC EMBL; AF011531; AAB65731.1; -  
CC EMBL; AF011532; AAB65732.1; -  
CC EMBL; AF011533; AAB65733.1; -  
CC EMBL; AF011534; AAB65734.1; -  
CC EMBL; AF011535; AAB65735.1; -  
CC EMBL; AF011536; AAB65736.1; -  
CC EMBL; AF011537; AAB65737.1; -  
CC EMBL; AF031237; AAB94735.1; -  
CC EMBL; AF052539; AAD18131.1; -  
CC EMBL; AY221093; AAC65971.1; -  
CC Genbank; HGNC:1606; CCR5.  
CC MIM; 601373; -  
CC GO; GO:0005768; C:endosome; TAS.  
CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
CC GO; GO:0016493; F:C-C chemokine receptor activity; NAS.  
CC GO; GO:0015026; F:coreceptor activity; TAS.  
CC GO; GO:0007267; P:cell-cell signaling; TAS.  
CC GO; GO:0006968; P:cellular defense response; TAS.  
CC GO; GO:0006935; P:chemotaxis; TAS.  
CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR GO; GO:0007125; P:invasive growth; TAS.  
DR GO; GO:0007203; P:phosphatidylinositol-4,5-bisphosphate hydro. . .; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCRHOOPS.  
DR PROSITE; PS00237; G-PROTEIN RECP\_F1.1; 1.  
DR PROSITE; PS50262; G-PROTEIN RECP\_F1.2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
KW Polymorphism.  
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 2 (POTENTIAL).  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 103 124 3 (POTENTIAL).  
  
Query Match 100.0%; Score 118; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.7e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 APYNVLLNTFQEFFGLNCS 22  
Db 249 APYNVLLNTFQEFFGLNCS 270  
|||||  
RESULT 6  
CKRS\_HYLLE STANDARD; PRT; 352 AA.  
AC O97883;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CKRS).  
GN CKRS OR CMKRS5.  
OS Hylobates leucogenys (White-cheeked gibbon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
OX NCBI\_TaxID=61853;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99416438; PubMed=10486970;  
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
RT "Sequence evolution of the CKRS chemokine receptor gene in primates.";  
RL Mol. Biol. Evol. 16:1145-1154 (1999).  
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
CC increasing the intracellular calcium ions level. May play a role  
CC in the control of granulocytic lineage proliferation or  
CC differentiation.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; AF075451; AAD19863.1; -  
CC InterPro; IPR000276; GPCR\_Rhodpsn.  
CC Pfam; PF00001; 7tm.1; 1.  
CC PRINTS; PR00237; GPCRHOOPS.  
CC PROSITE; PS00237; G-PROTEIN RECP\_F1.1; 1.  
CC PROSITE; PS50262; G-PROTEIN RECP\_F1.2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 2 (POTENTIAL).

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 4, 7e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNVILLNTFOEFFGLNCS 22  
 |||||  
 Db 249 APYNVILLNTFOEFFGLNCS 270

RESULT 7  
 CKR5\_HYLM  
 ID CKR5\_HYLM STANDARD; PRT; 352 AA.  
 AC Q95NC0;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKBR5.  
 OS Hylobates moloch (Silvery gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=81572;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 MIP-1-beta and RANTES and subsequently transduces a signal by  
 increasing the intracellular calcium ions level. May play a role  
 in the control of granulocytic lineage proliferation or  
 differentiation.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC

DR EMBL; AF177999; AAK43382.1;  
 DR InterPro; IPR000276; GPCR\_Rhodop.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 82 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40436 MW; 9623CA98340CF274 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 4, 7e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 APYNVILLNTFOEFFGLNCS 22  
 |||||  
 Db 249 APYNVILLNTFOEFFGLNCS 270

RESULT 8  
 CKR5\_HYLSY  
 ID CKR5\_HYLSY STANDARD; PRT; 352 AA.  
 AC Q95NC5;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 5 (CCR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKBR5.  
 OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=95950;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CCR5 chemokine receptor gene in primates."  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 MIP-1-beta and RANTES and subsequently transduces a signal by  
 increasing the intracellular calcium ions level. May play a role  
 in the control of granulocytic lineage proliferation or  
 differentiation.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC

DR EMBL; AF177884; AAK43367.1;  
 DR InterPro; IPR000276; GPCR\_Rhodop.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).



"Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains."

Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).

-I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

--S--

-I- SUBCELLULAR LOCATION: Integral membrane protein.

-I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

--S--

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--S--

EMBL; U7672; AAC51109.1; --  
EMBL; U73739; AAC51158.1; --  
EMBL; U96762; AAC34132.1; --  
EMBL; AF005660; AAB62554.1; --  
EMBL; AF005661; AAB62555.1; --  
EMBL; AF005662; AAB62556.1; --  
InterPro: IPR000276; GPCR\_Rhodpsn.  
Pfam: PF0001; 7tm.f.1;  
PRINTS; PR00237; GPCRRHODOPSN.  
PROSITE; PS00237; G PROTEIN RECP F1\_1; 1.  
PROSITE; PS0262; G PROTEIN RECP F1\_2; 1.  
G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

|     | DOMAIN<br>1 | DOMAIN<br>2 | DOMAIN<br>3      | DOMAIN<br>4 | DOMAIN<br>5 | DOMAIN<br>6 | DOMAIN<br>7 | DOMAIN<br>CYTOPLASMIC<br>(POTENTIAL) | DOMAIN<br>EXTRACELLULAR<br>(POTENTIAL) |
|-----|-------------|-------------|------------------|-------------|-------------|-------------|-------------|--------------------------------------|----------------------------------------|
| TFT | TRANSMEM    | TRANSMEM    | TRANSMEM         | TRANSMEM    | TRANSMEM    | TRANSMEM    | TRANSMEM    | CYTOPLASMIC (POTENTIAL)              | EXTRACELLULAR (POTENTIAL)              |
| F   | 31          | 59          | 69               | 125         | 142         | 261         | 241         | 1                                    | 1                                      |
| F   | 58          | 68          | 89               | 124         | 166         | 277         | 241         | 1                                    | 1                                      |
| F   | 88          | 89          | 102              | 141         | 198         | 301         | 352         | BY SIMILARITY                        | EXTRACELLULAR (POTENTIAL)              |
| F   | 89          | 89          | 102              | 141         | 198         | 301         | 352         | SULFATION (BY SIMILARITY)            | EXTRACELLULAR (POTENTIAL)              |
| F   | 103         | 124         | 124              | 125         | 166         | 261         | 277         | SULFATION (BY SIMILARITY)            | CYTOPLASMIC (POTENTIAL)                |
| F   | 125         | 141         | 124              | 125         | 166         | 261         | 277         | SULFATION (BY SIMILARITY)            | CYTOPLASMIC (POTENTIAL)                |
| F   | 142         | 166         | 141              | 142         | 198         | 277         | 301         | N-LINKED (GLCNAC... ) (POTENTIAL)    | EXTRACELLULAR (POTENTIAL)              |
| F   | 167         | 198         | 167              | 167         | 218         | 301         | 352         | M -> I (IN REF. 3)                   | EXTRACELLULAR (POTENTIAL)              |
| F   | 167         | 198         | 167              | 167         | 218         | 301         | 352         | I -> M (IN REF. 3)                   | EXTRACELLULAR (POTENTIAL)              |
| F   | 199         | 218         | 199              | 218         | 235         | 260         | 277         | CYTOPLASMIC (POTENTIAL)              | EXTRACELLULAR (POTENTIAL)              |
| F   | 219         | 235         | 219              | 235         | 260         | 277         | 301         | CYTOPLASMIC (POTENTIAL)              | EXTRACELLULAR (POTENTIAL)              |
| F   | 236         | 260         | 236              | 260         | 277         | 301         | 352         | CYTOPLASMIC (POTENTIAL)              | EXTRACELLULAR (POTENTIAL)              |
| F   | 261         | 277         | 261              | 277         | 301         | 352         | 352         | BY SIMILARITY                        | EXTRACELLULAR (POTENTIAL)              |
| F   | 278         | 301         | 278              | 301         | 352         | 352         | 352         | SULFATION (BY SIMILARITY)            | EXTRACELLULAR (POTENTIAL)              |
| F   | 302         | 352         | 302              | 352         | 352         | 352         | 352         | SULFATION (BY SIMILARITY)            | EXTRACELLULAR (POTENTIAL)              |
| F   | DISULFD     | MOD RES     | MOD RES          | MOD RES     | MOD RES     | MOD RES     | MOD RES     | SULFATION (BY SIMILARITY)            | EXTRACELLULAR (POTENTIAL)              |
| F   | MOD RES     | MOD RES     | MOD RES          | MOD RES     | MOD RES     | MOD RES     | MOD RES     | SULFATION (BY SIMILARITY)            | EXTRACELLULAR (POTENTIAL)              |
| F   | MOD RES     | MOD RES     | MOD RES          | MOD RES     | MOD RES     | MOD RES     | MOD RES     | SULFATION (BY SIMILARITY)            | EXTRACELLULAR (POTENTIAL)              |
| F   | MOD RES     | MOD RES     | MOD RES          | MOD RES     | MOD RES     | MOD RES     | MOD RES     | SULFATION (BY SIMILARITY)            | EXTRACELLULAR (POTENTIAL)              |
| F   | CONFLICT    | CONFLICT    | CONFLICT         | CONFLICT    | CONFLICT    | CONFLICT    | CONFLICT    | N-LINKED (GLCNAC... ) (POTENTIAL)    | EXTRACELLULAR (POTENTIAL)              |
| F   | CONFLICT    | CONFLICT    | CONFLICT         | CONFLICT    | CONFLICT    | CONFLICT    | CONFLICT    | M -> I (IN REF. 3)                   | EXTRACELLULAR (POTENTIAL)              |
| F   | CONFLICT    | CONFLICT    | CONFLICT         | CONFLICT    | CONFLICT    | CONFLICT    | CONFLICT    | I -> M (IN REF. 3)                   | EXTRACELLULAR (POTENTIAL)              |
| F   | SEQUENCE    | SEQUENCE    | SEQUENCE         | SEQUENCE    | SEQUENCE    | SEQUENCE    | SEQUENCE    | SEQUENCE                             | SEQUENCE                               |
| F   | 352 AA;     | 40507 MW;   | 58896C85909FACE2 | CCR64;      |             |             |             |                                      |                                        |

Query Match 100.0%; Score 118; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred.No. 4,7e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 APYNVILLANTFOEFFGLNCS 22  
db 249 APYNVILLANTFOEFFGLNCS 270

RESULT 10  
ID\_CKRS\_PANTRY STANDARD; PRT; 352 AA.  
AC P56440; O02778;  
DT 15-JUL-1998 (Rel. 36, Created)  
DD 15-JUL-1998 (Rel. 36, Last sequence update)  
DI 16-OCT-2001 (Rel. 40, Last annotation update)  
DE C-C chemokine receptor type 5 [C-C CKR-5] (CC-KKR-5) (CCR-5) (CCRS)

GN CCR5 OR CMGRS.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharon M., Sanson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX Zimmerman P.A., Buckler-White A., Alkhatib G.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98022612; PubMed=9359654;  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";  
 RL Aids Res. Hum. Retroviruses 13:1357-1366(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97426118; PubMed=9282822;  
 RA Zacharova V., Zachar V., Goustin A.S.;  
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural  
 RT HIV type 1 host.";  
 RL Aids Res. Hum. Retroviruses 13:1159-1161(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98090115; PubMed=9430250;  
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;  
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";  
 RL Aids Res. Hum. Retroviruses 13:1583-1587(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX Zhang Y., Ryder O.A., Zhang Y.;  
 RT "Sequence comparison of the CCR5 gene in primates and primate  
 RT phylogeny.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 DR EMBL; AF005663; AAB62557.1; -  
 DR EMBL; U94329; AAB58446.1; -  
 DR EMBL; AF011542; AAB65742.1; -  
 DR EMBL; U97666; AAC51670.1; -  
 DR EMBL; AF011540; AAB65740.1; -  
 DR EMBL; U89797; AAC03717.1; -  
 DR EMBL; AF17894; AAK43377.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSM.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 FT CARBOHYD 268 268 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CONFLICT 123 123 T -> S (IN REF. 1).  
 SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;  
 Query Match 100.0%; Score 118; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 APYNVILLNTTQEFGLNCS 22  
 Db 249 APYNVILLNTTQEFGLNCS 270  
 RESULT 11  
 CCR5\_PAPHA  
 ID CCR5\_PAPHA STANDARD; PRT; 352 AA.  
 AC P56441;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (CCR-5) (CCR-5).  
 GN CCR5 OR CMGRS.  
 OS Papio hamadryas (Hamadryas baboon), and  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Papio.  
 OX NCBI\_TaxID=9557, 9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.hamadryas;  
 RX Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharon M., Sanson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.hamadryas;  
 RX MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharon M., Sanson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=P.anubis;  
 RX Benton P.A., Timanov D.K., Shearer M.H., Lee D.R., Kennedy R.C.;  
 RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; AF005658; AAB2352.1; -  
 CC EMBL; AF105287; AAD20556.1; -  
 CC EMBL; AF105288; AAD20557.1; -  
 CC EMBL; AF105289; AAD20558.1; -  
 CC EMBL; AF105290; AAD20559.1; -  
 CC EMBL; AF023452; AAC63830.1; -  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.

CC Pfam; PF00001; 7tm\_1; 1.

CC PRINTS; PR00237; GPCR\_Rhodopsn.

CC PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

CC PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 31 58

FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124

FT DOMAIN 125 141

FT TRANSMEM 142 166

FT DOMAIN 167 198

FT TRANSMEM 199 218

FT DOMAIN 219 235

FT TRANSMEM 236 260

FT DOMAIN 261 277

FT TRANSMEM 278 301

FT DOMAIN 302 352

FT TRANSMEM 303 352

FT DISULFID 101 178

FT MOD\_RES 3 3

FT MOD\_RES 10 10

FT MOD\_RES 14 14

FT MOD\_RES 15 15

FT CARBOHYD 268 268

FT SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1F8B2 CRC64;

SQ

Query Match 100.0%; Score 118; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 4.7e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOFFGLNCS 22

DB 249 APYNIIVLLNTFOFFGLNCS 270

RESULT 12

CKR5\_PONPY

ID CKR5\_PONPY

AC 097881;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

GN CKR5 OR CMKRS.

OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.

OC NCBI\_TaxID=9600;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99416438; PubMed=10486970;

RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;

RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";

RL Mol. Biol. Evol. 16:1145-1154 (1999).

CC -|- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,

CC MIP-1-beta and RANTES and subsequently transduces a signal by

CC increasing the intracellular calcium ions level. May play a role

CC in the control of granulocytic lineage proliferation or

CC differentiation.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; AF075446; AAD19858.1; -

CC InterPro: IPR000276; GPCR\_Rhodopsn.

CC Pfam; PF00001; 7tm\_1; 1.

CC PRINTS; PR00237; GPCR\_Rhodopsn.

CC PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.

CC PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 31 58

FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 69 89

FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 103 124

FT DOMAIN 125 141

FT TRANSMEM 142 166

FT DOMAIN 167 198

FT TRANSMEM 199 218

FT DOMAIN 219 235

FT TRANSMEM 236 260

FT DOMAIN 261 277

FT TRANSMEM 278 301

FT DOMAIN 302 352

FT TRANSMEM 303 352

FT DISULFID 101 178

FT MOD\_RES 3 3

FT MOD\_RES 10 10

FT MOD\_RES 14 14

FT MOD\_RES 15 15

FT SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

SQ

Query Match 100.0%; Score 118; DB 1; Length 352;

Best Local Similarity 100.0%; Pred. No. 4.7e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOFFGLNCS 22

DB 249 APYNIIVLLNTFOFFGLNCS 270

RESULT 13

CKR5\_PYGBI

ID CKR5\_PYGBI

AC 097880;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

GN CKR5 OR CMKRS.

OS Pygathrix bieti (Black snub-nosed monkey) (Rhinothecus bieti).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;

OC Pygathrix.

OC NCBI\_TaxID=61621;

OX [1]

RP SEQUENCE FROM N.A.

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RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154 (1999).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075445; AAD19857.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 7 (POTENTIAL).
FT TRANSMEM 236 260 8 (POTENTIAL).
FT DOMAIN 261 277 9 (POTENTIAL).
FT TRANSMEM 278 301 10 (POTENTIAL).
FT DOMAIN 302 352 11 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 4366F142730F938F CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 249 APYNIIVLLNTFQFFGLNCS 270

RESULT 14
CKR5_PYGNE STANDARD; PRT; 352 AA.
AC O97882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CRK-5) (CCR-5) (CCR5).
GN CCR5 OR CMKGR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OC NCBI_TaxID=54133;

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EN SEQUENCE FROM N.A.
RP MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154 (1999).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075448; AAD19860.1; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 5 (POTENTIAL).
FT TRANSMEM 199 218 6 (POTENTIAL).
FT DOMAIN 219 235 7 (POTENTIAL).
FT TRANSMEM 236 260 8 (POTENTIAL).
FT DOMAIN 261 277 9 (POTENTIAL).
FT TRANSMEM 278 301 10 (POTENTIAL).
FT DOMAIN 302 352 11 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; FE4FD9D8D3B3E861 CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
DB 249 APYNIIVLLNTFQFFGLNCS 270

RESULT 15
CKR5_TRAFR STANDARD; PRT; 352 AA.
AC O97878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CRK-5) (CCR-5) (CCR5).
GN CCR5 OR CMKGR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Trachypithecus.

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OC NCBI_TaxID=54180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF075442; AAD19854.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP F1.2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 302 7 (POTENTIAL).
FT DOMAIN 303 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40496 MW; 4366F148C255938F CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 249 APYNIIVLLNTFOEFFGLNCS 270

RESULT 16
ID CCR5 TRAPH STANDARD; PRT; 352 AA.
AC O97879;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;

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```

OC Trachypithecus.
OX NCBI_TaxID=61618;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF075443; AAD19855.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPS.
CC PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
CC PROSITE; PS0262; G-PROTEIN RECP F1.2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 302 7 (POTENTIAL).
FT DOMAIN 303 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40509 MW; 4366F148D3A5938F CRC64;

Query Match 100.0%; Score 118; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
Db 249 APYNIIVLLNTFOEFFGLNCS 270

RESULT 17
ID CCR5 MOUSE STANDARD; PRT; 354 AA.
AC P51682; O35313; O35891; P97308; P97405; Q61867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (MIP-1
DE alpha receptor).
GN CCR5 OR CMKBR5.
OS Mus musculus (Mouse).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ; TISSUE=Spleen;  
 RX MEDLINE=96205938; PubMed=8631787;  
 RA Boring L., Gosling J., Montecarlo F.S., Lusis A.J., Tsou C.-L.,  
 RA Charo I.F.;  
 RT "Molecular cloning and functional expression of murine JE (monocyte  
 RT chemoattractant protein 1) and murine macrophage inflammatory protein  
 RT 1alpha receptors: evidence for two closely linked C-C chemokine  
 RT receptors on chromosome 9.";  
 RL J. Biol. Chem. 271:7551-7558(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
 RX MEDLINE=96278910; PubMed=8662890;  
 RA Meyer A., Coyle A.J., Proudfoot A.B.I., Wells T.N.C., Power C.A.;  
 RT "Cloning and characterization of a novel murine macrophage  
 RT inflammatory protein-1 alpha receptor.";  
 RL J. Biol. Chem. 271:14445-14451(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Ola;  
 RA Kuziel W.A., Beck M.A., Dawson T.C., Maeda N.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6, and NIH Swiss; TISSUE=Kidney, Liver, and Spleen;  
 RX MEDLINE=98001387; PubMed=9343222;  
 RA Kuhmann S.E., Platt E.J., Korak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 RT implicate specific amino acids in infections by simian and human  
 RT immunodeficiency viruses.";  
 RL J. Virol. 71:8642-8656(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=97404635; PubMed=9261347;  
 RA Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,  
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;  
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human  
 RT immunodeficiency virus type 1.";  
 RL J. Virol. 71:6305-6314(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Guo B., Kuno K., Harada A., Matsushima K.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Detected in monocyte/macrophage cell lines,  
 CC but not in nonhematopoietic cell lines.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL; U47036; AAC52454.1; -  
 CC EMBL; X94151; CAA63857.1; -  
 CC EMBL; U68565; AAB37273.1; -  
 CC EMBL; U83327; AAC53386.1; -  
 CC EMBL; AF022990; AAC53389.1; -  
 CC EMBL; AF019772; AAB71183.1; -  
 CC EMBL; D83648; BAA12024.1; -  
 CC MGD; MGI:107182; Ccr5.

DR GO; GO:0016493; F:C-C chemokine receptor activity; IDA.  
 DR GO; GO:0006952; P:defense response; IMP.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G PROTEIN RECF F1\_1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECF F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.  
 FT DOMAIN 1 32  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 33 60  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 61 70  
 FT TRANSMEM 71 91  
 FT EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 92 104  
 FT TRANSMEM 105 126  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 127 143  
 FT TRANSMEM 144 168  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 169 200  
 FT TRANSMEM 201 220  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 221 237  
 FT TRANSMEM 238 262  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 263 279  
 FT TRANSMEM 280 303  
 FT EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 304 354  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 103 180  
 FT CARBOHYD 270 270  
 FT VARIANT 11 11 I -> S.  
 FT VARIANT 62 62 K -> R.  
 FT VARIANT 66 66 V -> M.  
 FT VARIANT 97 97 I -> V.  
 FT VARIANT 109 109 V -> L.  
 FT VARIANT 156 156 V -> A.  
 FT VARIANT 160 160 F -> S.  
 FT VARIANT 185 185 P -> L.  
 FT VARIANT 213 213 I -> V.  
 FT VARIANT 318 318 I -> M.  
 FT VARIANT 337 337 V -> A.  
 FT CONFLICT 3 3 F -> L (IN REF. 2).  
 FT CONFLICT 80 80 L -> F (IN REF. 2).  
 FT CONFLICT 145 145 N -> I (IN REF. 5).  
 FT CONFLICT 190 190 H -> Y (IN REF. 3).  
 FT CONFLICT 208 208 P -> S (IN REF. 1).  
 SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;  
 Query Match 91.5%; Score 108; DB 1; Length 354;  
 Best Local Similarity 95.2%; Pred. No. 1.7e-09;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 PYNIVLLNTTQFFGLNCS 22  
 Db 252 PYNIVLLNTTQFFGLNCS 272  
 RESULT 18  
 CCR5 RAT  
 ID\_CCR5 RAT STANDARD; PRT; 354 AA.  
 AC 008556;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CCR-5) (CCR-5) (MIP-1  
 DE alpha receptor).  
 GN CCR5 OR CCR5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Brain;  
 RX MEDLINE=98334064; PubMed=9670989;  
 RA Speleiss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,  
 RA Berger M., Gebicke-Haerter P.J.;  
 RT "Cloning of rat HIV-1-chemokine coreceptor CCR5 from microglia and

upregulation of its mRNA in ischemic and endotoxinemic rat brain.";  
 J. Neurosci. Res. 53:16-28(1998).  
 [2]  
 SEQUENCE FROM N.A.  
 STRAIN=Sprague-Dawley;  
 MEDLINE=98318173; PubMed=9555467;  
 Jang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 "Chemokine receptor expression in cultured glia and rat experimental  
 allergic encephalomyelitis";  
 J. Neuroimmunol. 85:1-12(1998).  
 -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 MIP-1-beta and RANTES and subsequently transduces a signal by  
 increasing the intracellular calcium ions level.  
 -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 -----  
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 or send an email to license@isb-sib.ch).  
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 EMBL; Y12009; AAC72737.1; -;  
 EMBL; U77350; AAC03243.1; -;  
 InterPro; IPR000276; GPCR\_Rhodpsn.  
 Pfam; PF00001; 7tm.1; 1  
 PRINTS; PR00237; GPCRHOOPS.  
 PROSITE; PS00237; G-PROTEIN RECF F1\_1; 1.  
 PROSITE; PS0262; G-PROTEIN RECF F1\_2; 1.  
 G-protein coupled receptor; Transmembrane; Glycoprotein.  
 KW DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 33 60 1 (POTENTIAL).  
 FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 71 91 2 (POTENTIAL).  
 FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 105 126 3 (POTENTIAL).  
 FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 144 168 4 (POTENTIAL).  
 FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 201 220 5 (POTENTIAL).  
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 238 262 6 (POTENTIAL).  
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 280 303 7 (POTENTIAL).  
 FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 103 180 BY SIMILARITY.  
 FT CARBOHYD 270 270 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AAAC868D CRC64;  
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 Query Match 89.0%; Score 105; DB 1; Length 354;  
 Best Local Similarity 90.5%; Pred. No. 5.1e-09;  
 Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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 Qy 2 PYNIVLLNTFFQFFGLNCS 22  
 Db 252 PYNIVLLNTFFQFFGLNCS 272  
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 RESULT 19  
 CKR2 MACMU STANDARD; PRT; 360 AA.  
 ID CKR2 MACMU STANDARD; PRT; 360 AA.  
 AC 018753;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2)  
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R).  
 GN CCR2 OR CMKBR2.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;  
 Cercopitheciinae; Macaca.  
 NCBI\_TaxID=9544;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=21354176; PubMed=11461684;  
 Margulies B.J., Hauer D.A., Clements J.E.;  
 "Identification and comparison of eleven rhesus macaque chemokine  
 receptors";  
 AIDS Res. Hum. Retroviruses 17:981-986(2001).  
 -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 Transduces a signal by increasing the intracellular calcium ions  
 level.  
 -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 -!- ALTERNATIVE PRODUCTS:  
 Event=Alternative splicing; Named isoforms=2;  
 Name=B;  
 CC IsoId=O18793-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=O18793-2; Sequence=Not described;  
 -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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 -----  
 EMBL; AF013958; AAD11572.1; -;  
 InterPro; IPR000276; GPCR\_Rhodpsn.  
 Pfam; PF00001; 7tm.1; 1  
 PRINTS; PR00237; GPCRHOOPS.  
 PROSITE; PS00237; G-PROTEIN RECF F1\_1; 1.  
 PROSITE; PS0262; G-PROTEIN RECF F1\_2; 1.  
 G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 KW ALTERNATIVE SPLICING.  
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 43 70 1 (POTENTIAL).  
 FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 81 100 2 (POTENTIAL).  
 FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 115 136 3 (POTENTIAL).  
 FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 154 178 4 (POTENTIAL).  
 FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 207 226 5 (POTENTIAL).  
 FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 244 268 6 (POTENTIAL).  
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 286 303 7 (POTENTIAL).  
 FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 14 14 N-LINKED (GLCNAc. . .) (POTENTIAL).  
 FT MOD RES 26 26 SULFATION (BY SIMILARITY).  
 FT DISULFID 113 190 BY SIMILARITY.  
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;  
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 Query Match 87.3%; Score 103; DB 1; Length 360;  
 Best Local Similarity 90.0%; Pred. No. 1.1e-08;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
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 Qy 2 PYNIVLLNTFFQFFGLNCS 21  
 Db 258 PYNIVLLNTFFQFFGLNCS 277  
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 RESULT 20  
 CKR2 HUMAN STANDARD; PRT; 374 AA.  
 ID CKR2 HUMAN STANDARD; PRT; 374 AA.  
 AC P41597;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)





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Query Match 73.7%; Score 87; DB 1; Length 373;
Best Local Similarity 75.0%; Pred. NO. 3.5e-06;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PYNIVLLINTFOEFFGLNNC 21
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DB 271 PYNIVLELTTFQEFFGLMNC 290
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```

DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 KW PROSITE; PS50262; G-PROTEIN RECEPTOR FL2; 1.  
 FT G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 55 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 56 83 1 (POTENTIAL).  
 FT DOMAIN 84 93 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 94 114 2 (POTENTIAL).  
 FT DOMAIN 115 127 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 128 149 3 (POTENTIAL).  
 FT DOMAIN 150 166 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 167 191 4 (POTENTIAL).  
 FT DOMAIN 192 219 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 220 239 5 (POTENTIAL).  
 FT DOMAIN 240 256 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 257 281 6 (POTENTIAL).  
 FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 299 322 7 (POTENTIAL).  
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 126 203 BY SIMILARITY.  
 FT CONFLICT 39 39 Y -> H (IN REF. 1).  
 FT CONFLICT 184 184 A -> G (IN REF. 1).  
 FT CONFLICT 264 264 V -> G (IN REF. 1).  
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 66.9%; Score 79; DB 1; Length 373;  
 Best Local Similarity 70.0%; Pred. No. 6.3e-05;  
 Matches 14; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFQFFGLNLC 21  
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 Db 271 PYNIVLFLTFQFSLGNSNC 290

RESULT 23  
 CKRL HUMAN  
 ID CKRL HUMAN STANDARD; PRT; 355 AA.  
 AC P32246;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)  
 DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)  
 DE (RANTES-R) (HML45) (LD78 receptor).  
 DE CKR1 OR CMKR1 OR CMKR1.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP MEDLINE=93161416; PubMed=7679328;  
 RA Neote K., Digregorio D., Mak J.Y., Horuk R., Schall T.J.;  
 RT "Molecular cloning, functional expression, and signaling  
 RT characteristics of a C-C chemokine receptor.";  
 RL Cell 72:415-425 (1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=93240122; PubMed=7683036;  
 RA Gao J.-L., Kuhns D., Tiffany H.L., McDermott D., Li X., Francke U.,  
 RA Murphy P.M.;  
 RT "Structure and functional expression of the human macrophage  
 RT inflammatory protein 1 alpha/RANTES receptor.";  
 RL J. Exp. Med. 177:1421-1427 (1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Monocytes;  
 RX MEDLINE=94092629; PubMed=7505609;  
 RA Nomura H., Nielsen B.W., Matsumura K.;  
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative  
 RT leukocyte chemotactic peptide receptors.";  
 RL Int. Immunol. 5:1239-1249 (1993).  
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1 delta, RANTES, and MCP-3 and, less efficiently, to MIP-1-

CC beta or MCP-1 and subsequently transduces a signal by increasing  
 CC the intracellular calcium ions level. Responsible for affecting  
 CC stem cell proliferation.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Widely expressed in different hematopoietic  
 CC cells.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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 CC  
 CC EMBL; L09230; AAA58408.1; -;  
 CC EMBL; L10918; AAA36543.1; -;  
 CC EMBL; D10925; BAA01723.1; -;  
 CC PIR; A45177; A45177.  
 CC Genew; HGNC:1602; CCR1.  
 CC MIM; 601159; -;  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0004950; F:chemokine receptor activity; TAS.  
 CC GO; GO:0007155; P:cell adhesion; TAS.  
 CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.  
 CC GO; GO:0007287; P:cell-cell signaling; TAS.  
 CC GO; GO:006935; P:chemotaxis; TAS.  
 CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.  
 CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. .; TAS.  
 CC GO; GO:0006955; P:immune response; TAS.  
 CC GO; GO:0006954; P:inflammatory response; TAS.  
 CC GO; GO:0007125; P:invasive growth; TAS.  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC Pfam; PF00001; 7tm 1; 1.  
 CC PRINTS; PR00237; GPCR\_Rhodopsn.  
 CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 CC PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 60 1 (POTENTIAL).  
 FT DOMAIN 61 64 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 65 91 2 (POTENTIAL).  
 FT DOMAIN 92 107 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 108 129 3 (POTENTIAL).  
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 147 171 4 (POTENTIAL).  
 FT DOMAIN 172 197 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 198 223 5 (POTENTIAL).  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 264 6 (POTENTIAL).  
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 282 305 7 (POTENTIAL).  
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 106 183 BY SIMILARITY.  
 FT CONFLICT 337 337 E -> D (IN REF. 3).  
 SQ SEQUENCE 355 AA; 41172 MW; B2C100FFED275985 CRC64;

Query Match 47.5%; Score 56; DB 1; Length 355;  
 Best Local Similarity 40.0%; Pred. No. 0.24;  
 Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 PYNIVLLNTFQFFGLNLC 21  
 ||||| ||||| |||||  
 Db 254 PYNIVLLNTFQFFGLNLC 273

RESULT 24  
 RPOB\_PINTH  
 ID RPOB\_PINTH STANDARD; PRT; 1075 AA.  
 AC P41607;  
 DT 01-NOV-1995 (Rel. 32, Created)



CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
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 CC -----  
 DR EMBL: X85740; CAA59743.1; -.  
 DR EMBL: AB023888; BAA86965.1; -.  
 DR EMBL: AB023889; BAA86966.1; -.  
 DR EMBL: AB023890; BAA86967.1; -.  
 DR EMBL: AB023891; BAA86968.1; -.  
 DR EMBL: AB023892; BAA86969.1; -.  
 DR EMBL: AY322539; AAF84352.1; -.  
 DR F1R; A57160; A57160.  
 DR Genew; HGNC:1605; CCR4.  
 DR MIM; 604836; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.  
 DR GO; GO:0006935; P:chemotaxis; TAS.  
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.  
 DR GO; GO:0006955; P:immune response; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPT\_FL\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECPT\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Phosphorylation; Polymorphism.  
 FT DOMAIN 1 39  
 FT TRANSMEM 40 67  
 FT DOMAIN 68 77  
 FT TRANSMEM 78 98  
 FT DOMAIN 99 111  
 FT TRANSMEM 112 133  
 FT DOMAIN 134 150  
 FT TRANSMEM 151 175  
 FT DOMAIN 176 206  
 FT TRANSMEM 207 226  
 FT DOMAIN 227 242  
 FT TRANSMEM 243 267  
 FT DOMAIN 268 284  
 FT TRANSMEM 285 308  
 FT DOMAIN 309 360  
 FT CARBOHYD 183 183  
 FT CARBOHYD 194 194  
 FT DISULFID 110 187  
 FT VARIANT 130 130  
 FT VARIANT 178 178  
 FT VARIANT C->S.  
 FT SEQUENCE 360 AA; 41402 MW; 51BE12AD1FAFAFBF CRC64;  
 Query Match 44.9%; Score 53; DB 1; Length 360;  
 Best Local Similarity 52.4%; Pred.No. 0.71; Indels 0; Gaps 0;  
 Matches 11; Conservative 2; Mismatches 8;  
 QY 2 PYNVLNLTQFFGLNCS 22  
 |||||  
 Db 257 PYNVLFLTLVLEVLQDCT 277  
 RESULT 26  
 CCR3\_HUMAN  
 ID CCR3 HUMAN STANDARD; PRT; 355 AA.  
 AC P51677; Q15748; Q86WD2; Q9ULY8;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 3 (C-CR-3) (CCR-3) (CCR3)  
 DE (CCR3) (Eosinophil eotaxin receptor).  
 GN CCR3 OR CCR3R3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Monocytes;  
 RX MEDLINE=95348056; PubMed=7622448;  
 RA Combadiere C., Ahuja S.K., Murphy P.M.;  
 RT "Cloning and functional expression of a human eosinophil CC chemokine  
 RT receptor";  
 RL J. Biol. Chem. 270:16491-16494 (1995).  
 RN [2]  
 RP ERRATUM.  
 RA Combadiere C., Ahuja S.K., Murphy P.M.;  
 RL J. Biol. Chem. 270:30235-30235 (1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96235044; PubMed=8642344;  
 RA Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L.,  
 RA Sirotina A., Springer M.S.;  
 RT "Cloning, expression, and characterization of the human eosinophil  
 RT eotaxin receptor";  
 RL J. Exp. Med. 183:2349-2354 (1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96281895; PubMed=8676064;  
 RA Ponath P.D., Qin S., Post T.W., Wu L., Gerard N.P.,  
 RA Newman W., Gerard C., Mackay C.R.;  
 RT "Molecular cloning and characterization of a human eotaxin receptor  
 RT expressed selectively on eosinophils";  
 RL J. Exp. Med. 183:2737-2748 (1996).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96281895; PubMed=8676064;  
 RA Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;  
 RT "Partial resistance to infection by syncytium-inducing primary HIV-1  
 RT in exposed uninfected individuals homozygous for CCR5 32bp deletion";  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A., AND VARIANT SER-218.  
 RX MEDLINE=21040311; PubMed=11196669;  
 RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,  
 RA Hirai K., Tekunaga K.;  
 RT "New variations of human CC-chemokine receptors CCR3 and CCR4";  
 RL Genes Immun. 1:97-104 (1999).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22074933; PubMed=12079287;  
 RA Vijh S., Dayhoff D.E., Wang C.E., Imam Z., Ehrenberg P.K.,  
 RA Michael N.L.;  
 RT "Transcription regulation of human chemokine receptor CCR3: evidence  
 RT for a rare TATA-less promoter structure conserved between Drosophila  
 RT and humans";  
 RL Genomics 80:86-95 (2002).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center ([www.cdna.org](http://www.cdna.org));  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, Lung, and Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carnino R.P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,  
 CC eotaxin-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently  
 CC transduces a signal by increasing the intracellular calcium ions  
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: In eosinophils as well as trace amounts in  
 CC neutrophils and monocytes.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL: U28694; AAC50469.1; -  
 CC EMBL: U51241; AAB16831.1; -  
 CC EMBL: U49727; AAB09726.1; -  
 CC EMBL: AF026535; AAB25899.1; -  
 CC EMBL: AB023887; BAB86964.1; -  
 CC EMBL: AF247361; AAL85154.1; -  
 CC EMBL: AY221092; AAO65970.2; -  
 CC EMBL: BC033514; AAB33514.1; -  
 CC PIR: G02436; G02436.  
 CC Genbank: HGNC:1604; CCR3.  
 CC  
 CC MIM: 601268; -  
 CC GO: GO:0005887; C: integral to plasma membrane; TAS.  
 CC GO: GO:0004950; P: chemokine receptor activity; TAS.  
 CC GO: GO:0007155; P: cell adhesion; TAS.  
 CC GO: GO:0006968; P: cellular defense response; TAS.  
 CC GO: GO:0006935; P: chemotaxis; TAS.  
 CC GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.  
 CC GO: GO:0007189; P: G-protein signaling, coupled to cAMP nucleoside; TAS.  
 CC GO: GO:0006954; P: inflammatory response; TAS.  
 CC GO: GO:0007125; P: invasive growth; TAS.  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS: PR00237; GPCRHOPOPSN.  
 CC PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.  
 CC PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.  
 CC G-protein coupled receptor; Transmembrane; Polymorphism.  
 KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 62  
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 73 93  
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 108 129  
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 147 171  
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 204 223  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 264  
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 282 305  
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).

FT DISULFID 106 183 BY SIMILARITY.  
 FT VARIANT 218 218 C -> S (polymorphism found in about 7% of  
 FT the population; may show reduced  
 FT activity).  
 FT /FTID=VAR 010668.  
 FT CONFLICT 276 276 S -> T (IN REF. 4 AND 5).  
 SQ SEQUENCE 355 AA; 41043 MW; E95DCD7A6C643874 CRC64;  
 Query Match 44.1%; Score 52; DB 1; Length 355;  
 Best Local Similarity 40.0%; Pred. No. 1;  
 Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 PYNVILLNTQEFGLNLC 21  
 Db 254 PYNVALLSSQSTLFGNDC 273  
 ID\_CKR3 RAT STANDARD; PRT; 359 AA.  
 AC 054814; 055169;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)  
 DE (CCR3).  
 GN CCR3 OR CCR3R3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC STRAIN=Wistar; TISSUE=Spleen;  
 RX MEDLINE=98318173; PubMed=9655467;  
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 RT "Chemokine receptor expression in cultured glia and rat experimental  
 RT allergic encephalomyelitis".  
 RL J. Neuroimmunol. 86:11-12(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Spleen;  
 RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,  
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or  
 CC microglia.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL: AF003954; AAC03337.1; -  
 CC EMBL: Y13400; CAA73830.1; -  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS: PR00237; GPCRHOPOPSN.  
 CC PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.  
 CC PROSITE: PS00262; G PROTEIN RECEPTOR FL 2; 1.  
 CC G-protein coupled receptor; Transmembrane.  
 KW DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 44 63  
 FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 75 95 POTENTIAL.

FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 113 133 POTENTIAL.  
 FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 155 175 POTENTIAL.  
 FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 207 227 POTENTIAL.  
 FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 244 264 POTENTIAL.  
 FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 289 309 POTENTIAL.  
 FT DOMAIN 310 339 CYTOPLASMIC (POTENTIAL).  
 FT CONFLICT 164 184 F -> L (IN REF. 2).  
 SQ SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;  
 Query Match 44.1%; Score 52; DB 1; Length 359;  
 Best Local Similarity 50.0%; Pred. No. 1;  
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 Qy 2 PYNVLLNTFFQFGLNCS 21  
 Db 258 PYNVLLLSAFHSTLETSC 277  
 RESULT 28  
 CKR4\_MOUSE  
 ID CKR4\_MOUSE STANDARD; PRT; 360 AA.  
 AC P51680;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 4 (C-CR-4) (CCR-4) (CCR4).  
 GN CCR4 OR CMKCR4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;  
 RX MEDLINE=96136324; PubMed=8573157;  
 RA Hoogewerf A.J., Black D., Proudfoot A.E.I., Wells T.N.C., Power C.A.;  
 RT "Molecular cloning of murine CC CR-4 and high affinity binding of  
 chemokines to murine and human CC CR-4.";  
 RL Biochem. Biophys. Res. Commun. 218:337-343 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Cytotoxic T-cell;  
 RX MEDLINE=97335974; PubMed=9192769;  
 RA Yoon B.-S., Kim S.-H., Lyu M.S., Kozak C.A., Taub D.D., Kwon B.S.;  
 RT "Molecular cloning and characterization of a cDNA, CHEM1, encoding a  
 chemokine receptor with a homology to the human C-C chemokine  
 receptor, CCR-4.";  
 RL Blood 89:4448-4460 (1997).  
 RN [3]  
 RP FUNCTION.  
 RX MEDLINE=20273981; PubMed=10811868;  
 RA Buser R., Conquet F., Proudfoot A.E.I., Wells T.N.C., Power C.A.;  
 RT "A key role for CC chemokine receptor 4 in lipopolysaccharide-induced  
 endotoxic shock.";  
 RL J. Exp. Med. 191:1755-1764 (2000).  
 CC -1- FUNCTION: High affinity receptor for the C-C type chemokines  
 TARC/SCYA17 and MDC/SCYA22. The activity of this receptor is  
 mediated by G(i) proteins which activate a phosphatidylinositol-  
 calcium second messenger system. Could play a role in  
 lipopolysaccharide (LPS)-induced endotoxic shock. In the CNS,  
 could mediate hippocampal-neuron survival.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Expressed in the thymus, macrophages and T-  
 and B-cells.  
 CC -1- DEVELOPMENTAL STAGE: Low expression at 7.5 dpc and 12.5 dpc in the  
 yolk sac.  
 CC -1- PTM: IN NATURAL KILLER CELLS, SCYA22 BINDING INDUCES  
 PHOSPHORYLATION ON YET UNDEFINED SER/THR RESIDUES, MOST PROBABLY

CC BY BETA-ADRENERGIC RECEPTOR KINASES 1 AND 2 (BY SIMILARITY).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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 or send an email to license@isb-sib.ch).  
 CC EMBL; X90862; CAA62372.1; -;  
 DR EMBL; U15208; AAA92582.1; -;  
 DR PIR; J04587; J04587.  
 DR MGI; 107824; Ccr4.  
 GO; GO:0016493; F1-C-C chemokine receptor activity; IMP.  
 GO; GO:0006935; P:chemotaxis; IMP.  
 GO; GO:0006954; P:inflammatory response; IMP.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP Fl\_1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECP Fl\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 Phosphorylation.  
 KW DOMAIN 1 39 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 40 67 1 (POTENTIAL).  
 FT DOMAIN 68 77 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 78 98 2 (POTENTIAL).  
 FT DOMAIN 99 111 3 (POTENTIAL).  
 FT TRANSMEM 112 133 3 (POTENTIAL).  
 FT DOMAIN 134 150 4 (POTENTIAL).  
 FT TRANSMEM 151 175 5 (POTENTIAL).  
 FT DOMAIN 176 206 5 (POTENTIAL).  
 FT TRANSMEM 207 226 6 (POTENTIAL).  
 FT DOMAIN 227 242 7 (POTENTIAL).  
 FT TRANSMEM 243 267 7 (POTENTIAL).  
 FT DOMAIN 268 284 7 (POTENTIAL).  
 FT TRANSMEM 285 308 7 (POTENTIAL).  
 FT DOMAIN 309 360 7 (POTENTIAL).  
 FT DOMAIN 343 346 POLY-SER.  
 FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT DISULFID 110 187 BY SIMILARITY.  
 FT CONFLICT 4 4 T -> I (IN REF. 2).  
 FT CONFLICT 145 145 S -> T (IN REF. 2).  
 FT CONFLICT 181 181 E -> Q (IN REF. 2).  
 FT CONFLICT 205 205 E -> D (IN REF. 2).  
 FT CONFLICT 221 221 W -> C (IN REF. 2).  
 FT CONFLICT 241 241 V -> L (IN REF. 2).  
 FT CONFLICT 246 246 G -> A (IN REF. 2).  
 FT CONFLICT 293 293 G -> A (IN REF. 2).  
 FT CONFLICT 311 311 F -> S (IN REF. 2).  
 SQ SEQUENCE 360 AA; 41462 MW; 97BDB8C96D259AE3 CRC64;  
 Query Match 44.1%; Score 52; DB 1; Length 360;  
 Best Local Similarity 47.6%; Pred. No. 1;  
 Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
 Qy 2 PYNVLLNTFFQFGLNCS 22  
 Db 257 PYNVLFLETLEVLQDCT 277  
 RESULT 29  
 ACN2\_PANTR  
 ID ACN2\_PANTR STANDARD; PRT; 440 AA.  
 AC Q9N2A7;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Muscarinic acetylcholine receptor M2 (Fragment).

```

GN CHRM2.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 220;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver project.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
CC ADENYLATE CYCLASE INHIBITION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AB041392; BAA94477.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
CC PROSITE; PS0262; G PROTEIN RECP F1_2; 1.
CC Posttranslational modification: Glycoprotein; Transmembrane;
CC Phosphorylation; Multigene family; G-protein coupled receptor.
CC NON_TER 1 19
CC TRANSSEM <1 19 1 (POTENTIAL).
CC DOMAIN 20 33 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 34 54 2 (POTENTIAL).
CC DOMAIN 55 71 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 72 93 3 (POTENTIAL).
CC DOMAIN 94 113 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 114 136 4 (POTENTIAL).
CC DOMAIN 137 158 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 159 181 5 (POTENTIAL).
CC DOMAIN 182 362 CYTOPLASMIC (POTENTIAL).
CC TRANSSEM 363 383 6 (POTENTIAL).
CC DOMAIN 384 397 EXTRACELLULAR (POTENTIAL).
CC TRANSSEM 398 417 7 (POTENTIAL).
CC DOMAIN 418 440 CYTOPLASMIC (POTENTIAL).
CC DISULFID 70 150 BY SIMILARITY.
CC MOD_RES 420 420 PHOSPHORYLATION (POTENTIAL).
CC MOD_RES 424 424 PHOSPHORYLATION (POTENTIAL).
CC MOD_RES 439 439 PHOSPHORYLATION (POTENTIAL).
CC SEQUENCE 440 AA; 48854 MW; 12B0324E1D37DDF CRC64;
Query Match 44.1%; Score 52; DB 1; Length 440;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 1 APYNYVLLNTF 12
Db |||:|:|:|:|
375 APYNYVLLNTF 386
RESULT 30
ACM2 HUMAN
ID ACM2 HUMAN STANDARD; PRT; 466 AA.
AC P08172; Q9P1X9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Muscarinic acetylcholine receptor M2.

```

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GN CHRM2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=87263421; PubMed=3037705;
RA Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;
RT "Identification of a family of muscarinic acetylcholine receptor
RT genes.";
RL Science 237:527-532 (1987).
CC [2]
CC SEQUENCE FROM N.A.
CC MEDLINE=98166632; PubMed=3443095;
CC Peralta E.G., Ashkenazi A., Winslow J.W., Smith D.H.,
CC Ramachandran J., Capon D.J.;
CC "Distinct primary structures, ligand-binding properties and tissue-
CC specific expression of four human muscarinic acetylcholine
CC receptors.";
CC EMBO J. 6:3923-3929 (1987).
CC [3]
CC SEQUENCE FROM N.A.
CC TISSUE=Brain;
CC Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
CC "cDNA clones of human proteins involved in signal transduction
CC sequenced by the Guthrie cDNA resource center (www.cdna.org).";
CC Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC [4]
CC SEQUENCE OF 27-466 FROM N.A.
CC Kitano T., Kobayakawa H., Saitou N.;
CC "Silver project.";
CC Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS
CC ADENYLATE CYCLASE INHIBITION.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M16404; AAA51570.1; -
CC EMBL; X15264; CAA33335.1; -
CC EMBL; AF498916; AAM18939.1; -
CC EMBL; AB041391; BAA94476.1; -
CC PIR; S10126; S10126.
CC PDB; 1LUB; 19-JUN-02.
CC Genes; HGNC:1951; CHRM2.
CC MIM; 118493; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0004981; F: muscarinic acetylcholine receptor activity; TAS.
CC GO; GO:0007188; P: G-protein signaling, coupled to CAMP nucleo. .; TAS.
CC GO; GO:0007207; P: muscarinic acetyl choline receptor, phospho. .; TAS.
CC GO; GO:0007399; P: neurogenesis; TAS.
CC GO; GO:0009405; P: pathogenesis; TAS.
CC GO; GO:0008016; P: regulation of heart rate; TAS.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
CC PROSITE; PS0262; G PROTEIN RECP F1_2; 1.
CC Posttranslational modification: Glycoprotein; Transmembrane;
CC Phosphorylation; Multigene family; G-protein coupled receptor;
CC 3D-structure.
CC DOMAIN 1 22 EXTRACELLULAR (POTENTIAL).
FT

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|             |                                           |     |                                     |
|-------------|-------------------------------------------|-----|-------------------------------------|
| FT TRANSMEM | 23                                        | 45  | 1 (POTENTIAL).                      |
| FT DOMAIN   | 46                                        | 59  | CYTOPLASMIC (POTENTIAL).            |
| FT TRANSMEM | 60                                        | 80  | 2 (POTENTIAL).                      |
| FT DOMAIN   | 81                                        | 97  | EXTRACELLULAR (POTENTIAL).          |
| FT TRANSMEM | 98                                        | 119 | 3 (POTENTIAL).                      |
| FT DOMAIN   | 120                                       | 139 | CYTOPLASMIC (POTENTIAL).            |
| FT TRANSMEM | 140                                       | 162 | 4 (POTENTIAL).                      |
| FT DOMAIN   | 163                                       | 184 | EXTRACELLULAR (POTENTIAL).          |
| FT TRANSMEM | 185                                       | 207 | 5 (POTENTIAL).                      |
| FT DOMAIN   | 208                                       | 388 | CYTOPLASMIC (POTENTIAL).            |
| FT TRANSMEM | 389                                       | 409 | 6 (POTENTIAL).                      |
| FT DOMAIN   | 410                                       | 423 | EXTRACELLULAR (POTENTIAL).          |
| FT TRANSMEM | 424                                       | 443 | 7 (POTENTIAL).                      |
| FT DOMAIN   | 444                                       | 466 | CYTOPLASMIC (POTENTIAL).            |
| FT CARBOHYD | 2                                         | 2   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT CARBOHYD | 3                                         | 3   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT CARBOHYD | 6                                         | 6   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT CARBOHYD | 9                                         | 9   | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT DISULFID | 96                                        | 176 | BY SIMILARITY.                      |
| FT MOD RES  | 446                                       | 446 | PHOSPHORYLATION (POTENTIAL).        |
| FT MOD RES  | 450                                       | 450 | PHOSPHORYLATION (POTENTIAL).        |
| FT MOD RES  | 465                                       | 465 | PHOSPHORYLATION (POTENTIAL).        |
| SQ SEQUENCE | 466 AA; 51715 MW; 2FC2FD7748C22BEC CRC64; |     |                                     |

Query Match 44.1%; Score 52; DB 1; Length 466;  
 Best Local Similarity 66.7%; Pred. No. 1.3;  
 Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTF 12  
 Db 401 APYNVLLNTF 412

Search completed: March 4, 2004, 18:00:07  
 Job time : 8.38367 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:53:42 ; Search time 35.4694 Seconds  
(without alignments)  
195.701 Million cell updates/sec

Title: US-10-084-813-14

Perfect score: 118

Sequence: 1 APNVILLNTTQEPFGNNCS 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL 25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 118   | 100.0       | 333    | 4  | O14694      |
| 2          | 118   | 100.0       | 334    | 6  | Q9TUQ7      |
| 3          | 118   | 100.0       | 339    | 4  | Q9UN24      |
| 4          | 118   | 100.0       | 339    | 4  | Q9UN26      |
| 5          | 118   | 100.0       | 339    | 4  | Q9UN23      |
| 6          | 118   | 100.0       | 339    | 4  | Q9UBJ7      |
| 7          | 118   | 100.0       | 339    | 4  | Q9UN25      |
| 8          | 118   | 100.0       | 339    | 4  | Q9UN27      |
| 9          | 118   | 100.0       | 339    | 4  | Q9UBT9      |
| 10         | 118   | 100.0       | 339    | 6  | Q9TQW0      |
| 11         | 118   | 100.0       | 339    | 6  | Q9TQX1      |
| 12         | 118   | 100.0       | 339    | 6  | Q9TUN9      |
| 13         | 118   | 100.0       | 339    | 6  | Q9TUN8      |
| 14         | 118   | 100.0       | 339    | 6  | Q9TUT4      |
| 15         | 118   | 100.0       | 339    | 6  | Q9TUN9      |
| 16         | 118   | 100.0       | 339    | 6  | Q9TSQ1      |

Q9TUN8 cercopithec  
Q9TQW4 pan troglod  
Q9TUN4 pan troglod  
Q9TQW7 cercopithec  
Q9TUN5 erythrocebu  
Q9TUN9 saguinus sp  
Q9TQW0 macaca fasc  
Q9TUN9 macaca mula  
Q9TUN2 macaca fasc  
Q9TUN6 cercopithec  
Q9TQW6 colobus gue  
Q9TUN9 cercopithec  
Q9TUN3 macaca fasc  
Q9TUN7 macaca fusc  
Q9TUN0 papio papio  
Q9TUN6 papio papio  
Q9TUN5 cercopithec  
Q9TUN7 papio papio  
Q9TUN7 pan troglod  
Q9TUN3 pongo pygma  
Q9TUN5 papio papio  
Q9TUN0 macaca mula  
Q9TQW2 papio papio  
Q9TQW3 cercopithec  
Q9TUN8 cercopithec  
Q9TUN3 erythrocebu  
Q9TQW2 pongo pygma  
Q9TUN1 macaca mula  
Q9TUN6 macaca neme  
Q9TQW2 erythrocebu  
Q9TUN4 mandrillus  
Q9TQW3 mandrillus  
Q9TQW4 cercopithec  
Q9TUN0 macaca neme  
Q9TQW2 gorilla gor  
Q9TUN8 macaca mula  
Q9TUN1 macaca neme  
Q9TQW3 cercopithec  
Q9TUN5 pan troglod  
Q9TUN4 erythrocebu  
Q9TUN6 erythrocebu  
Q9TQW2 macaca neme  
Q9TQW1 macaca mula  
Q9TUN5 macaca neme  
Q9TUN2 macaca neme  
Q9TUN8 papio papio  
Q9TUN4 macaca mula  
Q9TUN6 papio papio  
Q9TQW4 cercopithec  
Q9TUN6 cercopithec  
Q9TUN7 macaca mula  
Q9TUN0 hylobates c  
Q9TQW2 cercopithec  
Q9TUN1 cercopithec  
Q9TUN9 papio papio  
Q9TUN2 macaca mula  
Q9TUN8 cercocebus  
Q9TQW3 cercocebus  
Q9TUN5 hylobates s  
Q9TUN4 cercopithec  
Q9TUN9 cercocebus  
Q9TUN1 colobus gue  
Q9TQW6 cercopithec  
Q9TUN3 miopithecus  
Q9TQW7 pan troglod  
Q9TUN4 cercopithec  
Q9TUN1 theropithec  
Q9TUN6 pan troglod  
Q9TUN8 trachypithe  
Q9TUN8 colobus pol  
Q9TUN4 cercopithec

90 118 100.0 352 6 Q95NC7  
 91 118 100.0 352 6 Q95NC0  
 92 118 100.0 352 6 Q95GN5  
 93 118 100.0 352 6 Q97975  
 94 118 100.0 352 6 Q9XT12  
 95 118 100.0 352 6 Q9XS35  
 96 118 100.0 352 6 Q9TV42  
 97 118 100.0 352 6 Q9XT13  
 98 118 100.0 352 6 Q95ND2  
 99 118 100.0 352 6 Q97776  
 100 118 100.0 352 6 Q97V93

## ALIGNMENTS

RESULT 1  
 O14694  
 ID O14694 PRELIMINARY; PRT; 333 AA.  
 AC O14694;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE CCR5 receptor (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RT Ho D.D.;  
 RL "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";  
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).  
 DR EMBL; AF01504; AAB85704.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR00276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 333 333  
 FT SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;  
 SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 100.0%; Score 118; DB 4; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYVILLNTFOFFGLNCS 22  
 DB 230 APYVILLNTFOFFGLNCS 251

RESULT 2  
 Q9TU07  
 ID Q9TU07 PRELIMINARY; PRT; 334 AA.  
 AC Q9TU07;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Erythrocybus patas (Red guenon) (Husar).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Erythrocybus.  
 OX NCBI\_TaxID=9538;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Kurstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF162049; AAD47804.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR00276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 334 334  
 FT SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;  
 SQ SEQUENCE 334 AA; 38460 MW; B19D0CEC667B69F0 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYVILLNTFOFFGLNCS 22  
 DB 237 APYVILLNTFOFFGLNCS 258

RESULT 3  
 Q9UN24  
 ID Q9UN24 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN24;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kurstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161919; AAD47676.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR00276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 339 339  
 FT SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;  
 SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 APYVILLNTFOFFGLNCS 22  
 DB 242 APYVILLNTFOFFGLNCS 263

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RESULT 4
Q9UN26
ID Q9UN26 PRELIMINARY; PRT; 339 AA.
AC Q9UN26;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161916; AAD47673.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39162 MW; A56369FE0529F4AB CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNVLLNTFOEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 242 APYNVLLNTFOEFFGLNCS 263

RESULT 5
Q9UN23
ID Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNVLLNTFOEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 242 APYNVLLNTFOEFFGLNCS 263

RESULT 6
Q9UBJ7
ID Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FF1F2F27A CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNVLLNTFOEFFGLNCS 22
| | | | | | | | | | | | | | | | | | | | | |
Db 242 APYNVLLNTFOEFFGLNCS 263

RESULT 7
Q9UN25
ID Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agly M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161918; AAD47675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39146 MW; 10FE05FE5371D4B3 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
|||||
DB 242 APYNVLLNTFQFFGLNCS 263

RESULT 8
Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39086 MW; 88AD8B44E2CB4EC2 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
|||||
DB 242 APYNVLLNTFQFFGLNCS 263

RESULT 9
Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39114 MW; 3C6369F92C29F4A7 CRC64;

Query Match 100.0%; Score 118; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVLLNTFQFFGLNCS 22
|||||
DB 242 APYNVLLNTFQFFGLNCS 263

RESULT 10
Q9TQW0 PRELIMINARY; PRT; 339 AA.
AC Q9TQW0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162024; AAD47779.1; -.
DR EMBL; AF161889; AAD47646.1; -.

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DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39036 MW; 5555FEAF2614D35C CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIIVLLNTQFEFFGLNCS 22
Db 242 APYNIIVLLNTQFEFFGLNCS 263

RESULT 11
Q9TUX1
ID Q9TUX1 PRELIMINARY; PRT; 339 AA.
AC Q9TUX1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161887; AAD47644.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39075 MW; 09257F8B834C4AE CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIIVLLNTQFEFFGLNCS 22
Db 242 APYNIIVLLNTQFEFFGLNCS 263

RESULT 12
Q9TUU9
ID Q9TUU9 PRELIMINARY; PRT; 339 AA.
AC Q9TUU9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161948; AAD47704.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIIVLLNTQFEFFGLNCS 22
Db 242 APYNIIVLLNTQFEFFGLNCS 263

RESULT 13
Q9TUW8
ID Q9TUW8 PRELIMINARY; PRT; 339 AA.
AC Q9TUW8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHHODOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

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Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 14
Q9TUT4 PRELIMINARY; PRT; 339 AA.
AC Q9TUT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161979; AAD47734.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 15
Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161979; AAD47734.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39092 MW; 84B51B9548E0703C CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 16
Q9TSQ1 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162023; AAD47778.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39216 MW; 847E935FA403E52D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 17
Q9TU08
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species."
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 16
Q9TSQ1 PRELIMINARY; PRT; 339 AA.
AC Q9TSQ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162023; AAD47778.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39216 MW; 847E935FA403E52D CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQFFGLNCS 22
 |||||
Db 242 APYNIVLLNTFQFFGLNCS 263

RESULT 17
Q9TU08
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ID QSTU08 PRELIMINARY; PRT; 339 AA.
AC QSTU08;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39049 MW; 6D1A93F66270F3ED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 242 APYNIVLLNTFOEFFGLNCS 263

RESULT 18
QSTQW4 PRELIMINARY; PRT; 339 AA.
AC QSTQW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39159 MW; 856995E882BAC0E84 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 242 APYNIVLLNTFOEFFGLNCS 263

RESULT 20
QSTQW7 PRELIMINARY; PRT; 339 AA.
AC QSTQW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

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DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8B8601D46A4 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 242 APYNIVLLNTFOEFFGLNCS 263

RESULT 19
QSTUW4 PRELIMINARY; PRT; 339 AA.
AC QSTUW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39159 MW; 856995E882BAC0E84 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22
Db 242 APYNIVLLNTFOEFFGLNCS 263

RESULT 20
QSTQW7 PRELIMINARY; PRT; 339 AA.
AC QSTQW7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

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OC Cercopithecinae; Cercopithecus.
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92EB03E2E2 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
DB 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 21
QY Q9TUQ5 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162054; AAD47809.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
DB 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 22
QY Q9TUR9 PRELIMINARY; PRT; 339 AA.
AC Q9TUR9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162015; AAD47770.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFOEFFGLNCS 22
DB 242 APYNIIVLLNTFOEFFGLNCS 263

RESULT 23
QY Q9TQT0 PRELIMINARY; PRT; 339 AA.
AC Q9TQT0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161954; AAD47710.1; -.

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DR EMBL; AF161950; AAD47706.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEFFGLNCS 22
Db 242 APYINVLLNTFQEFFGLNCS 263

RESULT 24
Q9TUN9
ID Q9TUN9 PRELIMINARY; PRT; 339 AA.
AC Q9TUN9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161972; AAD47727.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCB5BA96C2F98 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEFFGLNCS 22
Db 242 APYINVLLNTFQEFFGLNCS 263

RESULT 25
Q9TSN2
ID Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.

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AC Q9TSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD47709.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39137 MW; 9E626ED3288607C1 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYINVLLNTFQEFFGLNCS 22
Db 242 APYINVLLNTFQEFFGLNCS 263

RESULT 26
Q9TUR6
ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.

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KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39178 MW; 9DF2A6F446C55AED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQFFFGNNCS 22
DB 242 APYNVILLNTQFFFGNNCS 263

RESULT 27
Q9TQV6 PRELIMINARY; PRT; 339 AA.
AC Q9TQV6;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; RAD47760.1; -
DR EMBL; AF162006; RAD47755.1; -
DR EMBL; AF162001; RAD47756.1; -
DR EMBL; AF162002; RAD47757.1; -
DR EMBL; AF162003; RAD47758.1; -
DR EMBL; AF162004; RAD47759.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39168 MW; 6A4BF72FBFF566F CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQFFFGNNCS 22
DB 242 APYNVILLNTQFFFGNNCS 263

RESULT 28
Q9TUQ9 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ9;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.

```

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OS Cercopithecus mona.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Cercopithecus.
OX NCBI_TaxID=36226;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162041; RAD47796.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39019 MW; 7176F940AF1F3ED CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTQFFFGNNCS 22
DB 242 APYNVILLNTQFFFGNNCS 263

RESULT 29
Q9TSN3 PRELIMINARY; PRT; 339 AA.
AC Q9TSN3;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161951; RAD47707.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39098 MW; F0132E8BC44BF829 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;

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Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22  
|||||  
Db 242 APYNIVLLNTFOEFFGLNCS 263

## RESULT 30

Q9TUU7  
ID Q9TUU7 PRELIMINARY; PRT; 339 AA.  
AC Q9TUU7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5 (Fragment).  
GN CCR5.  
OS Macaca fuscata (Japanese macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9542;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstman K., Chen Z., Korber B., Oprea J., Stanton J., Agy M.,  
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
RT "Sequences of the CCR5 genes from diverse simian and prosimian  
RT species.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF161955; AAD4711.1; --  
DR GO: GO:0016021; C:integral to membrane; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR Pfam: PF00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCR\_Rhodopsn.  
DR PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.  
DR PROSITE: PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 339 339  
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 118; DB 6; Length 339;  
Best Local Similarity 100.0%; Pred. No. 2.1e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22  
|||||  
Db 242 APYNIVLLNTFOEFFGLNCS 263

Search completed: March 4, 2004, 18:02:56  
Job time : 36.4694 secs



## ALIGNMENTS

## RESULT 1

US-08-466-343D-2  
; Sequence 2, Application US/08466343D  
; Patent No. 6025154  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN  
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGNR10 (AS AMENDED)  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,343D  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-466-343D-2

Query Match 100.0%; Score 118; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLVLLNTFQEFFGLNCS 22  
Db 249 APYIVLLVLLNTFQEFFGLNCS 270

## RESULT 2

US-09-087-232A-13  
; Sequence 13, Application US/09087232A  
; Patent No. 6153431  
; GENERAL INFORMATION:  
; APPLICANT: Quillent et al.  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR  
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/087,232A  
; FILING DATE: 28 MAY 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/049,057  
; FILING DATE: 30 MAY 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOLE, LISA B.  
; REGISTRATION NUMBER: 35,225  
; REFERENCE/DOCKET NUMBER: AP 31115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 408-2628  
; TELEFAX: (212) 765-2519  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-09-087-232A-13

Query Match 100.0%; Score 118; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYIVLLVLLNTFQEFFGLNCS 22  
Db 249 APYIVLLVLLNTFQEFFGLNCS 270

## RESULT 3

US-08-861-105-14  
; Sequence 14, Application US/08861105  
; Patent No. 6258527  
; GENERAL INFORMATION:  
; APPLICANT: LITTMAN, DAN R.  
; APPLICANT: DENG, HONGKUI  
; APPLICANT: ELLMEIER, WILFRIED  
; APPLICANT: LANDAU, NATHANIEL R.  
; APPLICANT: LIU, RONG

; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH  
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,105  
; FILING DATE:  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/666,020  
; FILING DATE: 19-JUN-1996  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,319  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1049-1-004 N1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-861-105-14

Query Match 100.0%; Score 118; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22  
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 4  
US-08-575-967A-2  
; Sequence 2, Application US/08575967A  
; Patent No. 6265184  
; GENERAL INFORMATION:  
; APPLICANT: Gray et al.  
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 S. Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/575,967A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6265184and, Greta E.  
; REGISTRATION NUMBER: 35,302  
; REFERENCE/DOCKET NUMBER: 32918  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-485-1900  
; TELEFAX: 206-485-1662  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: /= "88C amino acid sequence"  
US-08-575-967A-2

Query Match 100.0%; Score 118; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22

Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 5  
US-09-045-583-52  
; Sequence 52, Application US/09045583  
; Patent No. 6287805  
; GENERAL INFORMATION:  
; APPLICANT: Graham, Gerard J. et al.  
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/045,583  
; FILING DATE: 20-WAR-98  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragoras, Amy B.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: MNI-044  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-09-045-583-52

Query Match 100.0%; Score 118; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFOEFFGLNCS 22  
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 6  
US-09-517-605-5  
; Sequence 5, Application US/09517605  
; Patent No. 6391567  
; GENERAL INFORMATION:  
; APPLICANT: Littman, Dan R.  
; APPLICANT: Kwon, Douglas S.  
; APPLICANT: van Kooyk, Yvette  
; APPLICANT: Geijtenbeck, Theo  
; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 1049-1-017  
; CURRENT APPLICATION NUMBER: US/09/517,605  
; CURRENT FILING DATE: 2000-03-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5

GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
APPLICANT: PARMENTIER, MARC  
APPLICANT: VASSART, GILBERT  
APPLICANT: LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,752  
FILING DATE: 9-APR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-833-752-5

Query Match 100.0%; Score 118; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYNVILLNTFOEFFGLNCS 22  
DB 249 APYNVILLNTFOEFFGLNCS 270

RESULT 7  
US-09-534-185-52  
Sequence 52, Application US/09534185  
Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Heptahelical Receptor Superfamily and Uses  
Therefor  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 52:  
US-09-534-185-52

Query Match 100.0%; Score 118; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYNVILLNTFOEFFGLNCS 22  
DB 249 APYNVILLNTFOEFFGLNCS 270

RESULT 8  
US-08-833-752-5  
Sequence 5, Application US/08833752  
Patent No. 6448375  
GENERAL INFORMATION:  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR1)  
TITLE OF INVENTION: HDGMR10  
FILE REFERENCE: 1488.1150006  
CURRENT APPLICATION NUMBER: US/09/502,783A  
CURRENT FILING DATE: 2001-08-23  
PRIOR APPLICATION NUMBER: 08/466,343  
PRIOR FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent In version 3.0  
SEQ ID NO 2  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-502-783A-2

Query Match 100.0%; Score 118; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYNVILLNTFOEFFGLNCS 22  
DB 249 APYNVILLNTFOEFFGLNCS 270

Query Match 100.0%; Score 118; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYNVILLNTFOEFFGLNCS 22  
DB 249 APYNVILLNTFOEFFGLNCS 270

Query Match 100.0%; Score 118; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.1e-12;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYNVILLNTFOEFFGLNCS 22  
DB 249 APYNVILLNTFOEFFGLNCS 270

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Db 249 APYNIVLLNTQEFFGLNCS 270

RESULT 10
US-09-796-202-1
; Sequence 1, Application US/09796202
; Patent No. 6548636
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/GHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-09-796-202-1

Query Match 100.0%; Score 118; DB 4; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTQEFFGLNCS 22
 |||||
Db 249 APYNIVLLNTQEFFGLNCS 270

RESULT 11
US-08-724-984A-2
; Sequence 2, Application US/08724984A
; Patent No. 6388055
; GENERAL INFORMATION:
; APPLICANT: Derk Bergema, Mary Brawner, and Usman Shabon
; TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-
; TITLE OF INVENTION: CCR5 Receptor
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: MICROSOFT WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,984A
; FILING DATE: October 3, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATG50023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270 5024
; TELEFAX: 610 270 5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-724-984A-2

Db 249 APYNIVLLNTQEFFGLNCS 270

Query Match 91.5%; Score 108; DB 4; Length 354;
Best Local Similarity 95.2%; Pred. No. 2.1e-10;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFFGLNCS 22
 |||||
Db 252 PYNIVLLNTQEFFGLNCS 272

RESULT 12
US-09-502-783A-9
; Sequence 9, Application US/09502783A
; Patent No. 6511826
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCRS
; TITLE OF INVENTION: HDGMR10
; FILE REFERENCE: 1488.1150006
; CURRENT APPLICATION NUMBER: US/09/502,783A
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 08/466,343
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Protein
US-09-502-783A-9

Query Match 87.3%; Score 103; DB 4; Length 329;
Best Local Similarity 90.0%; Pred. No. 1.4e-09;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTQEFFGLNCS 21
 |||||
Db 226 PYNIVLLNTQEFFGLSNC 245

RESULT 13
US-08-466-343D-9
; Sequence 9, Application US/08466343D
; Patent No. 6025154
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGMR10 (AS AMENDED)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,343D
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 9:
```



SEQUENCE CHARACTERISTICS:  
 LENGTH: 344 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-466-343D-9

Query Match 87.3%; Score 103; DB 3; Length 344;  
 Best Local Similarity 90.0%; Pred. No. 1.4e-09;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 PYNIVLLNTFQEFFGLNLC 21  
 DB 241 PYNIVLLNTFQEFFGLSNC 260

RESULT 14

US-08-461-244-3  
 ; Sequence 3, Application US/08461244  
 ; Patent No. 5776729  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soppet, Daniel R.  
 ; APPLICANT: Yi, Li  
 ; APPLICANT: Ruben, Steven M.  
 ; APPLICANT: Rosen, Craig A.  
 ; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
 ; STREET: 6 Becker Farm Road  
 ; CITY: Roseland  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07068

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/461,244  
 FILING DATE: 05-JUN-1995  
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
 NAME: Ferraro, Gregory D.  
 REGISTRATION NUMBER: 36,134  
 REFERENCE/DOCKET NUMBER: 325800-445  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 347 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-461-244-3

Query Match 87.3%; Score 103; DB 1; Length 347;  
 Best Local Similarity 90.0%; Pred. No. 1.5e-09;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 PYNIVLLNTFQEFFGLNLC 21  
 DB 245 PYNIVLLNTFQEFFGLSNC 264

RESULT 15

US-08-450-393A-4  
 ; Sequence 4, Application US/08450393A

Patent NO. 5707815  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charo, Israel  
 ; APPLICANT: Coughlin, Shaun  
 ; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
 ; TITLE OF INVENTION: PROTEIN RECEPTORS  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 ; STREET: 5 Palo Alto Square  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94306-2155  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/450,393A  
 ; FILING DATE: May 25, 1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cseri, Luann  
 ; REGISTRATION NUMBER: 31,822  
 ; REFERENCE/DOCKET NUMBER: UCAL-237/02US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-843-5165  
 ; TELEFAX: 415-8857-0663  
 ; TELEX: 380816COOLEYPA  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 360 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-450-393A-4

Query Match 87.3%; Score 103; DB 1; Length 360;  
 Best Local Similarity 90.0%; Pred. No. 1.5e-09;  
 Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 PYNIVLLNTFQEFFGLNLC 21  
 DB 258 PYNIVLLNTFQEFFGLSNC 277

RESULT 16

US-08-446-669-4  
 ; Sequence 4, Application US/08446669  
 ; Patent No. 6132987  
 ; GENERAL INFORMATION:

APPLICANT: Charo, Israel  
 APPLICANT: Coughlin, Shaun  
 TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
 TITLE OF INVENTION: PROTEIN RECEPTORS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
 STREET: 5 Palo Alto Square  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94306-2155

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/446,669  
 FILING DATE: May 25, 1995

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Neeley, Richard  
REGISTRATION NUMBER: 30,092  
REFERENCE/DOCKET NUMBER: UCAL-237/01US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-843-5000  
TELEFAX: 415-857-0663  
TELEX: 380816COOLEYPA  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-669-4

Query Match 87.3%; Score 103; DB 3; Length 360;  
Best Local Similarity 90.0%; Pred. No. 1.5e-09;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNNC 21  
DB 258 PYNIVLLNTFOEFFGLSNC 277

RESULT 17  
US-09-045-583-50  
Sequence 50, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-4214  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-045-583-50

Query Match 87.3%; Score 103; DB 3; Length 360;  
Best Local Similarity 90.0%; Pred. No. 1.5e-09;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNNC 21  
DB 258 PYNIVLLNTFOEFFGLSNC 277

## RESULT 18

US-09-045-583-51  
Sequence 51, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)742-4214  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-045-583-51

Query Match 87.3%; Score 103; DB 3; Length 360;  
Best Local Similarity 90.0%; Pred. No. 1.5e-09;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PYNIVLLNTFOEFFGLNNC 21  
DB 258 PYNIVLLNTFOEFFGLSNC 277

## RESULT 19

US-09-534-185-50  
Sequence 50, Application US/09534185  
Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Heptahelical Receptor Superfamily and Uses  
Therefor  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA

Query Match 87.3%; Score 103; DB 3; Length 360;  
Best Local Similarity 90.0%; Pred. No. 1.5e-09;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-534-185-50  
Query Match 87.3%; Score 103; DB 4; Length 360;  
Best Local Similarity 90.0%; Pred. No. 1.5e-09;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PYNIVLLNTFQFFGLNNC 21  
Db 258 PYNIVLLNTFQFFGLSNC 277  
RESULT 20  
US-09-534-185-51  
Sequence 51, Application US/09534185  
Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Heptahelical Receptor Superfamily and Uses  
Therefor  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-534-185-51  
Query Match 87.3%; Score 103; DB 4; Length 360;  
Best Local Similarity 90.0%; Pred. No. 1.5e-09;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PYNIVLLNTFQFFGLNNC 21  
Db 258 PYNIVLLNTFQFFGLSNC 277  
RESULT 21  
US-08-833-752-7  
Sequence 7, Application US/08833752  
Patent No. 6448375  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
APPLICANT: PARMENTIER, MARC  
APPLICANT: VASSART, GILBERT  
APPLICANT: LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobber, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,752  
FILING DATE: 9-APR-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6448375e  
US-08-833-752-7  
Query Match 87.3%; Score 103; DB 4; Length 360;  
Best Local Similarity 90.0%; Pred. No. 1.5e-09;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PYNIVLLNTFQFFGLNNC 21  
Db 258 PYNIVLLNTFQFFGLSNC 277  
RESULT 22  
US-09-131-827A-2

RESULT 24  
PCT-US95-00476-4  
; Sequence 4, Application PC/TUS9500476  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: MAMMALIAN MONOCLONAL ANTIBODIES TO THE PROTEIN RECEPTOR FOR GLUCAGON-LIKE GROWTH HORMONE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:

RESULT 25  
US-08-450-393A-2  
; Sequence 2, Application US/08450393A  
; Patent NO. 5707915  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; APPLICANT: Coughlin, Shaun  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; TITLE OF INVENTION: PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
; STREET: 5 palo Alto Square  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94306-2155  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,393A  
; FILING DATE: May 25, 1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cserit, Luann  
; REGISTRATION NUMBER: 31,822  
; REFERENCE/DOCKET NUMBER: UCAL-237/02US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-843-5165  
; TELEFAX: 415-8857-0663

RESULT 27  
PCT-US95-00476-2  
; Sequence 2, Application PC/TUS9500476  
; GENERAL INFORMATION:

RESULT 28  
 US-08-681-192-2  
 ; Sequence 2, Application US/08681192  
 ; Patent No. 6287801  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BERGSMÄ, DEBK  
 ; APPLICANT: ELSHOURBAGY, NABIL  
 ; APPLICANT: SARAU, HENRY  
 ; APPLICANT: RUBEN, STEVEN  
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNF878  
 ; NUMBER OF SEQUENCES: 6  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporation  
 ; STREET: 709 Swedeland Road  
 ; CITY: King of Prussia

```

1 STATE: PA
2
3 COUNTRY: USA
4
5 ZIP: 19406-2799
6
7 COMPUTER READABLE FORM:
8
9 MEDIUM TYPE: Diskette
10
11 COMPUTER: IBM Compatible
12
13 OPERATING SYSTEM: DOS
14
15 SOFTWARE: FastSeq Version 1.5
16
17 CURRENT APPLICATION DATA:
18
19 APPLICATION NUMBER: US/08/681,192
20
21 FILING DATE:
22
23 CLASSIFICATION: 530
24
25 PRIOR APPLICATION DATA:

```

```

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A.
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATC50014
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-681-192-2
;
Query Match 59.3%; Score 70; DB 3; Length 344;
Best Local Similarity 57.1%; Pred. No. 0.00063;
Matches 12; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTFQEFFGLNCC 21
Db 252 APYNTAFELSTFKHFLSDC 272

RESULT 29
US-09-087-232A-22
; Sequence 22, Application US/09087232A
; Patent No. 6153431
; GENERAL INFORMATION:
; APPLICANT: Oullient et al.
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/087,232A
; FILING DATE: 28 MAY 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/048,057
; FILING DATE: 30 MAY 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: KOLE, LISA B.
; REGISTRATION NUMBER: 35,225
; REFERENCE/DOCKET NUMBER: AP 31115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2628
; TELEFAX: (212) 765-2519
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-087-232A-22
;
Query Match 51.7%; Score 61; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIIVLLNTF 12
Db 14 APYNIIVLLNTF 25

RESULT 30
US-08-012-988A-2
; Sequence 2, Application US/08012988A
; Patent No. 5652133
; GENERAL INFORMATION:
; APPLICANT: Murphy, Philip M.
; TITLE OF INVENTION: Cloning and Expression of Human
; TITLE OF INVENTION: Macrophage Inflammatory Protein-1 alpha (MIP-1
; TITLE OF INVENTION: alpha)/RANTES Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,988A
; FILING DATE: 19930128
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-012-988A-2
;
Query Match 47.5%; Score 56; DB 1; Length 355;
Best Local Similarity 40.0%; Pred. No. 0.16;
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 PYNIIVLLNTFQEFFGLNCC 21
Db 254 PYNTILISVFDLFLETHCC 273

Search completed: March 4, 2004, 18:05:15
Job time : 15.1429 secs

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### RESULT 3

US-09-745-263-2  
; Sequence 2, Application US/09725285  
; Patent No. US20010000241A1  
; GENERAL INFORMATION:  
APPLICANT: Li, Yi

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/ APPLICANT: Ruben, Steven, M.
/ TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR
/ TITLE OF INVENTION: (CCRS Receptor)
/ FILE REFERENCE: 1488.1150003
/ CURRENT APPLICATION NUMBER: US/09/725,285
/ CURRENT FILING DATE: 2000-11-29
/ PRIOR APPLICATION NUMBER: 09/339,912
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: 09/195,662
/ PRIOR FILING DATE: 1998-11-18
/ PRIOR APPLICATION NUMBER: 08/466,343
/ PRIOR FILING DATE: 1995-06-06
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 2
/ LENGTH: 352
/ TYPE: PRT
/ ORGANISM: Artificial Sequence: Genomic
/ FEATURE:
/ OTHER INFORMATION: Deduced Amino Acid Sequence
/ US-09-725-285-2

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Query Match 100.0%; Score 118; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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249 APYNTV.I.I.NTFOEFFGLNCS 270

```

RESULT 4
; US-09-759-841-2
; Sequence 2, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Manuscros
; TITLE INVENTION: Assay Method
; FILE REFERENCE: PC10348ADME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-841-2

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US-09-759-841-2



```

RESULT 8
US-09-779-880A-22
; Sequence 22, Application US/09779880A
; Patent No. US20020061834A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Roschke, Viktor
; APPLICANT: Li, Yi
; APPLICANT: Ruben, Steven, M.
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGNRI.0
; FILE REFERENCE: 1488.115000C
; CURRENT APPLICATION NUMBER: US/09/779,880A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,258
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 60/187,999
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/234,336
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-880A-22
Query Match 100.0%; Score 118; DB 9; Length 352;

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Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYNIVLLNTFQEFFGLNCS 22  
DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 9  
US-09-813-653-15  
; Sequence 15, Application US/09813653  
; Patent No. US20020064770A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, John  
; APPLICANT: Wilson, Carol  
; APPLICANT: See, Raymond  
; APPLICANT: Tan Hehir, Christina  
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds  
; FILE REFERENCE: CNS-005  
; CURRENT APPLICATION NUMBER: US/09/813,653  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 60/190,946  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/190,996  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,299  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-813-653-15

Query Match 100.0%; Score 118; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22  
DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 10  
US-09-813-653-17  
; Sequence 17, Application US/09813653  
; Patent No. US20020064770A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, John  
; APPLICANT: Wilson, Carol  
; APPLICANT: See, Raymond  
; APPLICANT: Tan Hehir, Christina  
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds  
; FILE REFERENCE: CNS-005  
; CURRENT APPLICATION NUMBER: US/09/813,653  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 60/190,946  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/190,996  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,299  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-813-653-17

Query Match 100.0%; Score 118; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYNIVLLNTFQEFFGLNCS 22  
DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 11  
US-09-796-202-1  
; Sequence 1, Application US/09796202  
; Patent No. US20020068813A1  
; GENERAL INFORMATION:  
; APPLICANT: Dragic, Tatjana  
; APPLICANT: Olson, William  
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
; FILE REFERENCE: 2048/61010/JPW/SHS  
; CURRENT APPLICATION NUMBER: US/09/796,202  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: human  
US-09-796-202-1

Query Match 100.0%; Score 118; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22  
DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 12  
US-09-195-662A-2  
; Sequence 2, Application US/09195662A  
; Patent No. US20020076745A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGHR10 (CCR5 Receptor)  
; FILE REFERENCE: 1488.1150002  
; CURRENT APPLICATION NUMBER: US/09/195,662A  
; CURRENT FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/466,343  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Artificial Sequence: Genomic  
; FEATURE:  
; OTHER INFORMATION: Deduced Amino Acid Sequence  
US-09-195-662A-2

Query Match 100.0%; Score 118; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFQEFFGLNCS 22  
DB 249 APYNIVLLNTFQEFFGLNCS 270

RESULT 13  
US-09-339-912A-2  
; Sequence 2, Application US/09339912A  
; Patent No. US20020099176A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi

APPLICANT: Ruben, Steven, M.  
TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNE10  
FILE REFERENCE: 1488.1150003  
CURRENT APPLICATION NUMBER: US/09/339,912A  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 09/195,662  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 08/466,343  
PRIOR FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 2  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Artificial Sequence: Genomic  
FEATURE:  
OTHER INFORMATION: Deduced Amino Acid Sequence  
US-09-339-912A-2

Query Match 100.0%; Score 118; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFFQFFGLNCS 22  
DB 249 APYNIVLLNTFFQFFGLNCS 270

RESULT 14  
US-09-938-719-5  
Sequence 5, Application US/09938719  
Patent No. US20020106742A1  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/938,719  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 27-JULY-2000  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-938-719-5

Query Match 100.0%; Score 118; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 APYNIVLLNTFFQFFGLNCS 22  
DB 249 APYNIVLLNTFFQFFGLNCS 270

RESULT 15  
US-09-939-226-5  
Sequence 5, Application US/09939226  
Patent No. US20020110805A1  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/939,226  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 2000-07-27  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>

INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-939-226-5

Query Match 100.0%; Score 118; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNIVLLNTFFQFFGLNCS 22  
DB 249 APYNIVLLNTFFQFFGLNCS 270

RESULT 16  
US-09-938-703-5  
Sequence 5, Application US/09938703  
Patent No. US20020110870A1  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
PARMENTIER, MARC  
VASSART, GILBERT  
LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Krobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/938,703  
FILING DATE: 24-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/626,939  
FILING DATE: 2000-07-27  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: <Unknown>  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-938-703-5

Query Match 100.0%; Score 118; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0

QY 1 APYNVILLNTFQFFGLNCS 22  
|||||  
Db 249 APYNVILLNTFQFFGLNCS 270

RESULT 17  
US-09-502-783A-2  
Sequence 2, Application US/09502783A  
Patent No. US20020132269A1  
GENERAL INFORMATION:  
APPLICANT: Li, Yi  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR5)  
FILE REFERENCE: 1488.1150006  
CURRENT APPLICATION NUMBER: US/09/502,783A  
CURRENT FILING DATE: 2001-08-23  
PRIOR FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 2  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-502-783A-2

Query Match 100.0%; Score 118; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0

QY 1 APYNVILLNTFQFFGLNCS 22  
|||||  
Db 249 APYNVILLNTFQFFGLNCS 270

RESULT 18  
US-09-734-221A-14  
Sequence 14, Application US/09734221A  
Publication No. US20030096221A1  
GENERAL INFORMATION:  
APPLICANT: LITTMAN, DAN R.  
DENG, HONGKUI  
ELMEIER, WILFRIED  
LANDAU, NATHANIEL R.  
LIU, RONG  
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH  
MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
USES THEREOF  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
FLOOR  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/734,221A  
FILING DATE: 11-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/666,020  
FILING DATE: 19-JUN-1996  
APPLICATION NUMBER: US 08/227,319  
FILING DATE: 13-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1049-1-004 N2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-734-221A-14  
Query Match 100.0%; Score 118; DB 10; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFQFFGLNCS 22  
|||||  
Db 249 APYNVILLNTFQFFGLNCS 270

RESULT 19  
US-09-826-509-477  
Sequence 477, Application US/09826509  
Publication No. US20030204073A1  
GENERAL INFORMATION:  
APPLICANT: Lehmann-Bruinsma, Karin  
LIU, Chen W.  
APPLICANT: Lin, I-Lin

US-10-106-623-2

; CURRENT APPLICATION NUMBER: US/10/232,686  
; PRIOR FILING DATE: 2002-09-03  
; PRIOR APPLICATION NUMBER: 09/339,912  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 09/195,662  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/466,343  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-232-686-2

Query Match 100.0%; Score 118; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFQFFGLNCS 22  
DB 249 APYNVILLNTFQFFGLNCS 270

## RESULT 23

US-10-086-814-1  
; Sequence 1, Application US/1006814  
; Publication No. US20030092632A1  
; GENERAL INFORMATION:  
; APPLICANT: Dragic, Tatjana C.  
; APPLICANT: Olson, William C.  
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
; FILE REFERENCE: 61010-AB-1  
; CURRENT APPLICATION NUMBER: US/10/086,814  
; CURRENT FILING DATE: 2002-02-28  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-086-814-1

Query Match 100.0%; Score 118; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFQFFGLNCS 22  
DB 249 APYNVILLNTFQFFGLNCS 270

## RESULT 24

US-10-067-800-2  
; Sequence 2, Application US/10067800  
; Publication No. US20030100058A1  
; GENERAL INFORMATION:  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; CURRENT APPLICATION NUMBER: US/10/067,800  
; CURRENT FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: PCT/US01/04153  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 09/779,880  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/297,257  
; PRIOR FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: 60/310,458  
; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/328,447  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/341,725  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-800-2

Query Match 100.0%; Score 118; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFQFFGLNCS 22  
DB 249 APYNVILLNTFQFFGLNCS 270

## RESULT 25

US-10-067-800-22  
; Sequence 22, Application US/10067800  
; Publication No. US20030100058A1  
; GENERAL INFORMATION:  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.1150001  
; CURRENT APPLICATION NUMBER: US/10/067,800  
; CURRENT FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: PCT/US01/04153  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 09/779,880  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/297,257  
; PRIOR FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: 60/310,458  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/328,447  
; PRIOR FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/341,725  
; PRIOR FILING DATE: 2001-12-21  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 22  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-067-800-22

Query Match 100.0%; Score 118; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APYNVILLNTFQFFGLNCS 22  
DB 249 APYNVILLNTFQFFGLNCS 270

## RESULT 26

US-10-290-058A-6  
; Sequence 6, Application US/10290058A  
; Publication No. US20030104455A1  
; GENERAL INFORMATION:  
; APPLICANT: Silos-Santiago, Inmaculada  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; TITLE OF INVENTION: Urological Disorders Using 313, 333, 5464, 18817 or 33524  
; FILE REFERENCE: MEI01-289P1RM  
; CURRENT APPLICATION NUMBER: US/10/290,058A  
; CURRENT FILING DATE: 2002-11-07

```
; PRIOR APPLICATION NUMBER: 60/344,352
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-058A-6

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 27
US-10-225-567A-352
; Sequence 352, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 352
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-352

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 28
US-10-323-314-1
; Sequence 1, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPW/MAP/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-10-323-314-1

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 29
US-10-072-301-1
; Sequence 1, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN IMMUNODEF
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-301-1

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 APYNIVLLNTFOEFFGLNCS 22
Db 249 APYNIVLLNTFOEFFGLNCS 270

RESULT 30
US-10-164-649-52
; Sequence 52, Application US/10164649
; Publication No. US20030162943A1
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. US20030162943A1el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/164,649
; FILING DATE: 07-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
```

```

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-10-164-649-52

```

```

Query Match 100.0%; Score 118; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 APYNIIVLLINTFQEFFGLNCS 22
Db 249 APYNIIVLLINTFQEFFGLNCS 270

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Search completed: March 4, 2004, 18:22:53
Job time : 30.4082 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:07 ; Search time 42.7959 Seconds  
(without alignments)  
118.840 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YATVGEKFRNLYVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: A Genesep 29Jan04.\*

1: genesep1980s.\*

2: genesep1990s.\*

3: genesep2000s.\*

4: genesep2001s.\*

5: genesep2002s.\*

6: genesep2003as.\*

7: genesep2003bs.\*

8: genesep2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|-------|-------------|
| 1          | 95    | 100.0         | 18     | 4     | AAB88982    |
| 2          | 95    | 100.0         | 18     | 4     | AAB88997    |
| 3          | 95    | 100.0         | 27     | 5     | AAE14757    |
| 4          | 95    | 100.0         | 43     | 5     | AAE14756    |
| 5          | 95    | 100.0         | 58     | 5     | AAE14759    |
| 6          | 95    | 100.0         | 58     | 5     | AAE14755    |
| 7          | 95    | 100.0         | 268    | 7     | ADC10142    |
| 8          | 95    | 100.0         | 268    | 7     | ADC10144    |
| 9          | 95    | 100.0         | 332    | 2     | AAW26766    |
| 10         | 95    | 100.0         | 352    | 2     | AAW27407    |
| 11         | 95    | 100.0         | 352    | 2     | AAW27123    |
| 12         | 95    | 100.0         | 352    | 2     | AAW27125    |
| 13         | 95    | 100.0         | 352    | 2     | AAW07602    |
| 14         | 95    | 100.0         | 352    | 2     | AAW23835    |
| 15         | 95    | 100.0         | 352    | 2     | AAW88232    |
| 16         | 95    | 100.0         | 352    | 3     | AAW80128    |
| 17         | 95    | 100.0         | 352    | 4     | AAW79089    |
| 18         | 95    | 100.0         | 352    | 4     | AAW07046    |
| 19         | 95    | 100.0         | 352    | 4     | AAW07048    |
| 20         | 95    | 100.0         | 352    | 4     | AAW80111    |
| 21         | 95    | 100.0         | 352    | 4     | AAW04321    |
| 22         | 95    | 100.0         | 352    | 4     | AAW07037    |
| 23         | 95    | 100.0         | 352    | 4     | AAW07039    |
| 24         | 95    | 100.0         | 352    | 4     | AAW46858    |
| 25         | 95    | 100.0         | 352    | 4     | ABW56342    |
| 26         | 95    | 100.0         | 352    | 4     | ABW88982    |
| 27         | 95    | 100.0         | 352    | 4     | ABW88997    |
| 28         | 95    | 100.0         | 352    | 4     | AAU97150    |
| 29         | 95    | 100.0         | 352    | 5     | AAU97152    |
| 30         | 95    | 100.0         | 352    | 5     | AAW52829    |
| 31         | 95    | 100.0         | 352    | 5     | AAW52828    |
| 32         | 95    | 100.0         | 352    | 5     | ABG70597    |
| 33         | 95    | 100.0         | 352    | 5     | ABG92883    |
| 34         | 95    | 100.0         | 352    | 5     | ABG92880    |
| 35         | 95    | 100.0         | 352    | 5     | AAE25808    |
| 36         | 95    | 100.0         | 352    | 5     | AAE25811    |
| 37         | 95    | 100.0         | 352    | 5     | ABW81054    |
| 38         | 95    | 100.0         | 352    | 5     | ABW80343    |
| 39         | 95    | 100.0         | 352    | 6     | ABG75540    |
| 40         | 95    | 100.0         | 352    | 6     | ABW58602    |
| 41         | 95    | 100.0         | 352    | 6     | AAO29514    |
| 42         | 95    | 100.0         | 352    | 6     | ABU61654    |
| 43         | 95    | 100.0         | 352    | 6     | ABP97728    |
| 44         | 95    | 100.0         | 352    | 6     | ABP81933    |
| 45         | 95    | 100.0         | 352    | 7     | ADC03341    |
| 46         | 95    | 100.0         | 352    | 7     | ADC03359    |
| 47         | 95    | 100.0         | 371    | 2     | AAW23834    |
| 48         | 95    | 100.0         | 439    | 2     | AAW41280    |
| 49         | 85    | 89.5          | 354    | 7     | ADD44859    |
| 50         | 85    | 89.5          | 354    | 7     | ADD44863    |
| 51         | 80    | 84.2          | 354    | 2     | AAW54037    |
| 52         | 79    | 83.2          | 360    | 2     | AAW35833    |
| 53         | 79    | 83.2          | 360    | 2     | AAW80108    |
| 54         | 79    | 83.2          | 360    | 4     | AAU07613    |
| 55         | 79    | 83.2          | 360    | 4     | AAU07614    |
| 56         | 79    | 83.2          | 360    | 4     | ABW56340    |
| 57         | 79    | 83.2          | 360    | 6     | ABP97725    |
| 58         | 79    | 83.2          | 360    | 6     | ABP81987    |
| 59         | 79    | 83.2          | 360    | 6     | ABW88983    |
| 60         | 74    | 77.9          | 18     | 4     | ABW88983    |
| 61         | 73    | 76.8          | 18     | 4     | ABW88981    |
| 62         | 65    | 68.4          | 15     | 5     | AAE14758    |
| 63         | 65    | 68.4          | 332    | 5     | ABJ03698    |
| 64         | 65    | 68.4          | 332    | 5     | AAW03376    |
| 65         | 65    | 68.4          | 355    | 2     | AAW03377    |
| 66         | 65    | 68.4          | 355    | 2     | AAW01010    |
| 67         | 65    | 68.4          | 355    | 2     | AAW27124    |
| 68         | 65    | 68.4          | 355    | 2     | AAW31850    |
| 69         | 65    | 68.4          | 355    | 2     | AAW51744    |
| 70         | 65    | 68.4          | 355    | 2     | AAW51745    |
| 71         | 65    | 68.4          | 355    | 4     | AAW80109    |
| 72         | 65    | 68.4          | 355    | 4     | ABW56341    |
| 73         | 65    | 68.4          | 355    | 5     | AAE15320    |
| 74         | 65    | 68.4          | 355    | 5     | ABW07240    |
| 75         | 65    | 68.4          | 355    | 5     | ABW79520    |
| 76         | 65    | 68.4          | 355    | 5     | ABW07733    |
| 77         | 65    | 68.4          | 355    | 6     | ABG72634    |
| 78         | 65    | 68.4          | 355    | 6     | ABU09084    |
| 79         | 65    | 68.4          | 355    | 6     | ABP97726    |
| 80         | 65    | 68.4          | 355    | 6     | ABP81791    |
| 81         | 65    | 68.4          | 355    | 7     | ADC03343    |
| 82         | 65    | 68.4          | 356    | 7     | ADC25943    |
| 83         | 65    | 68.4          | 356    | 7     | ADC78873    |
| 84         | 65    | 68.4          | 355    | 2     | AAW07618    |
| 85         | 63    | 66.3          | 355    | 2     | AAW49807    |
| 86         | 63    | 66.3          | 355    | 2     | AAW56689    |
| 87         | 63    | 66.3          | 355    | 2     | AAW97868    |
| 88         | 63    | 66.3          | 355    | 4     | AAW80115    |
| 89         | 63    | 66.3          | 355    | 4     | ABW56343    |
| 90         | 63    | 66.3          | 355    | 4     | AAU80222    |
| 91         | 63    | 66.3          | 355    | 5     | AAU77932    |
| 92         | 63    | 66.3          | 355    | 6     | ABP97731    |
| 93         | 63    | 66.3          | 355    | 6     | ABP81794    |
| 94         | 63    | 66.3          | 358    | 5     | AAU77933    |
| 95         | 62    | 65.3          | 383    | 6     | ABP81684    |
| 96         | 61    | 64.2          | 355    | 2     | AAW29179    |
| 97         | 61    | 64.2          | 355    | 7     | ADD45360    |
| 98         | 61    | 64.2          | 365    | 2     | AAW48086    |

|     |    |      |     |   |          |           |
|-----|----|------|-----|---|----------|-----------|
| 99  | 61 | 64.2 | 365 | 3 | AA97077  | Primate ( |
| 100 | 61 | 64.2 | 365 | 6 | ABU03080 | Human den |

## ALIGNMENTS

|          |                                                                          |
|----------|--------------------------------------------------------------------------|
| RESULT 1 |                                                                          |
| AAB8982  |                                                                          |
| ID       | AAB8982 standard; peptide; 18 AA.                                        |
| XX       |                                                                          |
| XX       | AAB8982;                                                                 |
| XX       |                                                                          |
| XX       | 23-MAY-2001 (first entry)                                                |
| XX       |                                                                          |
| XX       | DE HIV gp120 protein binding peptide #75.                                |
| XX       |                                                                          |
| XX       | Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist; |
| KW       | replication; CCR5; CXCR4; CD4; STRL33.                                   |
| KW       |                                                                          |
| XX       |                                                                          |
| XX       | Homo sapiens.                                                            |
| OS       |                                                                          |
| XX       |                                                                          |
| XX       | WO200116182-A2.                                                          |
| PN       |                                                                          |
| XX       |                                                                          |
| XX       | 08-MAR-2001.                                                             |
| PD       |                                                                          |
| XX       |                                                                          |
| XX       | 25-AUG-2000; 2000WO-US023505.                                            |
| PF       |                                                                          |
| XX       |                                                                          |
| XX       | 27-AUG-1999; 99US-0151270P.                                              |
| PR       |                                                                          |
| XX       |                                                                          |
| XX       | (USSH ) US DEPT HEALTH & HUMAN SERVICES.                                 |
| PA       |                                                                          |
| XX       |                                                                          |
| XX       | Saxinger C;                                                              |
| PI       |                                                                          |

Novel polypeptides useful for treating HIV infection, have homology to regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33, and binds to HIV gp120 under physiological conditions.

Example 1; Page 37; 114pp; English.

The present invention describes a number of peptides which are able to bind to HIV glycoprotein 120 (gp120). These are similar to the human chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are useful in the treatment of HIV, as they prevent replication of the virus. The present sequence is an example of a peptide of the invention

Sequence 18 AA:

|    |                                                                           |
|----|---------------------------------------------------------------------------|
| XX | WO200116182-A2.                                                           |
| PN |                                                                           |
| XX |                                                                           |
| XX | 08-MAR-2001.                                                              |
| PD |                                                                           |
| XX |                                                                           |
| XX | 25-AUG-2000; 2000WO-US023505.                                             |
| PF |                                                                           |
| XX |                                                                           |
| XX | 27-AUG-1999; 99US-0151270P.                                               |
| PR |                                                                           |
| XX |                                                                           |
| XX | (USSH ) US DEPT HEALTH & HUMAN SERVICES.                                  |
| PA |                                                                           |
| XX |                                                                           |
| XX | Saxinger C;                                                               |
| PI |                                                                           |
| XX |                                                                           |
| DR | WPI; 2001-244398/25.                                                      |
| XX |                                                                           |
| PT | Novel polypeptides useful for treating HIV infection, have homology to    |
| XX | regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,   |
| PT | and binds to HIV gp120 under physiological conditions.                    |
| PT |                                                                           |
| XX |                                                                           |
| PS | Claim 21, Page 38; 114pp; English.                                        |
| XX |                                                                           |
| CC | The present invention describes a number of peptides which are able to    |
| CC | bind to HIV glycoprotein 120 (gp120). These are similar to the human      |
| CC | chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are     |
| CC | useful in the treatment of HIV, as they prevent replication of the virus. |
| CC | The present sequence is an example of a peptide of the invention          |
| XX |                                                                           |
| XX | Sequence 18 AA;                                                           |
| SO |                                                                           |

[illegible]

PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library  
 PT is useful to detect, treat and prevent HIV infection.

XX Example 2; Fig 2A; 28pp; English.

XX The invention relates to nucleic acid encoding a protein which interacts  
 CC with the carboxy terminus of the chemokine receptor CCR5 or of other  
 CC chemokine receptor family members. Molecules of the invention are used to  
 CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5  
 CC -derived peptides, or compounds derived from the protein of the invention  
 CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein  
 CC of the invention would block HIV infection. The present sequence is human  
 CC chemokine receptor CCR5 C-terminal fragment deletion mutant which is  
 CC incapable of interacting with the protein of the invention

XX Sequence 27 AA;

Query Match 100.0%; Score 95; DB 5; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
 |||||  
 Db 3 YAFVGEKFRNYLLVFFQK 20

RESULT 4

AAE14756  
 ID AAE14756 standard; peptide; 43 AA.

XX AAE14756;

DT 04-OCT-2002 (first entry)

DE Human CCR5 chemokine receptor deletion mutant fragment (aa 295-337).

KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;

KW human immunodeficiency virus; gene therapy; human; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 43 /note= "Wild-type Ser replaced by Glx"

XX EPI207202-A1.

XX 22-MAY-2002.

PF 12-NOV-2001; 2001EP-00126500.

XX 16-NOV-2000; 2000EP-00125052.

XX (MOEL/) MOELLING K.

XX Moelling K, Schwenecker M;

XX WPI; 2002-437464/47.

XX Nucleic acid encoding a protein which interacts with the carboxy terminus  
 PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library  
 PT is useful to detect, treat and prevent HIV infection.

XX Example 2; Fig 2A; 28pp; English.

XX The invention relates to nucleic acid encoding a protein which interacts  
 CC with the carboxy terminus of the chemokine receptor CCR5 or of other  
 CC chemokine receptor family members. Molecules of the invention are used to  
 CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5  
 CC -derived peptides, or compounds derived from the protein of the invention  
 CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein  
 CC of the invention would block HIV infection. The present sequence is human

CC chemokine receptor CCR5 C-terminal fragment deletion mutant which is  
 CC incapable of interacting with the protein of the invention

XX Sequence 43 AA;

Query Match 100.0%; Score 95; DB 5; Length 43;  
 Best Local Similarity 100.0%; Pred. No. 2e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
 |||||  
 Db 3 YAFVGEKFRNYLLVFFQK 20

RESULT 5

AAE14759  
 ID AAE14759 standard; peptide; 58 AA.

XX AAE14759;

DT 04-OCT-2002 (first entry)

DE Human CCR5 chemokine receptor C-terminal mutant fragment (aa 295-352).

KW Chemokine receptor CCR5; P2 protein; HIV infection; AIDS;

KW human immunodeficiency virus; gene therapy; human; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 58 /note= "Wild-type Leu replaced by Pro"

XX EPI207202-A1.

XX 22-MAY-2002.

PF 12-NOV-2001; 2001EP-00126500.

XX 16-NOV-2000; 2000EP-00125052.

XX (MOEL/) MOELLING K.

XX Moelling K, Schwenecker M;

XX WPI; 2002-437464/47.

XX Nucleic acid encoding a protein which interacts with the carboxy terminus  
 PT of the chemokine receptor CCR5 isolated from a human B cell cDNA library  
 PT is useful to detect, treat and prevent HIV infection.

XX Example 2; Fig 2A; 28pp; English.

XX The invention relates to nucleic acid encoding a protein which interacts  
 CC with the carboxy terminus of the chemokine receptor CCR5 or of other  
 CC chemokine receptor family members. Molecules of the invention are used to  
 CC detect, prevent and treat HIV infection and progression to AIDS. Any CCR5  
 CC -derived peptides, or compounds derived from the protein of the invention  
 CC (e.g. antagonist or mutants) that disrupt binding of CCR5 to the protein  
 CC of the invention would block HIV infection. The present sequence is human  
 CC chemokine receptor CCR5 C-terminal mutant fragment which is incapable of  
 CC interacting with the protein of the invention

XX Sequence 58 AA;

Query Match 100.0%; Score 95; DB 5; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
 |||||  
 Db 3 YAFVGEKFRNYLLVFFQK 20



CC polypeptide comprising one or more conservative substitutions. The NOVX  
CC polypeptide is useful for treating or preventing a pathology associated  
CC with the polypeptide e.g. disorders associated with aberrant expression  
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
CC endocrine, CNS and inflammatory disorders. They can also be used in  
CC various detection and screening assays, chromosome mapping, tissue typing  
CC and predictive medicine. This sequence corresponds to one of the  
CC polypeptides of the invention.

XX SQ Sequence 268 AA;

Query Match 100.0%; Score 95; DB 7; Length 268;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 213 YAFVGEKFRNLLVFFQK 230

RESULT 8

ADCl0144

ID ADCl0144 standard; protein; 268 AA.

XX AC ADCl0144;

XX DT 18-DEC-2003 (first entry)

XX DE Human NOVX polypeptide SEQ ID NO: 164.

XX cytotactic; antidiabetic; anorectic; cerebroprotective; neuroprotective;  
KW antiinflammatory; gene therapy; antisense therapy; thyromimetic; NOVX;  
KW pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder;  
KW inflammatory disorder; chromosome mapping; tissue typing;  
KW predictive medicine.

XX OS Homo sapiens.

XX PN WC2003000842-A2.

XX PD 03-JAN-2003.

XX PF 04-JUN-2002; 2002WO-US017443.

XX PR 04-JUN-2001; 2001US-0295607P.

XX PR 04-JUN-2001; 2001US-0295661P.

XX PR 06-JUN-2001; 2001US-0296404P.

XX PR 06-JUN-2001; 2001US-0296418P.

XX PR 07-JUN-2001; 2001US-0296575P.

XX PR 11-JUN-2001; 2001US-0297414P.

XX PR 12-JUN-2001; 2001US-0295573P.

XX PR 12-JUN-2001; 2001US-0297567P.

XX PR 14-JUN-2001; 2001US-0298285P.

XX PR 15-JUN-2001; 2001US-0298528P.

XX PR 18-JUN-2001; 2001US-0299133P.

XX PR 19-JUN-2001; 2001US-0299230P.

XX PR 21-JUN-2001; 2001US-0299949P.

XX PR 22-JUN-2001; 2001US-0300177P.

XX PR 26-JUN-2001; 2001US-0300883P.

XX PR 28-JUN-2001; 2001US-0301530P.

XX PR 28-JUN-2001; 2001US-0301550P.

XX PR 03-JUL-2001; 2001US-0302951P.

XX PR 31-JUL-2001; 2001US-0308909P.

XX PR 14-SEP-2001; 2001US-0322979P.

XX PR 25-SEP-2001; 2001US-0324669P.

XX PR 03-DEC-2001; 2001US-0337477P.

XX PR 14-DEC-2001; 2001US-0341562P.

XX PR 21-FEB-2002; 2002US-0358656P.

XX PR 21-FEB-2002; 2002US-0359122P.

XX PR 22-FEB-2002; 2002US-0358978P.

XX PR 22-FEB-2002; 2002US-0359034P.

XX PR 22-FEB-2002; 2002US-0359121P.

PR 27-FEB-2002; 2002US-0359364P.  
PR 01-MAR-2002; 2002US-0360858P.  
PR 12-MAR-2002; 2002US-0363430P.  
PR 12-MAR-2002; 2002US-0363676P.  
PR 10-APR-2002; 2002US-0371346P.  
PR 10-MAY-2002; 2002US-0379444P.  
PR 04-JUN-2002; 2002US-00379444.

XX (CURA-) CURAGEN CORP.

XX AGee ML, Anderson DW, Berghs C, Casman SJ, Catterton E;  
PI Dipippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;  
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, Kekuda R;  
PI Khramsov NV, Li L, Liu X, Malyankar UM, Miller CE, Millet I;  
PI Ort T, Padigaru M, Patturajan M, Pena CE, Rastelli L, Rieger DK;  
PI Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G, Spaderna SK;  
PI Spytek KA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobrook JP;  
PI Burgess CE, Lepley DM;

XX WPI; 2003-210149/20.

XX N-PSDB; ADCl0143.

XX New isolated NOVX polypeptides and nucleic acid molecules useful for  
PT treating, preventing and diagnosing pathological conditions with NOVX-  
PT associated disorders, such as cancer, obesity, diabetes and inflammatory  
PT or CNS diseases.

XX Claim 1; SEQ ID NO 164; 772pp; English.

XX The invention relates to novel isolated polypeptides, mature form of the  
CC polypeptide, a sequence that is 95% identical to the polypeptide or the  
CC polypeptide comprising one or more conservative substitutions. The NOVX  
CC polypeptide is useful for treating or preventing a pathology associated  
CC with the polypeptide e.g. disorders associated with aberrant expression  
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and  
CC endocrine, CNS and inflammatory disorders. They can also be used in  
CC various detection and screening assays, chromosome mapping, tissue typing  
CC and predictive medicine. This sequence corresponds to one of the  
CC polypeptides of the invention.

XX SQ Sequence 268 AA;

Query Match 100.0%; Score 95; DB 7; Length 268;

Best Local Similarity 100.0%; Pred. No. 1.4e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

DB 213 YAFVGEKFRNLLVFFQK 230

RESULT 9

AAW26766

ID AAW26766 standard; protein; 332 AA.

XX AC AAW26766;

XX DT 21-MAY-1998 (first entry)

XX DE Human chemokine receptor MMLR-CCR.

XX Mammalian mixed lymphocyte receptor; chemokine receptor; MMLR-CCR; human;  
KW monocyte; macrophage; chemotaxis; haematopoiesis; infection;  
KW inflammation; proliferative disease; cardiovascular disease; tumour;  
KW rheumatoid arthritis; alveolitis; atherosclerosis;  
KW chronic granulomatous disease; asthma; myasthenia gravis; diabetes;  
KW inflammatory bowel disease; toxic shock syndrome; septic shock;  
KW Chediak-Higashi syndrome; therapy; diagnosis.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 107..128

FT Misc-difference 121 /note= "conserved peptide"  
 FT FT /note= "a claimed polypeptide has isoleucine at residue  
 FT 121"  
 XX  
 PN WO9741225-A2.  
 XX  
 PD 06-NOV-1997.  
 XX  
 PF 25-APR-1997; 97WO-US006993.  
 XX  
 PR 26-APR-1996; 96US-00638081.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Au-Young J, Bandman O, Coleman R, Wilde CG;  
 XX  
 DR WPI; 1997-549729/50.  
 XX  
 DR N-PSDB; AAT99542.  
 XX  
 PT Polynucleotide encoding MMLR-CCR or MPH-CCR chemokine receptor - useful  
 PT to study, diagnose and treat, e.g. infection, inflammation, solid tumour  
 PT and proliferative and cardiovascular disease.  
 XX  
 PS Claim 8; Page 37-38; 59pp; English.  
 XX  
 CC This protein comprises human MMLR-CCR, a novel C-C chemokine receptor  
 CC associated with monocyte/macrophage infiltration and chemotaxis and  
 CC haematopoiesis. The amino acid sequence was deduced from a cDNA clone  
 CC (see AAT99542) obtained from a cDNA library made from mononuclear cells  
 CC collected on day 2 of a mixed lymphocyte culture, i.e. cells associated  
 CC with inflammation and immunomodulation. Another novel chemokine receptor,  
 CC MPH-CCR (see AAT36767), is also claimed. MMLR-CCR contains 7  
 CC transmembrane spanning segments connected by a series of intracellular  
 CC and extracellular loops. MMLR-CCR and MPH-CCR can be used to study,  
 CC diagnose and treat disease states in which normal leukocyte function is  
 CC perturbed by normal leukopoiesis or inappropriate activation via  
 CC chemokine agonists or antagonists, such as infection, inflammation,  
 CC proliferative disease, tumorigenesis, autoimmune disease, abnormal cell  
 CC proliferation, solid tumours, cardiovascular disease, rheumatoid  
 CC arthritis, alveolitis, atherosclerosis, chronic granulomatous disease,  
 CC asthma, myasthenia gravis, diabetes, inflammatory bowel disease, toxic  
 CC shock syndrome, septic shock and Chediak-Higashi syndrome  
 XX  
 SQ Sequence 332 AA;  
 Query Match 100.0%; Score 95; DB 2; Length 332;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFNRYLLVFFQK 18  
 DB 277 YAFVGEKFNRYLLVFFQK 294  
 RESULT 10  
 AAW27407  
 ID AAW27407 standard; protein; 352 AA.  
 XX  
 AC AAW27407;  
 XX  
 DT 14-APR-1998 (first entry)  
 XX  
 DE Human CCR5.  
 XX  
 KW Human Cys-Cys chemokine receptor 5; CCR5; human immunodeficiency virus;  
 KW type 1; type 2; HIV-1; HIV-2; diagnosis; treatment; prevention;  
 KW inflammatory disease; rheumatoid arthritis; glomerulonephritis; asthma;  
 KW idiopathic pulmonary fibrosis; psoriasis; viral infection; cancer;  
 KW atherosclerosis; autoimmune disorder.  
 XX  
 OS Homo sapiens.  
 XX

PN WO9732019-A2.  
 XX  
 PD 04-SEP-1997.  
 XX  
 PF 28-FEB-1997; 97WO-BE000023.  
 XX  
 PR 01-MAR-1996; 96EP-00870021.  
 XX  
 PR 06-AUG-1996; 96EP-00870102.  
 XX  
 PA (EURO-) EUROSCREEN SA.  
 XX  
 PI Samson M, Parmentier M, Vassart G, Libert F;  
 XX  
 DR WPI; 1997-479829/44.  
 XX  
 DR N-PSDB; AAT90117.  
 XX  
 PT Active and inactive forms of human CC chemokine receptor CCR-5 - useful  
 PT to diagnose, prevent and/or treat inflammatory disorders, autoimmune  
 PT disease and viral infection.  
 XX  
 PS Claim 4; Fig 1b-c; 94pp; English.  
 XX  
 CC The present sequence is human CC (Cys-Cys) chemokine receptor 5 (CCR5),  
 CC which is stimulated by MIP-1 alpha, MIP-1 beta or RANTES chemokines, but  
 CC not by monocyte chemoattractant protein 1 (MCP-1), MCP-2, MCP-3, but  
 CC chemokines. Active CCR-5 is also a receptor of human immunodeficiency  
 CC virus type 1 or type 2 (HIV-1 or HIV-2). CCR5 or its cDNA can be used to  
 CC diagnose, treat and/or prevent inflammatory diseases, e.g. rheumatoid  
 CC arthritis, glomerulonephritis, asthma, idiopathic pulmonary fibrosis and  
 CC psoriasis, viral infections, especially HIV-1 or HIV-2 infection, cancer,  
 CC atherosclerosis and autoimmune disorders  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 95; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFNRYLLVFFQK 18  
 DB 297 YAFVGEKFNRYLLVFFQK 314  
 RESULT 11  
 AAW27123  
 ID AAW27123 standard; protein; 352 AA.  
 XX  
 AC AAW27123;  
 XX  
 DT 14-DEC-1997 (first entry)  
 XX  
 DE Human chemokine receptor 88C.  
 XX  
 KW Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;  
 KW asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;  
 KW diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;  
 KW modulator; antibody; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..32 /label= Extracellular\_domain  
 FT FT 56..67 /label= Intracellular\_domain  
 FT FT 89..112 /label= Extracellular\_domain  
 FT FT 125..145 /label= Extracellular\_domain  
 FT FT 166..191 /label= Intracellular\_domain  
 FT FT 213..235 /label= Extracellular\_domain  
 FT FT

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FT Domain /label= Intracellular_domain
FT 259..290
FT /label= Extracellular_domain
FT 301..352
FT /label= Intracellular_domain
XX WO9722698-A2.
XX
XX 26-JUN-1997.
XX
XX 20-DEC-1996; 96WO-US020759.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX WPI; 1997-341689/31.
XX N-PSDB; AAT85161.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 16; Page 47-48; 65pp; English.
XX
XX This polypeptide sequence comprises novel human chemokine receptor 88C, a
XX G protein coupled receptor that is involved in leukocyte trafficking. Its
XX amino sequence was deduced from a cDNA clone (AAT85161) isolated from a
XX macrophage library. It shows 62% identity to CCKXR1. Chemokine receptor
XX 88-2B (see AAW27124) has also been identified. 88C and 88-2B receptors
XX and their polypeptide fragments can be produced in transformed host
XX cells. The receptors, peptides comprising one or more of the
XX extracellular or intracellular domains, and anti-receptor antibodies can
XX be used to modulate receptor activities, particularly ligand and G
XX protein binding, and are potentially potentially useful in the treatment
XX of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX infection, AIDS, inflammatory conditions, pathological immune response,
XX abnormal haematopoietic processes etc
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNLLVFFQK 18
XX |||||
XX 297 YAFVGEKFRNLLVFFQK 314
XX
XX Db
XX
XX RESULT 12
XX AAW27125
XX ID AAW27125 standard; protein; 352 AA.
XX
XX AC AAW27125;
XX
XX 14-DEC-1997 (first entry)
XX
XX Macaque chemokine receptor 88C.
XX
XX Chemokine receptor 88C; atherosclerosis; rheumatoid arthritis; tumour;
XX asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy;
XX diagnosis; leukocyte trafficking; G protein coupled receptor; ligand;
XX modulator; antibody.
XX
XX Macaca sp.
XX
XX WO9722698-A2.
XX
XX 26-JUN-1997.

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XX 20-DEC-1996; 96WO-US020759.
XX
XX 20-DEC-1995; 95US-00575967.
XX
XX 07-JUN-1996; 96US-00661393.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray PW, Schweickart VL, Raport CJ;
XX WPI; 1997-341689/31.
XX N-PSDB; AAT85163.
XX
XX New nucleic acid encoding chemokine receptors 88-2B and 88C - used to
XX modulate leukocyte trafficking, e.g. for treatment of inflammation,
XX tumours, viral infections, auto-immune diseases, etc.
XX
XX Claim 36; Page 57-58; 65pp; English.
XX
XX This polypeptide sequence comprises macaque chemokine receptor 88C, a G
XX protein coupled receptor that is involved in leukocyte trafficking. Its
XX amino sequence was deduced from a 88C DNA (AAT85163) isolated by PCR
XX amplification. It shows 9% identity to human 88C (AAW27123). 88C
XX receptors and their polypeptide fragments can be produced in transformed
XX host cells. The receptors, peptides comprising one or more of the
XX extracellular or intracellular domains, and anti-receptor antibodies can
XX be used to modulate receptor activities, particularly ligand and G
XX protein binding, and are potentially potentially useful in the treatment
XX of atherosclerosis, rheumatoid arthritis, tumours, asthma, viral
XX infection, AIDS, inflammatory conditions, pathological immune response,
XX abnormal haematopoietic processes etc. A hybridoma that produces an
XX antibody that specifically binds to macaque 88C is claimed
XX
XX Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 2; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNLLVFFQK 18
XX |||||
XX 297 YAFVGEKFRNLLVFFQK 314
XX
XX Db
XX
XX RESULT 13
XX AAW07602
XX ID AAW07602 standard; protein; 352 AA.
XX
XX AC AAW07602;
XX
XX 26-FEB-1997 (first entry)
XX
XX Human G-protein chemokine receptor HDGMR10.
XX
XX G-protein chemokine receptor; HDGMR10; signal transduction;
XX haematopoiesis; leukaemia; inflammation; rheumatoid arthritis; diagnosis;
XX therapy.
XX
XX Homo sapiens.
XX
XX WO9639437-A1.
XX
XX 12-DEC-1996.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX 06-JUN-1995; 95WO-US007173.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Li Y, Ruben SM;
XX
XX WPI; 1997-043072/04.

```

DR N-PSDB; AAT44042.  
 XX Human G-protein chemokine receptor, HDGNR10 - useful to identify  
 PT (antagonists, for treatment of haematopoiesis, leukaemia, chronic and  
 PT acute inflammation, rheumatoid arthritis, etc.  
 XX  
 XX Claim 1; Page 44-46; 61pp; English.  
 XX  
 XX Novel human mature G-protein chemokine receptor HDGNR10 (AAW07602) is a 7  
 CC -transmembrane protein involved in signal transduction. Its amino acid  
 CC sequence was deduced from a cDNA clone (AAT44042) isolated from a human  
 CC monocyte library. Isolation of the cDNA allows prodn. of recombinant  
 CC HDGNR10 in host, e.g. E. coli, COS or Sf9, cells. The recombinant  
 CC receptor can be used to identify agonists or antagonists of the receptor;  
 CC such cpds. can be used to treat conditions related to the under- and over  
 CC -expression of G-protein chemokine receptors  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 95; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNYLLVFFQK 18  
 DB 297 YAFVGEKFRNYLLVFFQK 314  
 RESULT 14  
 AAW23835  
 ID AAW23835 standard; protein; 352 AA.  
 AC AAW23835;  
 XX  
 DT 08-JUN-1998 (first entry)  
 XX  
 DE Human CC chemokine receptor 5 (CCR5).  
 XX  
 XX CC chemokine receptor 5; CCR5; G-protein coupled receptor;  
 KW human immunodeficiency virus; HIV; CD4; AIDS; therapy; transgenic animal.  
 KW  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Domain /label= I  
 FT /note= "transmembrane domain"  
 FT 104..126  
 FT /label= III  
 FT /note= "transmembrane domain"  
 FT 109..120  
 FT /note= "extracellular loop-1 (Claim 19)"  
 FT 143..171  
 FT /label= IV  
 FT /note= "transmembrane domain"  
 FT 187..210  
 FT /note= "extracellular loop-2 (Claim 19)"  
 FT 194..219  
 FT /label= V  
 FT /note= "transmembrane domain"  
 FT 238..258  
 FT /label= VI  
 FT /note= "transmembrane domain"  
 FT 261..276  
 FT /note= "extracellular loop-3 (Claim 19)"  
 FT 277..300  
 FT /label= VII  
 FT /note= "transmembrane domain"  
 FT  
 XX WO9745543-A2.  
 XX  
 XX 04-DEC-1997.  
 XX

PF 28-MAY-1997; 97WO-US009586.  
 XX  
 PR 28-MAY-1996; 96US-0018508P.  
 XX  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Combadriere C, Feng Y, Berger EA, Alkhatib G, Murphy PM;  
 PI Broder CC, Kennedy PE;  
 XX  
 XX WPI: 1998-032650/03.  
 DR N-PSDB; AAT76920.  
 XX  
 CC chemokine receptor 5 polypeptide - used to inhibit membrane fusion  
 PT between HIV and a target cell.  
 XX  
 XX Claim 68; Fig 1C; 70pp; English.  
 XX  
 XX This protein sequence comprises of a novel human macrophage-selective CC  
 CC chemokine receptor that has been designated CCR5. The sequence was  
 CC deduced from an isolated cDNA clone (see AAT76920). An Alai27Leu variant  
 CC (see W238340 of CCR5 was also identified. The susceptibility of human  
 CC macrophages to HIV infection depends on cell surface expression of CD4  
 CC and CCR5. CCR5 is a member of the 7-transmembrane superfamily of G-  
 CC protein coupled cell surface molecules. It plays an essential role in the  
 CC membrane fusion step of infection by some HIV isolates. The establishment  
 CC of stable, non-human cell lines and transgenic mammals having cells that  
 CC coexpress human CD4 and CCR5 provides valuable tools for research of HIV  
 CC infection. Antibodies that bind to CCR5, CCR5 variants, and CCR5-binding  
 CC agents capable of blocking membrane fusion between HIV and target cells  
 CC represent potential anti-HIV therapeutics for macrophage tropic strains  
 CC of HIV  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 95; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNYLLVFFQK 18  
 DB 297 YAFVGEKFRNYLLVFFQK 314  
 RESULT 15  
 AAW88232  
 ID AAW88232 standard; protein; 352 AA.  
 XX  
 AC AAW88232;  
 XX  
 DT 15-MAR-1999 (first entry)  
 XX  
 DE HIV-1 co-receptor CCR5.  
 XX  
 KW HIV-1; CCR5; CCR5m303; co-receptor; infection; diagnosis; AIDS;  
 KW gene therapy, human.  
 XX  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Domain /label= I  
 FT /note= "transmembrane domain 1"  
 FT 67..87  
 FT /note= "transmembrane domain 2"  
 FT /note= "transmembrane domain 3"  
 FT /note= "transmembrane domain 4"  
 FT /note= "transmembrane domain 5"  
 FT 103..124  
 FT /note= "transmembrane domain 1"  
 FT 142..167  
 FT /note= "transmembrane domain 2"  
 FT 200..223  
 FT /note= "transmembrane domain 3"  
 FT 236..260  
 FT /note= "transmembrane domain 4"  
 FT /note= "transmembrane domain 5"



FT /note= "transmembrane domain 6"  
 FT 275...301  
 FT /note= "transmembrane domain 7"

XX W09854317-A1.

XX 03-DEC-1998.

XX 29-MAY-1998; 98WO-EP003437.

XX 30-MAY-1997; 97US-0048057P.

XX (MOND-) FOND MONDIALE RECH & PREVENTION SIDA.

XX Beretta A, Quillent C, Arenzana Siesdedos F, Braun J;

XX WPI; 1999-059835/05.

XX N-PSDB; AAV84126.

XX New CCR5 variant protein of the HIV-1 co-receptor - useful in developing  
 resistance of CCR5-expressing cells to HIV-1 infection.

XX Disclosure; Page 34-35; 55pp; English.

CC This is the amino acid sequence of wild-type human CCR5, which serves as  
 a co-receptor for infection by macrophage-tropic (M-tropic) strains of  
 HIV-1. The invention relates to the identification of a CCR5 variant (see  
 AAV84231), designated CCR5m303, comprising the first two transmembrane  
 domains of wild-type CCR5, but lacking transmembrane domains 3-7. The  
 presence of the CCR5m303 variant with the wild type CCR5 allele shows a  
 positive correlation with resistance to infection with M-tropic HIV-1  
 strains, and may indicate slower progression of the disease. The  
 detection of CCR5 variants may be used to identify individuals at lower  
 risk of infection relative to the general population who, if infected,  
 may exhibit slower progression to AIDS. Probes and primers (see AAV84127-  
 36) are provided for use in diagnostic methods for detecting the presence  
 of such variants. A method is provided for inhibiting HIV-1 infection of  
 a cell expressing the CCR5 receptor. This involves introducing a nucleic  
 acid encoding a CCR5 variant into the cell, thereby reducing the number  
 of functional CCR5 molecules present on the cell surface

XX Sequence 352 AA;

Query Match 100.0%; Score 95; DB 2; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18  
 |||||  
 DB 297 YAFVGEKFRNVLVFFQK 314

RESULT 16

AAV80128  
 ID AAV80128 standard; protein; 352 AA.

XX AC AAV80128;

XX 19-MAY-2000 (first entry)

XX Human G-protein chemokine receptor HDGNR10 SEQ ID NO:2.

XX Human; G-protein coupled receptor; G-protein chemokine receptor; HDGNR10;  
 KW diagnosis; haematopoiesis; wound healing; coagulation; angiogenesis;  
 KW tumour; infection; leukaemia; psoriasis; allergy;  
 KW T-cell mediated autoimmune disease; atherosclerosis; anaphylaxis;  
 KW inflammation; allergic reaction; silicosis; sarcoidosis;  
 KW rheumatoid arthritis; hyper-eosinophilia syndrome.

XX Homo sapiens.

XX US025154-A.

XX

PD 15-FEB-2000.

XX 06-JUN-1995; 95US-00466343.

XX 06-JUN-1995; 95US-00466343.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Li Y, Ruben SM;

XX WPI; 2000-181807/16.

XX N-PSDB; AAZ91481.

XX Isolated nucleic acid encoding human G-protein chemokine receptor useful  
 for diagnostic assays, scientific research and screening for compounds  
 which bind to and activate or inhibit activation of the receptor  
 polypeptides.

XX Claim 1; Fig 1; 22pp; English.

XX The present sequence represents a human G-protein chemokine receptor  
 designated HDGNR10. HDGNR10 polynucleotides are useful in methods of  
 screening for compounds which bind to and either: (1) activate the  
 HDGNR10 polypeptides causing stimulation of haematopoiesis, wound  
 healing, coagulation, and angiogenesis; treatment of solid tumours,  
 chronic infections, leukaemia, T-cell mediated autoimmune diseases,  
 parasitic infections, psoriasis, and to stimulate growth factor activity;  
 or (2) inhibit activation of the HDGNR10 polypeptides which is useful for  
 preventing and/or treating allergy, atherosclerosis, anaphylaxis,  
 malignancy, chronic and acute inflammation, histamine and immunoglobulin  
 E-mediated allergic reactions, prostaglandin-independent fever, bone  
 marrow failure, silicosis, sarcoidosis, rheumatoid arthritis shock and  
 hyper-eosinophilia syndrome. The polynucleotides are also useful for  
 diagnostic assays for detecting diseases related to mutations in the  
 nucleic acid sequences encoding the polypeptides and for detecting an  
 altered level of the soluble form of the receptor polypeptides. The  
 polynucleotides are also useful for in vitro purposes related to  
 scientific research, synthesis of DNA and manufacture of DNA vectors  
 Sequence 352 AA;

Query Match 100.0%; Score 95; DB 3; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18  
 |||||  
 DB 297 YAFVGEKFRNVLVFFQK 314

RESULT 17

AAV79089  
 ID AAV79089 standard; protein; 352 AA.

XX AC AAV79089;

XX 10-DEC-2001 (first entry)

XX Amino acid sequence of human CCR5 protein.

XX Human; receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120;

XX C-type lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection; CCR5.

XX Homo sapiens.

XX WO200164752-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006322.

XX 02-MAR-2000; 2000US-00517605.

XX

PA (UNY ) UNIV NEW YORK STATE.  
 PA (UNY-) UNIV NIJMEGEN.  
 XX  
 PI Littman DR, Kwon D, Van Kooyk Y, Geijtenbeek T;  
 XX  
 XX WPI; 2001-602565/68.  
 XX  
 XX An antibody for the treatment or prevention of HIV-infection comprises a  
 PT gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of  
 PT DC-SIGN due to concomitant conformational change.  
 XX  
 XX Disclosure; Page 118-119; 131pp; English.  
 XX  
 CC The specification describes an antibody which is specific for an  
 CC antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or  
 CC is exposed upon gp120 binding of DC-SIGN due to concomitant  
 CC conformational change. DC-SIGN is a receptor that is specifically  
 CC expressed on dendritic cells and facilitates infection of T lymphocytes  
 CC with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. DC  
 CC -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes)  
 CC with high affinity. The antibody of the invention inhibits the trans  
 CC enhancement of HIV entry into a T cell or macrophage facilitated by  
 CC dendritic cells. The antibody is useful to treat or prevent HIV  
 CC infection. The present sequence represents a human CCR5 protein, which is  
 CC a translocation promoting agent that interacts with CD4. This receptor  
 CC functions in HIV-1 entry into cells  
 XX  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 95; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNVLVFFOK 18  
 DB 297 YAFVGEKFRNVLVFFOK 314  
 RESULT 18  
 AAE07046  
 ID AAE07046 standard; protein; 352 AA.  
 XX  
 XX AAE07046;  
 AC  
 DT 16-OCT-2001 (first entry)  
 XX  
 XX Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.  
 DE  
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;  
 KW cytosolic; immunosuppressive; nontropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..36 /label= Extracellular\_domain  
 FT Domain 37..305 /label= Transmembrane\_domain  
 FT Domain 37..58 /label= Transmembrane\_domain  
 FT Domain 59..67 /label= Intracellular\_loop\_1  
 FT Domain 68..88 /label= Transmembrane\_domain  
 FT Domain 89..102 /label= Extracellular\_loop\_1  
 FT Domain 103..124 /label= Transmembrane\_domain  
 FT Domain 125..141 /label= Transmembrane\_domain  
 FT Domain 142..166 /label= Transmembrane\_domain  
 FT Domain 167..195 /label= Transmembrane\_domain  
 FT Domain 196..223 /label= Transmembrane\_domain  
 FT Domain 224..235 /label= Transmembrane\_domain  
 FT Domain 236..260 /label= Transmembrane\_domain  
 FT Domain 261..274 /label= Transmembrane\_domain  
 FT Domain 287..305 /label= Transmembrane\_domain  
 FT Domain 306..352 /label= Transmembrane\_domain  
 XX  
 XX WO200158916-A2.  
 XX  
 XX 16-AUG-2001.  
 PD  
 XX  
 XX 09-FEB-2001; 2001WO-US004153.  
 PP  
 XX  
 XX 09-FEB-2000; 2000US-0181258P.  
 PR  
 XX 09-MAR-2000; 2000US-0187999P.  
 PR  
 XX 22-SEP-2000; 2000US-0234336P.  
 PR  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 PI  
 XX WPI; 2001-488966/53.  
 DR  
 XX N-PSDB; AAD13282.  
 DR  
 XX  
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor  
 PT (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 PT neurodegenerative disorders.  
 PT  
 XX Claim 102; Fig 1; 518pp; English.  
 PS  
 XX The invention relates to human G-protein chemokine receptor (CCR5)  
 CC HDGNR10 polypeptides and polynucleotides. CCR5 HDGNR10 antibodies are  
 CC useful for treating, preventing or ameliorating a disease or disorder  
 CC associated with inflammation, defective or aberrant chemotaxis of immune  
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's  
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell  
 CC interaction. The disease or disorder may also be an infectious disease  
 CC (e.g. a viral infection such as an early stage HIV infection, a  
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune  
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The  
 CC disease or disorder may be associated with aberrant CCR5 expression, lack  
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand  
 CC function. CCR5 HDGNR10 protein is used as a food additive or preservative  
 CC to increase or decrease storage capabilities. CCR5 HDGNR10 DNA are useful  
 CC for chromosome identification and in gene therapy. CCR5 HDGNR10 DNA, the  
 CC protein, antibodies, agonists and antagonists are also useful in the  
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal  
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,  
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)  
 CC

CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The  
 CC present sequence is human CCR5 HDGMR10 protein  
 CC  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YAFVGEKFRNLLVFFQK 18  
 |||||  
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 19  
 AAE07048  
 ID AAE07048 standard; protein; 352 AA.  
 XX AC AAE07048;  
 XX DT 16-OCT-2001 (first entry)  
 XX DE Human G-protein chemokine receptor (CCR5) HDGMR10 protein #2.  
 XX KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnery;  
 KW cytostatic; immunosuppressive; nontropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.  
 XX OS Homo sapiens.  
 XX PN WO200158916-A2.  
 XX PD 16-AUG-2001.  
 XX PF 09-FEB-2001; 2001WO-US0004153.  
 XX PR 09-FEB-2000; 2000US-0181258P.  
 XX PR 09-MAR-2000; 2000US-0187999P.  
 XX PR 22-SEP-2000; 2000US-0234336P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX DR WPI; 2001-488966/53.  
 XX DR N-PSDB; AAD13299.  
 XX PT Isolated nucleic acid encoding a human G-protein chemokine receptor  
 PT (CCR5) HDGMR10 polypeptide, useful for preventing or treating autoimmune  
 PT diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 PT neurodegenerative disorders.  
 XX PS Example 40; Page 504-505; 518pp; English.

CC The invention relates to human G-protein chemokine receptor (CCR5)  
 CC HDGMR10 polypeptides and polynucleotides. CCR5 HDGMR10 antibodies are  
 CC useful for treating, preventing or ameliorating a disease or disorder  
 CC associated with inflammation, defective or aberrant chemotaxis of immune  
 CC cells, HIV infection (such as Pneumocystis carinii pneumonia or Kaposi's  
 CC sarcoma) or defective or aberrant T-cell antigen presenting cell  
 CC interaction. The disease or disorder may also be an infectious disease  
 CC (e.g. a viral infection such as an early stage HIV infection, a  
 CC cytomegalovirus infection, or a poxvirus infection), an autoimmune  
 CC disease (e.g. rheumatoid arthritis) or a neurodegenerative disorder. The  
 CC disease or disorder may be associated with aberrant CCR5 expression, lack  
 CC of CCR5 function, aberrant CCR5 ligand expression, or lack of CCR5 ligand  
 CC function. CCR5 HDGMR10 protein is used as a food additive or preservative

CC to increase or decrease storage capabilities. CCR5 HDGMR10 DNA are useful  
 CC for chromosome identification and in gene therapy. CCR5 HDGMR10 DNA,  
 CC protein, antibodies, agonists and antagonists are also useful in the  
 CC diagnosis, treatment and prevention of cancer (breast, ovary, adrenal  
 CC gland, bone, bone marrow, gastrointestinal tract, liver, lung,  
 CC urogenital); immune disorders (Addison's disease, allergies, autoimmune  
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis)  
 CC ; cardiovascular disorders (myocardial ischaemias) and wound healing. The  
 CC present sequence is human CCR5 HDGMR10 protein  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;

Best Local Similarity 100.0%; Pred. No. 1.9e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YAFVGEKFRNLLVFFQK 18

|||||

DB 297 YAFVGEKFRNLLVFFQK 314

# RESULT 20

AAG80111  
 ID AAG80111 standard; protein; 352 AA.

XX AC AAG80111;

XX DT 17-JAN-2002 (first entry)

XX DE Human CCR5 protein.

XX KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;  
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;  
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;  
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;  
 KW antirheumatic; antiarthritic.

XX OS Homo sapiens.

XX PN WO200172830-A2.

XX PD 04-OCT-2001.

XX PF 02-APR-2001; 2001WO-EP003708.

XX PR 31-MAR-2000; 2000DE-01016013.

XX PA (IPFP-) IPF PHARM GMBH.

XX PI (FORS/) FORSMANN U.

XX PI Forsemann W, Adermann K, Heitland A, Spodsborg N;

XX DR WPI; 2001-626256/72.

XX PT Diagnostic agent containing two or more receptor-specific ligands, useful  
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand  
 PT inhibitors.

XX PS Disclosure; Page 10; 26pp; German.

XX CC This invention describes a novel diagnostic agent (A) comprising at least  
 CC two different ligands (I) for receptors (II) that are implicated in  
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal  
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.  
 CC Also inhibitors of (I) are used therapeutically against tumors (and their  
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel  
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),  
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,  
 CC endocrine, motor or urogenital systems or skin are affected, and bone  
 CC marrow diseases. The products of the invention are chemokine derivatives  
 CC which have cytostatic, antiinflammatory, antiasthmatic,  
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.

CC Chemokines act on specific tumor and inflammatory cells through a  
 CC constellation of chemokine receptors (CR), which control migration and  
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine  
 CC fragments used to illustrate the method of the invention  
 XX  
 SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||  
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 21  
 AAE04321  
 ID AAE04321 standard; protein; 352 AA.

XX AC AAE04321;  
 XX DT 04-SEP-2001 (first entry)  
 XX DE Human chemokine receptor (CCR), CC-CR-5 related protein #2.

XX KW Human; transformed mammalian cell; CD4; reporter gene; translocation;  
 KW human immuno deficiency virus; HIV; long terminal repeat; LTR; therapy;  
 KW chemokine receptor; CCR; cellular dysfunction; HIV infection; cofactor;  
 KW CC-CR-5; envelope glycoprotein; anti-HIV.

XX OS Homo sapiens.

XX PN US6258527-B1.

XX PD 10-JUL-2001.

XX PF 21-MAY-1997; 97US-00861105.

XX PR 20-MAY-1996; 96US-0017157P.

XX PR 19-JUN-1996; 96US-0020043P.

XX PR 19-MAY-1997; 97US-00858660.

XX PA (AARO-) AARON DIAMOND AIDS RES CENT.

XX PA (UUNY ) UNIV NEW YORK STATE.

XX PI Littman DR, Deng H, Ellmeier W, Landau NR, Liu R;

XX DR WPI; 2001-417127/44.

XX DR N-PSDB; AAD08577.

XX PT Transformed mammalian cell (T) that contains a CD4 gene, reporter gene  
 and HIV LTR for identification of drugs and antibodies for treatment of  
 HIV.

XX PS Disclosure; Col 47-50; 37pp; English.

XX CC The present invention relates to a transformed mammalian cell that  
 CC contains a gene encoding CD4, a construct encoding a reporter gene under  
 CC the regulation of an human immuno deficiency virus (HIV) long terminal  
 CC repeat (LTR) and that has been transduced with a vector encoding a human  
 CC chemokine receptor (CCR) where the CD4 and the CCR are present on the  
 CC cell surface of transformed mammalian cell. The invention is useful for  
 CC identifying drugs or antibodies that interfere with the translocation of  
 CC HIV into transformed mammalian cell or for identifying a human chemokine  
 CC receptor that facilitates the infection of a particular HIV strain into  
 CC the transformed mammalian cell. Compounds identified can be used to treat  
 CC cellular dysfunction and to prevent or combat HIV infection. The present  
 CC sequence is a human chemokine receptor (CCR), CC-CR-5 related protein.  
 CC CC-CR-5 is the principal cofactor for entry mediated by the envelope  
 CC glycoproteins of primary macrophage-tropic strains of HIV-1

XX SQ Sequence 352 AA;

Query Match 100.0%; Score 95; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||  
 DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 22  
 AAE07037  
 ID AAE07037 standard; protein; 352 AA.

XX AC AAE07037;

XX DT 16-OCT-2001 (first entry)

XX DE Human G-protein chemokine receptor (CCR5) HDGNR10 protein #1.

XX KW Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;  
 KW cytosolic; immunosuppressive; neutropenic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;  
 KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..36 /label= Extracellular\_domain

FT Domain 37..305 /label= Transmembrane\_domain

FT Domain 37..58 /label= Transmembrane\_domain

FT Domain 59..67 /label= Intracellular\_loop\_1

FT Domain 68..88 /label= Transmembrane\_domain

FT Domain 89..102 /label= Extracellular\_loop\_1

FT Domain 103..124 /label= Transmembrane\_domain

FT Domain 125..141 /label= Extracellular\_loop\_2

FT Domain 142..166 /label= Transmembrane\_domain

FT Domain 167..195 /label= Extracellular\_loop\_2

FT Domain 196..223 /label= Transmembrane\_domain

FT Domain 224..235 /label= Extracellular\_loop\_3

FT Domain 236..260 /label= Transmembrane\_domain

FT Domain 261..274 /label= Extracellular\_loop\_3

FT Domain 287..305 /label= Transmembrane\_domain

FT Domain 306..352 /label= Extracellular\_domain

XX

PN W0200158915-A2.  
 XX 16-AUG-2001.  
 XX 09-FEB-2001; 2001WO-US004152.  
 XX 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 XX 22-SEP-2000; 2000US-0234336P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 PI WPI; 2001-488965/53.  
 XX N-PSDB; AAD13181.  
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor  
 (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 neurodegenerative disorders.  
 XX Claim 102; Fig 1; 495pp; English.  
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10  
 protein. CCR5 HDGNR10 cDNA is included in ATCC Deposit No: 97183. CCR5  
 HDGNR10 antibodies are useful for treating, preventing or ameliorating a  
 disease or disorder associated with inflammation, defective or aberrant  
 chemotaxis of immune cells, HIV infection (such as Pneumocystis carinii  
 pneumonia or Kaposi's sarcoma) or defective or aberrant T-cell antigen  
 presenting cell interaction. The disease or disorder may also be an  
 infectious disease (e.g. a viral infection such as an early stage HIV  
 infection, a cytomegalovirus infection, or a poxvirus infection), an  
 autoimmune disease (e.g. rheumatoid arthritis), a neurodegenerative  
 disorder. The disease or disorder may be associated with aberrant CCR5  
 expression, lack of CCR5 function, aberrant CCR5 ligand expression, or  
 lack of CCR5 ligand function. CCR5 HDGNR10 protein is used as a food  
 additive or preservative to increase or decrease storage capabilities.  
 CC CCR5 HDGNR10 DNA are useful for chromosome identification and in gene  
 therapy. CCR5 HDGNR10 DNA, protein, antibodies, agonists and antagonists  
 are also useful in the diagnosis, treatment and prevention of cancer  
 (breast, ovary, adrenal gland, bone, bone marrow, gastrointestinal tract,  
 liver, lung, urogenital); immune disorders (Addison's disease, allergies,  
 autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,  
 Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 colitis); cardiovascular disorders (myocardial ischaemias) and wound  
 healing  
 XX Sequence 352 AA;  
 SQ Query Match 100.0%; Score 95; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNLLVFFQK 18  
 DB 297 YAFVGEKFRNLLVFFQK 314  
 RESULT 23  
 AAE07039  
 ID AAE07039 standard; protein; 352 AA.  
 XX AAE07039;  
 AC AAE07039;  
 XX 16-OCT-2001 (first entry)  
 DT Human G-protein chemokine receptor (CCR5) HDGNR10 protein #2.  
 XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation; HIV;  
 KW human immunodeficiency virus; antimicrobial; vasodilator; vulnerary;  
 KW cytostatic; immunosuppressive; nootropic; neuroprotective; gene therapy;  
 KW neurodegenerative disorder; Kaposi's sarcoma; autoimmune disease;

KW rheumatoid arthritis; cancer; breast; ovary; adrenal gland; bone marrow;  
 KW gastrointestinal tract; lung; liver; immune disorder; Addison's disease;  
 KW haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; allergy;  
 KW multiple sclerosis; ulcerative colitis; Crohn's disease; wound healing;  
 KW cardiovascular disorder; myocardial ischaemia.  
 XX Homo sapiens.  
 XX W0200158915-A2.  
 XX 16-AUG-2001.  
 XX 09-FEB-2001; 2001WO-US004152.  
 XX 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Roschke V, Li Y, Ruben SM;  
 PI WPI; 2001-488965/53.  
 XX N-PSDB; AAD13198.  
 XX Isolated nucleic acid encoding a human G-protein chemokine receptor  
 (CCR5) HDGNR10 polypeptide, useful for preventing or treating autoimmune  
 diseases e.g. rheumatoid arthritis, hyperproliferative disorders and  
 neurodegenerative disorders.  
 XX Example 40; Page 486-487; 495pp; English.  
 XX The present sequence is human G-protein chemokine receptor (CCR5) HDGNR10  
 protein. CCR5 HDGNR10 antibodies are useful for treating, preventing or  
 ameliorating a disease or disorder associated with inflammation, such as  
 defective or aberrant chemotaxis of immune cells, HIV infection (such as  
 Pneumocystis carinii pneumonia or Kaposi's sarcoma) or defective or  
 aberrant T-cell antigen presenting cell interaction. The disease or  
 disorder may also be an infectious disease (e.g. a viral infection such  
 as an early stage HIV infection, a cytomegalovirus infection, or a  
 poxvirus infection), an autoimmune disease (e.g. rheumatoid arthritis) or  
 a neurodegenerative disorder. The disease or disorder may be associated  
 with aberrant CCR5 expression, lack of CCR5 function, aberrant CCR5  
 ligand expression, or lack of CCR5 ligand function. CCR5 HDGNR10 protein  
 is used as a food additive or preservative to increase or decrease  
 storage capabilities. CCR5 HDGNR10 DNA are useful for chromosome  
 identification and in gene therapy. CCR5 HDGNR10 DNA, protein,  
 antibodies, agonists and antagonists are also useful in the diagnosis,  
 treatment and prevention of cancer (breast, ovary, adrenal gland, bone,  
 bone marrow, gastrointestinal tract, liver, lung, urogenital); immune  
 disorders (Addison's disease, allergies, autoimmune haemolytic anaemia,  
 Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative  
 colitis); cardiovascular disorders (myocardial ischaemias) and wound healing  
 XX Sequence 352 AA;  
 SQ Query Match 100.0%; Score 95; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNLLVFFQK 18  
 DB 297 YAFVGEKFRNLLVFFQK 314  
 RESULT 24  
 AAB46858  
 ID AAB46858 standard; protein; 352 AA.  
 XX AAB46858;  
 AC AAB46858;  
 XX 16-AUG-2001 (revised)  
 DT

DT 02-AUG-2001 (revised)  
 DT 04-MAY-2001 (first entry)  
 XX Human HDGMR10 protein.  
 XX HDGMR10; human; G-protein chemokine receptor; anti-inflammatory;  
 KW immunomodulatory; anticoagulant; antiallergic; immunosuppressive;  
 KW cytotactic; antiparasitic; antipsoriatic; antirheumatic; antiarthritic;  
 KW vasotropic; gene therapy; haematopoiesis; wound healing; coagulation;  
 KW angiogenesis; solid tumour; infection; leukemia; growth factor activity;  
 KW T-cell mediated autoimmune disease; psoriasis; allergy; atherogenesis;  
 KW anaphylaxis; malignancy; inflammation; histamine; IgE; silicosis; shock;  
 KW immunoglobulin E-mediated allergic reaction; rheumatoid arthritis;  
 KW prostaglandin-independent fever; bone marrow failure; sarcoidosis;  
 KW hyper-eosinophilic syndrome; vulnery.  
 XX Homo sapiens.  
 XX US2001000241-A1.  
 XX 12-APR-2001.  
 XX 29-NOV-2000; 2000US-00725285.  
 XX 06-JUN-1995; 95US-00466343.  
 XX 18-NOV-1998; 98US-00195662.  
 XX 25-JUN-1999; 99US-00339912.  
 XX (LIYY/) LI Y.  
 XX (RUBE/) RUBEN S. M.  
 XX Li Y, Ruben SM;  
 XX WPI; 2001-226317/23.  
 XX N-PSDB; AAF26390.  
 XX New human G-protein chemokine receptor polypeptides and polynucleotides,  
 XX useful for identifying (ant)agonists to the G-protein chemokine receptor.  
 XX Claim 1a; Page 15; 2pp; English.  
 XX This invention describes a novel receptor polypeptide (I) selected from  
 CC (i) a fully defined 329 amino acid sequence (II) fully disclosed in the  
 CC specification; and (ii) a polypeptide encoded by the cDNA contained in a  
 CC plasmid, and fragments, analogs and derivatives of the polypeptide. The  
 CC products of the invention have antiinflammatory, immunomodulatory,  
 CC anticoagulant, antiallergic, immunosuppressive, vulnery, cytostatic,  
 CC antiparasitic, antipsoriatic, antirheumatic, antiarthritic and vasotropic  
 CC activity and can be used for gene therapy. The G-protein chemokine  
 CC receptors, HDGMR10, (I) are useful for screening for compounds which  
 CC activate or inhibit activation of (I). The products of the invention can  
 CC also be used for stimulating haematopoiesis, wound healing, coagulation,  
 CC cell mediated autoimmune diseases, chronic infections, leukemia, T-  
 CC angiogenesis, treating solid tumours, parasitic infections, psoriasis, and  
 CC stimulating growth factor activity. HDGMR10 is useful for treating  
 CC allergy, atherogenesis, anaphylaxis, malignancy, chronic and acute  
 CC inflammation, histamine and immunoglobulin E (IgE)-mediated allergic  
 CC reactions, prostaglandin-independent fever, bone marrow failure,  
 CC silicosis, sarcoidosis, rheumatoid arthritis, shock and hyper-  
 CC eosinophilic syndrome. (N.B. This record was resubmitted to correct  
 CC errors in the keyword formatting)  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 95; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||  
 DB 297 YAFVGEKFRNLLVFFQK 314  
 |||||  
 RESULT 26  
 AAB83354  
 ID AAB83354 standard; protein; 352 AA.  
 XX  
 AC AAB83354;  
 XX  
 DT 09-OCT-2001 (first entry)  
 XX  
 DE Human CCR5 protein sequence.  
 XX Chemotactic chemokine receptor 5; gpl20; CD4; therapy; HIV; CCR5;  
 KW human immunodeficiency virus; anti-inflammatory disease; human.  
 XX Homo sapiens.  
 XX EP1118858-A2.  
 PN  
 XX

RESULT 25  
 ABB56342  
 ID ABB56342 standard; protein; 352 AA.  
 XX  
 AC ABB56342;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Non-endogenous human GPCR protein, SEQ ID NO: 477.  
 KW Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;  
 KW constitutively activated GPCR; agonist; disease.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO200177172-A2.  
 PN  
 XX 18-OCT-2001.  
 XX  
 XX 05-APR-2001; 2001WO-US011098.  
 XX  
 XX 07-APR-2000; 2000US-0195747P.  
 XX  
 XX (AREN-) ARENA PHARM INC.  
 XX Lehmann-Bruinsma K, Liaw CW, Lin I;  
 XX WPI; 2001-648759/74.  
 XX N-PSDB; ASI97978.  
 XX  
 XX Identifying agonists of G protein-coupled receptors (GPCRs) for use in  
 PT disease treatment, comprises contacting candidate compounds with versions  
 PT of GPCRs.  
 XX  
 PS Claim 1; Page 277-278; 394pp; English.  
 XX  
 XX The invention relates to G protein-coupled receptors (GPCRs) for which  
 CC the endogenous ligand has been identified. Non-endogenous constitutively  
 CC activated versions of known GPCRs are used in the invention for the  
 CC direct identification of candidate compounds as receptor agonists,  
 CC inverse agonists or partial agonists. Such agonists are useful as  
 CC therapeutic agents for diseases or disorders associated with GPCRs. The  
 CC present sequence is a non-endogenous version of a known human GPCR  
 XX Sequence 352 AA;  
 SQ  
 Query Match 100.0%; Score 95; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||  
 DB 297 YAFVGEKFRNLLVFFQK 314  
 |||||  
 RESULT 26  
 AAB83354  
 ID AAB83354 standard; protein; 352 AA.  
 XX  
 AC AAB83354;  
 XX  
 DT 09-OCT-2001 (first entry)  
 XX  
 DE Human CCR5 protein sequence.  
 XX Chemotactic chemokine receptor 5; gpl20; CD4; therapy; HIV; CCR5;  
 KW human immunodeficiency virus; anti-inflammatory disease; human.  
 XX Homo sapiens.  
 XX EP1118858-A2.  
 PN  
 XX

PD 25-JUL-2001.  
XX  
FF 03-JAN-2001; 2001EP-00300020.  
XX  
PR 12-JAN-2000; 2000GB-00000659.  
PR 12-JAN-2000; 2000GB-00000661.  
PR 12-JAN-2000; 2000GB-00000663.  
XX (PFIZ ) PFIZER LTD.  
FA (PFIZ ) PFIZER INC.  
XX  
XX Dobbs S, Perros M, Rickett GA;  
XX  
XX WPI; 2001-477089/52.  
DR N-PSDB; AAF87099.  
XX  
XX Determining if an agent can modulate CCR5-gp120 interaction, comprises  
PT incubating the agent with CCR5 and gp120 and determining if the agent  
PT modulates the interaction.  
XX  
XX Claim 1; Page 110; 113pp; English.  
XX  
XX This sequence represents the human CCR5 protein sequence. The invention  
CC relates to a method for determining whether an agent is capable of  
CC modulating the interaction of chemotactic chemokine receptor 5 (CCR5)  
CC with gp120, comprising incubating the agent with CCR5 and gp120 and  
CC determining whether the agent modulates the interaction, where gp120 is  
CC associated with CD4, and where the interaction is a low affinity binding.  
CC The method is used to identify an agent capable of modulating the  
CC interaction of CCR5 with gp120. An agent identified by the method is used  
CC to prepare a pharmaceutical composition for the treatment of a disease or  
CC condition associated with CCR5 and gp120 interaction, to treat a subject  
CC with a disease or condition associated with CCR5 and gp120 interaction,  
CC and for preparing a pharmaceutical for treating human immunodeficiency  
CC virus (HIV). It can also be used to treat anti-inflammatory diseases. The method  
CC is commercially useful, amenable to high throughput screening, and  
CC detects interaction of gp120 with cells expressing only CCR5  
XX  
XX Sequence 352 AA;  
Query Match 100.0%; Score 95; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YAFVGEKFRNYLLVFFQK 18  
DB 297 YAFVGEKFRNYLLVFFQK 314  
RESULT 27  
AAB82948  
ID AAB82948 standard; protein; 352 AA.  
AC AAB82948;  
XX  
XX 21-DEC-2001 (first entry)  
XX  
XX Human HIV-1 co-receptor CCR5.  
DE CCR5; chemokine; co-receptor; human immunodeficiency virus type 1; HIV-1;  
KW infection; therapy; vaccine; anti-HIV-1.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FT Binding-site 2..18  
FT /note= "binds to HIV-1 gp120"  
XX  
XX WO200164710-A2.  
PN  
XX  
XX 07-SEP-2001.  
PD  
XX  
XX 28-FEB-2001; 2001WO-US006699.

XX 29-FEB-2000; 2000US-0185667P.  
PR 19-MAY-2000; 2000US-0205839P.  
PR 07-FEB-2001; 2001US-0267231P.  
XX  
XX (PROG-) PROGENICS PHARM INC.  
FA (AARO-) AARON DIAMOND AIDS RES CENT.  
XX  
XX Dragic T, Olson WC;  
XX  
XX WPI; 2001-611273/70.  
DR N-PSDB; AAH26903.  
XX  
XX Novel compounds comprising specific amino acids within CCR5 (HIV 1 co-  
PT receptor) amino terminal domain including negatively charged and two  
PT sulfated tyrosine residues is useful for treating HIV infection in  
PT humans.  
XX  
XX Claim 1; Page 30; 163pp; English.  
XX  
XX The present sequence is that of human HIV-1 co-receptor CCR5. Amino acids  
CC 2-18 in the N-terminal region of CCR5 comprise an HIV-1 gp120-binding  
CC site that determines the specificity of the interaction between CCR5 and  
CC HIV-1 gp120. Post-translational sulfation of the tyrosine residues in the  
CC CCR5 N-terminus is required for gp120 binding and may critically modulate  
CC the susceptibility of target cells to HIV-1 infection in vivo. The  
CC invention provides claimed sulfated peptides (see AAB82947) that are  
CC based on the CCR5 N-terminal region and which are effective for  
CC inhibiting HIV-1 binding to CCR5. These peptides are used in claimed  
CC methods of inhibiting HIV infection of CD4+ cells, of preventing CD4+  
CC cells from becoming infected with HIV, of treating a subject whose CD4+  
CC cells are infected with HIV, and of identifying an agent which inhibits  
CC binding of a CCR5 ligand to a CCR5 receptor. The methods may be carried  
CC out in a subject, especially a human, infected (therapeutic method), not  
CC infected with HIV (prophylactic method), or in a subject who is not  
CC infected with, but has been exposed to, HIV  
XX  
XX Sequence 352 AA;  
Query Match 100.0%; Score 95; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YAFVGEKFRNYLLVFFQK 18  
DB 297 YAFVGEKFRNYLLVFFQK 314  
RESULT 28  
AAU97150  
ID AAU97150 standard; protein; 352 AA.  
XX  
XX AAU97150;  
AC  
XX  
XX 13-AUG-2002 (first entry)  
XX  
XX Human G-protein chemokine receptor (CCR5) HDGNR10 #1.  
DE  
XX  
XX Human; G-protein chemokine receptor; CCR5; HDGNR10; inflammation;  
KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;  
KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;  
KW hyperproliferative disease; neurological disease; receptor.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2002048786-A1.  
PN  
XX  
XX 25-APR-2002.  
PD  
XX  
XX 09-FEB-2001; 2001US-00779879.  
PF  
XX  
XX 04-FEB-2000; 2000US-0181258P.  
PR  
XX 09-MAR-2000; 2000US-0187999P.  
PR

PR 22-SEP-2000; 2000US-0234336P.  
 XX (ROSE/) ROSEN C A.  
 PA (ROSC/) ROSCHKE V.  
 PA (LIYV/) LI Y.  
 PA (RUBE/) RUBEN S M.  
 XX  
 PI Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX WPI; 2002-434754/46.  
 DR N-PSDB; ABK51853.  
 XX  
 PT New nucleic acid encoding an antibody specific for the G-protein  
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.  
 PT inflammation.  
 XX  
 PS Claim 61; Fig 1; 180pp; English.  
 XX  
 CC The present invention relates to the isolation of a novel human G-protein  
 CC chemokine receptor (CCR5) designated HDGMR10, and polynucleotide  
 CC sequences encoding it. The invention also describes antibodies that bind  
 CC human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide  
 CC sequences encoding the antibodies. The antibodies are useful for treating  
 CC or preventing inflammation, defective or aberrant chemotaxis of immune  
 CC cells and T-cell/antigen-presenting cell interactions, infections and  
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral  
 CC infections (especially early-stage human immune deficiency virus (HIV),  
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions  
 CC associated with aberrant or deficient expression of the CCR5 receptor or  
 CC its ligands. The antibodies are also useful to determine CCR5 expression,  
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other  
 CC hyperproliferative diseases. The polynucleotide sequences encoding human  
 CC G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the  
 CC recombinant receptor, and in the treatment of a wide range of diseases  
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.  
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The  
 CC present sequence represents human G-protein chemokine receptor (CCR5)  
 CC HDGMR10 #1  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 95; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||  
 Db 297 YAFVGEKFRNLLVFFQK 314  
 RESULT 29  
 AAU97152  
 ID AAU97152 standard; protein; 352 AA.  
 XX  
 AC AAU97152;  
 XX  
 DT 13-AUG-2002 (first entry)  
 XX  
 DE Human G-protein chemokine receptor (CCR5) HDGMR10 #2.  
 XX  
 KW Human; G-protein chemokine receptor; CCR5; HDGMR10; inflammation;  
 KW immune cell chemotaxis; autoimmune disease; rheumatoid arthritis;  
 KW neurodegeneration; viral infection; Kaposi sarcoma; cancer;  
 KW hyperproliferative disease; neurological disease; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 OS US2002048786-A1.  
 XX  
 PN 25-APR-2002.  
 XX  
 PD 09-FEB-2001; 2001US-00779879.  
 XX

PR 09-FEB-2000; 2000US-0181258P.  
 PR 09-MAR-2000; 2000US-0187999P.  
 PR 22-SEP-2000; 2000US-0234336P.  
 XX  
 PA (ROSE/) ROSEN C A.  
 PA (ROSC/) ROSCHKE V.  
 PA (LIYV/) LI Y.  
 PA (RUBE/) RUBEN S M.  
 XX  
 PI Rosen CA, Roschke V, Li Y, Ruben SM;  
 XX WPI; 2002-434754/46.  
 DR N-PSDB; ABK51870.  
 XX  
 PT New nucleic acid encoding an antibody specific for the G-protein  
 PT chemokine receptor CCR5, useful for treatment and diagnosis of e.g.  
 PT inflammation.  
 XX  
 PS Disclosure; Page 165-166; 180pp; English.  
 XX  
 CC The present invention relates to the isolation of a novel human G-protein  
 CC chemokine receptor (CCR5) designated HDGMR10, and polynucleotide  
 CC sequences encoding it. The invention also describes antibodies that bind  
 CC human G-protein chemokine receptor (CCR5) HDGMR10 and polynucleotide  
 CC sequences encoding the antibodies. The antibodies are useful for treating  
 CC or preventing inflammation, defective or aberrant chemotaxis of immune  
 CC cells and T-cell/antigen-presenting cell interactions, infections and  
 CC autoimmune diseases, rheumatoid arthritis, neurodegeneration, viral  
 CC infections (especially early-stage human immune deficiency virus (HIV),  
 CC cytomegalovirus or pox virus infections, Kaposi sarcoma, or conditions  
 CC associated with aberrant or deficient expression of the CCR5 receptor or  
 CC its ligands. The antibodies are also useful to determine CCR5 expression,  
 CC e.g. for diagnosis, prognosis and monitoring of cancer and other  
 CC hyperproliferative diseases. The polynucleotide sequences encoding human  
 CC G-protein chemokine receptor (CCR5) HDGMR10 can be used to produce the  
 CC recombinant receptor, and in the treatment of a wide range of diseases  
 CC such as infectious diseases (e.g. influenza), neurological diseases (e.g.  
 CC Parkinson's disease), and hyperproliferative disorders (e.g. cancer). The  
 CC present sequence represents human G-protein chemokine receptor (CCR5)  
 CC HDGMR10 #2  
 XX  
 SQ Sequence 352 AA;  
 Query Match 100.0%; Score 95; DB 5; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||  
 Db 297 YAFVGEKFRNLLVFFQK 314  
 RESULT 30  
 AAU52829  
 ID AAU52829 standard; protein; 352 AA.  
 XX  
 AC AAU52829;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Human CCR5 Gln 55 variant.  
 XX  
 KW CCR5; CC chemokine receptor 5; human; HIV infection;  
 KW human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
 KW drug screening; identification; variant.  
 XX  
 OS Homo sapiens.  
 XX  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 55  
 FT /note= "Glu replaces wild-type Leu; encoded by CTG"  
 FT Misc-difference 58  
 FT /note= "Encoded by AGC"  
 FT



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XX WO200171346-A2.
XX
XX
XX PD 27-SEP-2001.
XX
XX PF 21-MAR-2001; 2001WO-US009155.
XX
XX PR 21-MAR-2000; 2000US-0190946P.
XX PR 21-MAR-2000; 2000US-0190996P.
XX PR 21-MAR-2000; 2000US-0191299P.
XX PR 20-MAR-2001; 2001US-00813448.
XX PR 20-MAR-2001; 2001US-00813651.
XX PR 20-MAR-2001; 2001US-00813653.
XX
XX PA (CONS-) CONSENSUS PHARM INC.
XX
XX PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX
XX DR WPI; 2002-010610/01.
XX DR N-PSDB; ABA02318.
XX
XX PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
XX PT comprises binding a molecule from library to a molecule having binding
XX PT property corresponding to CCR5 and identifying bound molecule.
XX
XX PS Example 3; Fig 4B; 50pp; English.
XX
XX CC The invention relates to a method for identifying a binding compound for
XX CC chemokine receptor 5 (CCR5). The method involves screening a library
XX CC of test molecules (particularly peptides) with immobilised CCR5, and then
XX CC identifying those molecules which bind. The invention also relates to
XX CC CCR5-binding molecules identified using the method of the invention,
XX CC methods for identifying consensus motifs for CCR5-binding peptides, a
XX CC transfer vector encoding tagged CCR5, a computer-aided method for
XX CC determining the relative binding affinity of a test molecule to CCR5 and
XX CC a computer aided drug screening assay that utilises the three-dimensional
XX CC structure of CCR5. Compounds identified using the methods of the
XX CC invention are useful for treating or preventing HIV (human
XX CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
XX CC syndrome) in a patient. The methods of the invention may also be used to
XX CC identify agonists or antagonists of the interaction of CCR5 with its
XX CC natural ligand, and to determine a binding motif for CCR5. The present
XX CC sequence represents a naturally occurring variant of human CCR5 in which
XX CC there is a glutamine, rather than a leucine, at position 55
XX
XX SQ Sequence 352 AA;
XX
XX Query Match 100.0%; Score 95; DB 5; Length 352;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-07;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YAFVGEKFRNVLVFFQK 18
XX Db 297 YAFVGEKFRNVLVFFQK 314
XX
XX Search completed: March 4, 2004, 17:59:25
XX Job time : 43.7959 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 4, 2004, 17:54:12 ; Search time 9.18367 Seconds  
(without alignments)  
188.535 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKFNVLVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 78:\*\*

1: PIR1:\*\*

2: PIR2:\*\*

3: PIR3:\*\*

4: PIR4:\*\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 95    | 100.0       | 352    | 2 A43113 | chemokine (C-C) re |
| 2          | 79    | 83.2        | 360    | 2 J22443 | chemokine (C-C) re |
| 3          | 65    | 68.4        | 355    | 2 G02436 | chemokine (C-C) re |
| 4          | 64    | 67.4        | 359    | 2 I49341 | MIP-1 alpha recept |
| 5          | 63    | 66.3        | 355    | 2 J05067 | G protein-coupled  |
| 6          | 62    | 65.3        | 383    | 2 S55594 | G protein-coupled  |
| 7          | 61    | 64.2        | 359    | 2 J05068 | G protein-coupled  |
| 8          | 60    | 63.2        | 355    | 2 A45177 | chemokine (C-C) re |
| 9          | 58    | 61.1        | 354    | 2 I58186 | probable G protein |
| 10         | 57    | 60.0        | 355    | 2 J04304 | orphan G protein-c |
| 11         | 57    | 60.0        | 360    | 2 A57160 | chemokine (C-C) re |
| 12         | 53    | 55.8        | 355    | 2 I49339 | macrophage inflam  |
| 13         | 53    | 55.8        | 356    | 2 J49340 | MIP-1 alpha recept |
| 14         | 52    | 54.7        | 360    | 2 J04587 | chemokine (C-C) re |
| 15         | 52    | 54.7        | 378    | 2 B55735 | lymphocyte-specifi |
| 16         | 50    | 52.6        | 356    | 2 S42096 | interleukin-8 rece |
| 17         | 50    | 52.6        | 359    | 2 A48921 | interleukin-8 rece |
| 18         | 50    | 52.6        | 360    | 2 A53611 | interleukin-8 rece |
| 19         | 50    | 52.6        | 378    | 2 A56800 | G protein-coupled  |
| 20         | 49    | 51.6        | 76     | 2 E95247 | hypothetical prote |
| 21         | 49    | 51.6        | 76     | 2 B96112 | hypothetical prote |
| 22         | 49    | 51.6        | 374    | 2 I38450 | chemokine (C-C) re |
| 23         | 48    | 50.5        | 367    | 2 J03049 | interferon-inducib |
| 24         | 47    | 49.5        | 358    | 2 A53752 | interleukin-8 rece |
| 25         | 47    | 49.5        | 378    | 2 A55735 | G protein-coupled  |
| 26         | 46    | 48.4        | 354    | 2 A23669 | interleukin-8 rece |
| 27         | 46    | 48.4        | 355    | 2 J01231 | interleukin-8 rece |
| 28         | 45.5  | 47.9        | 377    | 2 B97185 | glycosyltransferas |
| 29         | 45    | 47.4        | 350    | 2 JN0621 | G protein-coupled  |

|     |      |      |      |          |                     |
|-----|------|------|------|----------|---------------------|
| 30  | 45   | 47.4 | 359  | 2 J01104 | angiotensin II rec  |
| 31  | 45   | 47.4 | 359  | 2 S44425 | angiotensin II rec  |
| 32  | 45   | 47.4 | 359  | 2 J01194 | angiotensin II rec  |
| 33  | 45   | 47.4 | 359  | 2 A48857 | angiotensin II rec  |
| 34  | 45   | 47.4 | 359  | 2 A42656 | angiotensin II rec  |
| 35  | 45   | 47.4 | 359  | 2 J01516 | angiotensin II rec  |
| 36  | 45   | 47.4 | 359  | 2 S15403 | angiotensin II rec  |
| 37  | 45   | 47.4 | 359  | 2 JH0621 | angiotensin II rec  |
| 38  | 45   | 47.4 | 359  | 2 J02134 | angiotensin II rec  |
| 39  | 44   | 46.3 | 358  | 2 G02670 | IL8-related recept  |
| 40  | 44   | 46.3 | 375  | 2 J05069 | G protein-coupled   |
| 41  | 43   | 45.3 | 119  | 2 C81207 | hypothetical prote  |
| 42  | 43   | 45.3 | 259  | 2 E64514 | hypothetical prote  |
| 43  | 43   | 45.3 | 293  | 2 T03883 | hypothetical prote  |
| 44  | 43   | 45.3 | 297  | 2 C02070 | sugar transport pr  |
| 45  | 43   | 45.3 | 333  | 2 I65989 | G protein-coupled   |
| 46  | 43   | 45.3 | 350  | 2 S43497 | opsin, 563nm - whi  |
| 47  | 43   | 45.3 | 362  | 2 A37783 | iodopsin - chicken  |
| 48  | 43   | 45.3 | 364  | 1 OOHUR  | opsin, red-sensiti  |
| 49  | 43   | 45.3 | 364  | 1 OOHUG  | opsin, green-sensi  |
| 50  | 43   | 45.3 | 1060 | 2 T30823 | bumetanide sensiti  |
| 51  | 42.5 | 44.7 | 180  | 2 B07020 | hypothetical prote  |
| 52  | 42.5 | 44.7 | 180  | 2 E85570 | hypothetical prote  |
| 53  | 42.5 | 44.7 | 189  | 2 G64805 | ybC protein - Esc   |
| 54  | 42.5 | 44.7 | 855  | 2 A45713 | Env transmembrane   |
| 55  | 42   | 44.2 | 629  | 2 T34370 | hypothetical prote  |
| 56  | 41   | 43.2 | 110  | 2 A6410  | envelope protein (  |
| 57  | 41   | 43.2 | 110  | 2 D82455 | hypothetical prote  |
| 58  | 41   | 43.2 | 203  | 2 T32822 | hypothetical prote  |
| 59  | 41   | 43.2 | 326  | 2 G98835 | conserved hypothet  |
| 60  | 41   | 43.2 | 350  | 2 A39445 | interleukin-8 rece  |
| 61  | 41   | 43.2 | 365  | 2 B46191 | cone visual pigmen  |
| 62  | 41   | 43.2 | 369  | 2 S33250 | red visual pigment  |
| 63  | 41   | 43.2 | 375  | 2 J05509 | G protein-coupled   |
| 64  | 41   | 43.2 | 397  | 2 E70317 | hypothetical prote  |
| 65  | 41   | 43.2 | 632  | 2 E96723 | hypothetical prote  |
| 66  | 41   | 43.2 | 919  | 2 S42842 | Ti6G12.2 protein -  |
| 67  | 40.5 | 42.6 | 323  | 1 Q0BED3 | HHRF3 protein - hu  |
| 68  | 40.5 | 42.6 | 927  | 2 T43110 | lactacin 481/lacto  |
| 69  | 40   | 42.1 | 231  | 2 C69300 | conserved hypothet  |
| 70  | 40   | 42.1 | 271  | 2 T18056 | ATPase homolog A55  |
| 71  | 40   | 42.1 | 301  | 2 S56211 | probable membrane   |
| 72  | 40   | 42.1 | 340  | 2 T44330 | glycosyl transfera  |
| 73  | 40   | 42.1 | 349  | 2 C96738 | unknown protein F3  |
| 74  | 40   | 42.1 | 354  | 2 T09353 | G protein-coupled   |
| 75  | 40   | 42.1 | 371  | 2 J05498 | G protein-coupled   |
| 76  | 40   | 42.1 | 421  | 2 T33811 | hypothetical prote  |
| 77  | 40   | 42.1 | 425  | 2 T23560 | hypothetical prote  |
| 78  | 40   | 42.1 | 543  | 2 T39345 | probable metabolit  |
| 79  | 40   | 42.1 | 608  | 2 T18445 | hypothetical prote  |
| 80  | 40   | 42.1 | 744  | 2 A70385 | DNA gyrase A subun  |
| 81  | 40   | 42.1 | 834  | 2 E69380 | methyl-accepting c  |
| 82  | 40   | 42.1 | 969  | 2 H69425 | modification methy  |
| 83  | 40   | 42.1 | 1024 | 1 RNQ8BF | DNA-directed RNA p  |
| 84  | 40   | 42.1 | 1802 | 2 G71616 | hypothetical prote  |
| 85  | 39.5 | 41.6 | 932  | 2 F84465 | hypothetical prote  |
| 86  | 39   | 41.1 | 167  | 2 F81263 | probable lipoprote  |
| 87  | 39   | 41.1 | 193  | 2 AG1988 | hypothetical protei |
| 88  | 39   | 41.1 | 211  | 2 G83718 | DNA-binding protei  |
| 89  | 39   | 41.1 | 273  | 2 T51512 | hypothetical prote  |
| 90  | 39   | 41.1 | 274  | 2 T41009 | hypothetical prote  |
| 91  | 39   | 41.1 | 274  | 2 E91185 | probable ATP-bindi  |
| 92  | 39   | 41.1 | 274  | 2 C86032 | probable ATP-bindi  |
| 93  | 39   | 41.1 | 274  | 2 S47791 | hypothetical prote  |
| 94  | 39   | 41.1 | 274  | 2 AI0979 | probable exported   |
| 95  | 39   | 41.1 | 305  | 2 T43972 | hypothetical prote  |
| 96  | 39   | 41.1 | 310  | 2 T30004 | hypothetical prote  |
| 97  | 39   | 41.1 | 340  | 2 T09304 | G protein-coupled   |
| 98  | 39   | 41.1 | 351  | 2 B42009 | FWLP-related recep  |
| 99  | 39   | 41.1 | 391  | 2 T32714 | hypothetical prote  |
| 100 | 39   | 41.1 | 507  | 2 T38653 | trp-asp repeat pro  |

## ALIGNMENTS

RESULT 1  
A31113  
chemokine (C-C) receptor 5 - human  
N/Alternate names: C-C CKR-5; CCR5  
C/Species: Homo sapiens (man)  
C/Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 20-Jun-2000  
C/Accession: A43113; S71808; A58832; G02653; A58833  
R/Sanson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
Biochemistry 35, 3362-3367, 1996  
A/Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
A/Reference number: A43113; MUID:96241590; PMID:8639485  
A/Accession: A43113  
A/Molecule type: mRNA  
A/Residues: 1-352 <SAM1>  
A/Cross-references: GB:X91492; NID:g1262810; PIDN:CAA62796.1; PID:g1262811  
R/Sanson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liegnard, C.; Farber, C.M.; Saragosti  
M.; Imai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Parmentier, M.  
Nature 382, 722-725, 1996  
A/Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the *CCR5* gene  
A/Reference number: S71808; MUID:96345670; PMID:8751444  
A/Accession: S71808  
A/Status: nucleic acid sequence not shown; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 182-206/207-230 <SAM2>  
A/Accession: A58834  
A/Status: nucleic acid sequence not shown; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-184, 'TKDSHLCAGPAAACHGILLGNPKNSASVSK' <SAM3>  
A/Cross-references: GB:X99393; NID:g1524062; PIDN:CAA67767.1; PID:g1524063  
A/Note: this frameshift mutation results in a non-functional receptor but confers a degree of resistance to HIV-1 infection  
R/Combadere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.  
J. Leukoc. Biol. 60, 147-152, 1996  
A/Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor  
A/Reference number: A58832; MUID:96295970; PMID:8699119  
A/Accession: A58832  
A/Molecule type: mRNA  
A/Residues: 1-352 <COM1>  
A/Cross-references: GB:U57840; NID:g1502408; PIDN:AAB17071.1; PID:g1502409  
A/Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
R/Combadere, C.  
Submitted to the EMBL Data Library, May 1996  
A/Reference number: H01541  
A/Accession: G02653  
A/Status: translated from GB/EMBL/DDBJ  
A/Molecule type: mRNA  
A/Residues: 1-89, 'L', '91-352 <COM2>  
A/Cross-references: EMBL:U57840  
R/Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.  
J. Biol. Chem. 271, 17161-17166, 1996  
A/Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor  
A/Reference number: A58833; MUID:96291862; PMID:8663314  
A/Accession: A58833  
A/Molecule type: mRNA  
A/Residues: 1-352 <RAP>  
A/Cross-references: GB:U54994; NID:g1457945; PIDN:AA50598.1; PID:g1457946  
C/Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30574) and dual-tropic strains of HIV-1 bind to a complex of chemokine receptor and MIP-1alpha  
C/Genetics:  
A/Status: GDB:CMKBR5; CCR5; CKR-5; CC-CKR-5; CKR5; ChemR13  
A/Cross-references: GDB:1230510; OMIM:601373  
A/Map position: 3p21-3p21  
C/Function:  
A/Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES  
A/Note: probably acts to control granulocyte proliferation and differentiation  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
F/32-56/Domain: transmembrane #status predicted <TM1>  
F/67-87/Domain: transmembrane #status predicted <TM2>  
F/103-124/Domain: transmembrane #status predicted <TM3>

F/142-166/Domain: transmembrane #status predicted <TM4>  
F/193-218/Domain: transmembrane #status predicted <TM5>  
F/236-257/Domain: transmembrane #status predicted <TM6>  
F/285-300/Domain: transmembrane #status predicted <TM7>  
F/20-269,101-178/Disulfide bonds: #status predicted  
F/268/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F/336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted  
F/340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 100.0%; Score 95; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 3.2e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
|||||

DB 297 YAFVGEKFRNYLLVFFQK 314  
|||||

## RESULT 2

JC2443  
chemokine (C-C) receptor 2, splice form B - human  
N/Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemoattractant protein 1  
C/Species: Homo sapiens (man)  
C/Date: 21-Feb-1995 #sequence\_revision 05-Apr-1995 #text\_change 20-Jun-2000  
C/Accession: JC2443; I38463  
R/Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.  
Biochem. Biophys. Res. Commun. 202, 1156-1162, 1994  
A/Title: cDNA cloning and functional expression of a human monocyte chemoattractant protein 1  
A/Reference number: JC2443; MUID:94324942; PMID:8048929  
A/Accession: JC2443  
A/Molecule type: mRNA  
A/Residues: 1-360 <YAM>  
A/Cross-references: DDJB:D29884; NID:g531246; PIDN:BAA06253.1; PID:g531247  
R/Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
A/Title: Molecular cloning and functional expression of two monocyte chemoattractant protein 1  
A/Reference number: A53477; MUID:94195821; PMID:8146186  
A/Accession: I38463  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-360 <RES>  
A/Cross-references: EMBL:U03905; NID:g472557; PIDN:AAA19120.1; PID:g472558  
C/Genetics:  
A/Status: GDB:CMKBR2  
A/Cross-references: GDB:337364; OMIM:601267  
A/Map position: 3p21-3p21  
C/Superfamily: vertebrate rhodopsin  
C/Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

F/81-100/Domain: transmembrane #status predicted <TM1>  
F/115-136/Domain: transmembrane #status predicted <TM2>  
F/154-178/Domain: transmembrane #status predicted <TM3>  
F/207-226/Domain: transmembrane #status predicted <TM4>  
F/244-268/Domain: transmembrane #status predicted <TM5>  
F/287-309/Domain: transmembrane #status predicted <TM6>  
F/314/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F/113-190/Disulfide bonds: #status predicted

Query Match 83.2%; Score 79; DB 2; Length 360;  
Best Local Similarity 83.3%; Pred. No. 1.6e-05;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
|||||

DB 305 YAFVGEKFRNYLLVFFQK 322  
|||||

## RESULT 3

G02436  
chemokine (C-C) receptor 3 - human  
N/Alternate names: C-C CKR-3  
C/Species: Homo sapiens (man)  
C/Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 04-Mar-2000

N; Alternate names: chemokine receptor-like protein TER1; GPR-CV6

C; Species: Homo sapiens (man)

C; Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 21-Jul-2000

R; Zaballos, A.; Varona, R.; Gutierrez, J.; Lind, P.; Marquez, G.

Biochem. Biophys. Res. Commun. 227, 846-853, 1996

A; Title: Molecular cloning and RNA expression of two new human chemokine receptor-like

A; Reference number: JC5067; MUID:197040707; PMID:8886020

A; Accession: JC5067

A; Molecule type: DNA

A; Residues: 1-355 <ZAB>

A; Cross-references: EMBL:Z79782; NID:gl668735; PIDN:CA802142.1; PID:gl668736

R; Napolitano, M.; Zingoni, A.; Bernardini, G.; Spinetti, G.; Rocchi, M.; Santoni, A.

submitted to the EMBL Data Library, June 1996

A; Reference number: H01714

A; Accession: G02776

A; Status: translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-355 <NAP>

A; Cross-references: EMBL:U62556; NID:gl468978; PID:gl468979

R; Borner, T.I.

submitted to the EMBL Data Library, January 1996

A; Reference number: H01154

A; Accession: G02387

A; Status: preliminary; translated from GB/EMBL/DBJ

A; Molecule type: DNA

A; Residues: 1-355 <BON>

A; Cross-references: EMBL:U45983; NID:gl245056; PID:gl245057

C; Comment: This protein belongs to the family of beta chemokine receptors.

C; Genetics:

A; Gene: GDB:CMKBR8; CMKBR2; TER1; CKR-L1

A; Cross-references: GDB:6053733; OMIM:601834

A; Map position: 3p21-3p21

C; Superfamily: vertebrate rhodopsin

C; Keywords: G protein-coupled receptor; transmembrane protein

F; 36-63/Domain: transmembrane #status predicted <TM1>

F; 73-94/Domain: transmembrane #status predicted <TM2>

F; 108-129/Domain: transmembrane #status predicted <TM3>

F; 147-171/Domain: transmembrane #status predicted <TM4>

F; 200-222/Domain: transmembrane #status predicted <TM5>

F; 239-260/Domain: transmembrane #status predicted <TM6>

F; 281-304/Domain: transmembrane #status predicted <TM7>

Query Match 66.3%; Score 63; DB 2; Length 355;

Best Local Similarity 66.7%; Pred. No. 0.0076;

Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18

|||||:|

DB 300 YAFVGEKFKHLSEIFQK 317

RESULT 6

SS5594

G protein-coupled receptor E1 - equine herpesvirus 2

C; Species: equine herpesvirus 2

C; Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 13-Aug-1999

C; Accession: S55594

R; Telford, B.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A; Title: The DNA sequence of equine herpesvirus 2.

A; Reference number: S55594; MUID:95302501; PMID:7783207

A; Accession: S55594

A; Status: preliminary; nucleic acid sequence not shown

A; Molecule type: DNA

A; Residues: 1-383 <TEL>

A; Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173

C; Superfamily: vertebrate rhodopsin

C; Keywords: G protein-coupled receptor

Query Match 65.3%; Score 62; DB 2; Length 383;

Best Local Similarity 75.0%; Pred. No. 0.012;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 YAFVGEKFRNYLLVFF 16
DB 340 YAFVGEKFRNYLLVFF 355

RESULT 7
JC5068
G protein-coupled receptor CKR-L3 - human
C:Species: Homo sapiens (man)
C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C:Accession: JC5068
R:Zaballos, A.; Varona, R.; Guierrez, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A:Title: Molecular cloning and RNA expression of two new human chemokine receptor-like 9
A:Reference number: JC5067; MUID:97040707; PMID:8886020
A:Molecule type: DNA
A:Residues: 1-369 <ZAB>
A:CROSS-references: EMBL:Z79784; NID:gl668738; PIDN:CAB02144.1; PID:gl668738
C:Comment: This protein belongs to the family of alpha chemokine receptors.
C:Genetics:
A:Gene: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A:Map position: 6q27-6q27
A:CROSS-references: GDB:5370639; OMIM:601835
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein
F:42-68/Domain: transmembrane #status predicted <TM1>
F:79-99/Domain: transmembrane #status predicted <TM2>
F:115-136/Domain: transmembrane #status predicted <TM3>
F:160-180/Domain: transmembrane #status predicted <TM4>
F:212-233/Domain: transmembrane #status predicted <TM5>
F:250-271/Domain: transmembrane #status predicted <TM6>
F:292-315/Domain: transmembrane #status predicted <TM7>

Query Match 64.2%; Score 61; DB 2; Length 369;
Best Local Similarity 76.9%; Pred. No. 0.017;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13
DB 311 YAFVGEKFRNYLL 323

RESULT 8
A45177
chemokine (C-C) receptor 1 - human
N:Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C:Accession: A45177; J55671
R:Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A:Title: Molecular cloning, functional expression, and signaling characteristics of a C-
A:Reference number: A45177; MUID:93161416; PMID:7679328
A:Accession: A45177
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-355 <NEO>
A:CROSS-references: GB:110918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A:Experimental source: HL60 cells
A:Note: sequence extracted from NCBI backbone (NCBIP:124876)
R:Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A:Title: Structure and functional expression of the human macrophage inflammatory 1 alpha
A:Reference number: I55671; MUID:93240122; PMID:7683036
A:Accession: I55671
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-355 <RES>
A:CROSS-references: GB:110918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C:Genetics:
A:Gene: GDB:CMKBR1; CMKBR-1

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A:CROSS-references: GDB:138446; OMIM:601159
A:Map position: 3p21-3p21
C:Superfamily: vertebrate rhodopsin
C:Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; t
F:36-60/Domain: transmembrane #status predicted <TM1>
F:71-91/Domain: transmembrane #status predicted <TM2>
F:108-129/Domain: transmembrane #status predicted <TM3>
F:147-171/Domain: transmembrane #status predicted <TM4>
F:205-223/Domain: transmembrane #status predicted <TM5>
F:240-264/Domain: transmembrane #status predicted <TM6>
F:288-305/Domain: transmembrane #status predicted <TM7>
F:5/Binding site: carbohydrate (Agn) (covalent) #status predicted
F:24-273.106-183/Disulfide bonds: #status predicted
F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 63.2%; Score 60; DB 2; Length 355;
Best Local Similarity 61.1%; Pred. No. 0.024;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 301 YAFVGEKFRNYLLVFFQK 318

RESULT 9
I58186
probable G protein-coupled receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C:Accession: I58186
R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A:Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and
A:Reference number: I58186; MUID:94323113; PMID:8047298
A:Accession: I58186
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-354 <RES>
A:CROSS-references: EMBL:U04808; NID:g2558635; PIDN:AA87093.1; PID:g439861
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor

Query Match 61.1%; Score 58; DB 2; Length 354;
Best Local Similarity 61.1%; Pred. No. 0.053;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
DB 294 YAFVGEKFRNYLLVFFQK 311

RESULT 10
JC4304
orphan G protein-coupled receptor - human
N:Alternate names: V28 protein
C:Species: Homo sapiens (man)
C>Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C:Accession: JC4304
R:Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 293-299, 1995
A:Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to
A:Reference number: JC4304; MUID:96011651; PMID:7590284
A:Accession: JC4304
A:Molecule type: mRNA
A:Residues: 1-355 <RAP>
A:CROSS-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A:Experimental source: peripheral blood mononuclear cell
A:Comment: This protein is a cell-surface receptor which recognizes extracellular signa
C:Comment: This protein is a key regulator of many immune and homeostatic responses, an
C:Genetics:
A:Gene: V28
A:Map position: 3pter-p21
C:Superfamily: vertebrate rhodopsin

```

C:Keywords: G protein-coupled receptor; lymphokine; transmembrane protein  
 F:35-57/Domain: transmembrane #status predicted <TM1>  
 F:66-88/Domain: transmembrane #status predicted <TM2>  
 F:104-125/Domain: transmembrane #status predicted <TM3>  
 F:146-165/Domain: transmembrane #status predicted <TM4>  
 F:197-217/Domain: transmembrane #status predicted <TM5>  
 F:230-254/Domain: transmembrane #status predicted <TM6>  
 F:275-296/Domain: transmembrane #status predicted <TM7>

Query Match 60.0%; Score 57; DB 2; Length 355;  
 Best Local Similarity 61.1%; Pred. No. 0.078;  
 Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18  
 |||||:|||||:  
 Db 293 YAFAGEKFRNLYLVFFQK 310  
 |||||:|||||:

RESULT 11  
 I49339  
 chemokine (C-C) receptor 4 - human  
 N:Alternate names: C-C CKR-4  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
 C:Accession: A57160  
 R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogwerf, A.J.; Proudfoot, A.E.I.; W  
 J. Biol. Chem. 270, 19495-19500, 1995  
 A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor cl  
 A:Reference number: A57160; MUID:95370289; PMID:7642634  
 A:Accession: A57160  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <POW>  
 A:Cross-references: GB:X85740; NID:gl370103; PIDN:CAA59743.1; PID:g971452  
 A:Note: source clone K5-5  
 C:Genetics:  
 A:Gene: GDB:CMKBR4  
 A:Cross-references: GDB:677463  
 A:Map position: 3p21-3p21  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot  
 F:40-65/Domain: transmembrane #status predicted <TM1>  
 F:76-97/Domain: transmembrane #status predicted <TM2>  
 F:112-133/Domain: transmembrane #status predicted <TM3>  
 F:151-175/Domain: transmembrane #status predicted <TM4>  
 F:208-226/Domain: transmembrane #status predicted <TM5>  
 F:243-264/Domain: transmembrane #status predicted <TM6>  
 F:291-308/Domain: transmembrane #status predicted <TM7>  
 F:29-276,110-187/Disulfide bonds: #status predicted  
 F:72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted  
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 60.0%; Score 57; DB 2; Length 360;  
 Best Local Similarity 58.8%; Pred. No. 0.079;  
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 17  
 |||||:|||||:  
 Db 304 YPFLGKFRKYLQLEK 320  
 |||||:|||||:

RESULT 12  
 I49339  
 macrophage inflammatory protein-1 alpha receptor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
 C:Accession: I49339  
 R:Gao, J.L.; Murphy, P.M.  
 J. Biol. Chem. 270, 17494-17501, 1995  
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemoki  
 A:Reference number: I49339; MUID:95340546; PMID:7542241

A:Accession: I49339  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-355 <RES>  
 A:Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g881548  
 C:Superfamily: vertebrate rhodopsin

Query Match 55.8%; Score 53; DB 2; Length 355;  
 Best Local Similarity 55.6%; Pred. No. 0.37;  
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18  
 |||||:|||||:  
 Db 301 YFVGKFRKYLQLEK 318  
 |||||:|||||:

RESULT 13  
 I49340  
 MIP-1 alpha receptor like-1 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
 C:Accession: I49340  
 R:Gao, J.L.; Murphy, P.M.  
 J. Biol. Chem. 270, 17494-17501, 1995  
 A:Title: Cloning and differential tissue-specific expression of three mouse beta chemoki  
 A:Reference number: I49339; MUID:95340546; PMID:7542241  
 A:Accession: I49340  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-356 <RES>  
 A:Cross-references: EMBL:U28405; NID:g881549; PIDN:AAA89154.1; PID:g881550  
 C:Superfamily: vertebrate rhodopsin

Query Match 55.8%; Score 53; DB 2; Length 356;  
 Best Local Similarity 50.0%; Pred. No. 0.37;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18  
 |||||:|||||:  
 Db 302 YFVGKFRKYLQLEK 319  
 |||||:|||||:

RESULT 14  
 JC4587  
 chemokine (C-C) receptor 4 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000  
 C:Accession: JC4587  
 R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.  
 Biochem. Biophys. Res. Commun. 218, 337-343, 1996  
 A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines to  
 A:Reference number: JC4587; MUID:96136324; PMID:8573157  
 A:Accession: JC4587  
 A:Molecule type: mRNA  
 A:Residues: 1-360 <HOOW>  
 A:Cross-references: EMBL:X90862; NID:gl167851; PIDN:CAA62372.1; PID:gl167852  
 A:Experimental source: thymus  
 C:Genetics:  
 A:Gene: cc ckr-4  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: glycoprotein; phosphoprotein; receptor; thymus  
 F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pred  
 F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
 F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 54.7%; Score 52; DB 2; Length 360;  
 Best Local Similarity 52.9%; Pred. No. 0.55;  
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 17  
 |||||:|||||:  
 Db 304 YPFLGKFRKYLQLEK 320  
 |||||:|||||:

## RESULT 15

B55735  
 Lymphocyte-specific G protein-coupled receptor EB11 - human  
 N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-Aug-1999  
 C;Accession: B55735  
 C;Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled receptor  
 A;Reference number: A55735; MUID:95154835; PMID:7851893  
 A;Accession: B55735  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-378 <SCH>  
 A;Cross-references: GB:L131581; NID:9468319; PIDN:AAA74231.1; PID:9468320  
 R;Burgstahler, R.; Kempkes, B.; Staube, K.; Lipp, M.  
 submitted to the EMBL Data Library, February 1995  
 A;Description: The expression of the chemokine receptor BLR2/EB11 is specifically transcribed in Burkitt's lymphoma cells.  
 A;Reference number: S52443  
 A;Accession: S52443  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 21-378 <BUR>  
 A;Cross-references: EMBL:X84702  
 C;Genetics:  
 A;Gene: GDB:CMKBR7; EB11; BLR2; CCR7  
 A;Cross-references: GDB:342065; OMIM:600242  
 A;Map position: 17q12-17q21.2  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor

Query Match 54.78; Score 52; DB 2; Length 378;  
 Best Local Similarity 58.8%; Pred. No. 0.57; Indels 5; Gaps 0;  
 Matches 10; Conservative 2; Mismatches 5

QY 1 YAFVGGKFRNYLLVFFQ 17  
 |||||  
 DB 326 YAFVGGKFRNYLLVFFQ 342

## RESULT 16

S42096  
 Interleukin-8 receptor - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 26-Aug-1999  
 C;Accession: S42096  
 R;Gobli, A.E.; Wang, S.; Zhou, Y.; Oeberg, K.  
 submitted to the EMBL Data Library, February 1994  
 A;Description: Molecular cloning of the rat IL8 receptor.  
 A;Reference number: S42096  
 A;Accession: S42096  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-356 <GOB>  
 A;Cross-references: EMBL:X77797  
 C;Superfamily: vertebrate rhodopsin  
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.6%; Score 50; DB 2; Length 356;  
 Best Local Similarity 69.2%; Pred. No. 1.2;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGGKFRNYLL 13  
 |||||  
 DB 310 YAFVGGKFRNYLL 322

## RESULT 17

A48921  
 Interleukin-8 receptor type B - mouse

N;Alternate names: G-protein coupled receptor Gpcr16  
 C;Species: Mus musculus (house mouse)  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1999  
 C;Accession: A48921; A53677; I49348; I55421; H48909; I53774  
 R;Cerratti, D.P.; Nelson, N.; Kozlosky, C.J.; Morrissey, P.J.; Copeland, N.G.; Gilbert, Genomics 18, 410-413, 1993  
 A;Title: The murine homologue of the human interleukin-8 receptor type B maps near the A;Reference number: A48921; MUID:94117014; PMID:8288247  
 A;Accession: A48921  
 A;Molecule type: DNA  
 A;Residues: 1-359 <CER>  
 A;Cross-references: GB:L23637; NID:9435093; PIDN:AAA9305.1; PID:9435094  
 R;Suzuki, H.; Prado, G.N.; Wilkinson, N.; Navarro, J.  
 J. Biol. Chem. 269, 18263-18266, 1994  
 A;Title: The N terminus of interleukin-8 (IL-8) receptor confers high affinity binding A;Reference number: A53677; MUID:94308043; PMID:7518426  
 A;Accession: A53677  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-359 <SUZ>  
 A;Cross-references: GB:L25549  
 A;Note: sequence extracted from NCBI backbone (NCBIP:149812)  
 R;Lee, J.; Cacalano, G.; Camarato, T.; Toy, K.; Moore, M.W.; Wood, W.I.  
 J. Immunol. 155, 2158-2164, 1995  
 A;Title: Chemokine binding and activities mediated by the mouse IL-8 receptor.  
 A;Reference number: I49348; MUID:95363183; PMID:7636264  
 A;Accession: I49348  
 A;Status: preliminary; translated from GB/EMBL/DBDJB  
 A;Molecule type: DNA  
 A;Residues: 1-359 <RES>  
 A;Cross-references: EMBL:U31207; NID:9950174; PIDN:AA52239.1; PID:9950175  
 R;Bozic, C.R.; Gerard, N.P.; von Döckert, G.; Kolakowski, L.F.  
 J. Biol. Chem. 269, 29355-29358, 1994  
 A;Title: The murine interleukin 8 type B receptor homologue and its ligands. Expression A;Reference number: I55421; MUID:95050766; PMID:7961903  
 A;Accession: I55421  
 A;Status: preliminary; translated from GB/EMBL/DBDJB  
 A;Molecule type: DNA  
 A;Residues: 1-359 <RE2>  
 A;Cross-references: GB:L13239; NID:9293665; PIDN:AAA62109.1; PID:9293666  
 R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N. Genomics 18, 175-184, 1993  
 A;Title: Identification, chromosomal location, and genome organization of mammalian G-p A;Reference number: A48909; MUID:94116980; PMID:8288218  
 A;Accession: H48909  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 145-258 <WIL>  
 A;Cross-references: GB:L20337; NID:9438800; PIDN:AAA16853.1; PID:9438801  
 R;Harada, A.; Kuno, K.; Nomura, H.; Mukaida, N.; Murakami, S.; Matsushima, K. Gene 142, 297-300, 1994  
 A;Title: Cloning of a cDNA encoding a mouse homolog of the interleukin-8 receptor.  
 A;Reference number: I53774; MUID:94252584; PMID:8194768  
 A;Accession: I53774  
 A;Status: preliminary; translated from GB/EMBL/DBDJB  
 A;Molecule type: mRNA  
 A;Residues: 1-359 <RE3>  
 A;Cross-references: GB:D17630; NID:9493671; PIDN:BAA04536.1; PID:9493672  
 C;Genetics:  
 A;Gene: IL8rb  
 A;Introns: #status absent  
 C;Superfamily: G protein-coupled receptor; glycoprotein; transmembrane protein  
 C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
 F;49-74/Domain: transmembrane #status predicted <TM1>  
 F;84-106/Domain: transmembrane #status predicted <TM2>  
 F;120-141/Domain: transmembrane #status predicted <TM3>  
 F;163-182/Domain: transmembrane #status predicted <TM4>  
 F;213-234/Domain: transmembrane #status predicted <TM5>  
 F;251-271/Domain: transmembrane #status predicted <TM6>  
 F;308-328/Domain: transmembrane #status predicted <TM7>

Query Match 52.6%; Score 50; DB 2; Length 359;  
 Best Local Similarity 69.2%; Pred. No. 1.2;

A;Accession: A45680  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-378 <BIR>  
A;Cross-references: GB:L08176; NID:gl83484; PID:gl83485  
A;Experimental source: B-lymphocytes  
A;Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIPI:127095)  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 52.6%; Score 50; DB 2; Length 378;  
Best Local Similarity 52.9%; Pred. No. 1.2;  
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQ 17  
||||| : :  
Db 326 YAFIGVKFRNDFKLEK 342

RESULT 20  
E95247  
hypothetical protein SP2115 [imported] - Streptococcus pneumoniae (strain TIGR4)  
C;Species: Streptococcus pneumoniae  
C;Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
C;Accession: E95247  
R;Fetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid  
on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,  
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A;Reference number: A95000; MUID:21357209; PMID:11463916  
A;Accession: E95247  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-76 <KUR>  
A;Cross-references: GB:AE005672; PIDN:AAK76174.1; PID:gl4973627; GSPDB:GN00164; TIGR:SP4  
A;Experimental source: strain TIGR4  
C;Genetics:  
A;Gene: SP2115

Query Match 51.6%; Score 49; DB 2; Length 76;  
Best Local Similarity 62.5%; Pred. No. 0.37;  
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFF 16  
||||| : :  
Db 24 YAFKGDFFNYLAVVF 39

RESULT 21  
B98112  
hypothetical protein spr1925 [imported] - Streptococcus pneumoniae (strain R6)  
C;Species: Streptococcus pneumoniae  
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
C;Accession: B98112  
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E  
e, B.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A;Reference number: A97872; MUID:21429245; PMID:11544234  
A;Accession: B98112  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-76 <KUR>  
A;Cross-references: GB:AE007317; PIDN:AAL00727.1; PID:gl15459622; GSPDB:GN00174  
C;Genetics:  
A;Gene: spr1925

Query Match 51.6%; Score 49; DB 2; Length 76;  
Best Local Similarity 62.5%; Pred. No. 0.37;



Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFF 16  
 |||||:|||||  
 Db 24 YAFKGDFFNYLAVF 39

## RESULT 22

I38450  
 Chemokine (C-C) receptor 2, splice form A - human  
 N:Alternate names: C-C CR-2; monocyte chemoattractant protein 1 receptor; monocyte chem  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 13-Aug-1999  
 C:Accession: I38450  
 R:Charo, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
 A:Title: Molecular cloning and functional expression of two monocyte chemoattractant pro  
 A:Reference number: A53477; MUID:94195821; PMID:8146186  
 A:Accession: I38450  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-374 <RES>  
 A:Cross-references: EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:9472556  
 C:Genetics:  
 A:Gene: GDB:CMKBR2  
 A:Cross-references: GDB:337364; OMIM:601267  
 A:Map position: 3p21-3p21  
 C:Superfamily: vertebrate rhodopsin

C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran  
 F:44-68/Domain: transmembrane #status predicted <TM1>  
 F:79-99/Domain: transmembrane #status predicted <TM2>  
 F:115-136/Domain: transmembrane #status predicted <TM3>  
 F:154-178/Domain: transmembrane #status predicted <TM4>  
 F:208-226/Domain: transmembrane #status predicted <TM5>  
 F:244-265/Domain: transmembrane #status predicted <TM6>  
 F:292-309/Domain: transmembrane #status predicted <TM7>  
 F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 51.6%; Score 49; DB 2; Length 374;

Best Local Similarity 90.0%; Pred. No. 1.8;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRN 10  
 |||||:|||||  
 Db 305 YAFVGEKFRS 314

## RESULT 23

JE0349  
 interferon-inducible protein 10 (IP-10) receptor - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000  
 C:Accession: JE0349  
 R:Tamari, M.; Tomimaga, Y.; Yatsunami, K.; Narumi, S.  
 Biochem. Biophys. Res. Commun. 251, 41-48, 1998  
 A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its  
 A:Reference number: JE0349; MUID:99009219; PMID:9790904  
 A:Accession: JE0349  
 A:Molecule type: mRNA  
 A:Residues: 1-367 <TAM>  
 A:Cross-references: DDBJ:AB003174; NID:g3798731; PIDN:BAA34045.1; PID:g3798732  
 C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.  
 C:Superfamily: vertebrate rhodopsin

Query Match 50.5%; Score 48; DB 2; Length 367;  
 Best Local Similarity 50.0%; Pred. No. 2.6;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||:|||||  
 Db 317 YAFVGVKFRQWMLFTR 334

## RESULT 24

A53752  
 interleukin-8 receptor (clone 5B1a) - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: A53752  
 R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Navarroz  
 J. Biol. Chem. 269, 12391-12394, 1994  
 A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.  
 A:Reference number: A53752; MUID:94230294; PMID:8175642  
 A:Accession: A53752  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-358 <PRA>  
 A:Cross-references: GB:L24445; NID:g437661; PIDN:AAA31378.1; PID:g437662  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 49.5%; Score 47; DB 2; Length 358;  
 Best Local Similarity 69.2%; Pred. No. 3.8;  
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLL 13  
 |||||:|||||  
 Db 312 YAFVGEKFRYGLL 324

## RESULT 25

A55735  
 G protein-coupled receptor EB11 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 24-Nov-1999  
 C:Accession: A55735  
 R:Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B  
 Genomics 23, 643-650, 1994  
 A:Title: Cloning of human and mouse EB11, a lymphoid-specific G-protein-coupled recepto  
 A:Reference number: A55735; MUID:95154835; PMID:7851893  
 A:Accession: A55735  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-378 <SCH>  
 A:Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor

Query Match 49.5%; Score 47; DB 2; Length 378;  
 Best Local Similarity 52.9%; Pred. No. 4;  
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQ 17  
 |||||:|||||  
 Db 326 YAFVGEKFRSDLFKLFK 342

## RESULT 26

A23669  
 interleukin-8 receptor, high affinity - rabbit  
 N:Alternate names: FMLP receptor  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 05-Nov-1999  
 C:Accession: A23669  
 R:Thomas, K.M.; Pyun, H.Y.; Navarroz, J.  
 J. Biol. Chem. 265, 20061-20064, 1990  
 A:Title: Molecular cloning of the fMet-Leu-Phe receptor from neutrophils.  
 A:Reference number: A23669; MUID:91056034; PMID:1700779  
 A:Accession: A23669  
 A:Molecule type: mRNA  
 A:Residues: 1-354 <THO>  
 A:Cross-references: GB:M58021; NID:g165442; PIDN:AAA31377.1; PID:g165443  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein; neutrophil

Query Match 50.5%; Score 48; DB 2; Length 367;  
 Best Local Similarity 50.0%; Pred. No. 2.6;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||:|||||  
 Db 317 YAFVGVKFRQWMLFTR 334

Query Match 48.4%; Score 46; DB 2; Length 354;  
Best Local Similarity 61.5%; Pred. No. 5.5;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLL 13  
| | | | |  
309 YAFIQGNFRNGFL 321

Db

RESULT 27  
JQ1231  
interleukin-8 receptor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 05-Nov-1999  
C:Accession: JQ1231; A46483  
R;Beckmann, M.P.; Munger, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, B.; Biemann, M.P.; Res. Commun. 179, 784-789, 1991  
A:Title: Molecular characterization of the interleukin-8 receptor.  
A:Reference number: JQ1231; MUID:91378994; PMID:1898400  
A:Accession: JQ1231  
A:Molecule type: DNA  
A:Residues: 1-355 <BEC>  
A:Cross-references: GB:M74240; NID:g165438; PIDN:AAA31375.1; PID:g165439  
J. Immunol. 148, 1261-1264, 1992  
R;Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.  
A:Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.  
A:Reference number: A46483; MUID:92148149; PMID:1737938  
A:Accession: A46483  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-355 <LEE>  
A:Cross-references: GB:M82873; NID:g165440; PIDN:AAA31376.1; PID:g165441  
A:Experimental source: neutrophils  
A:Note: sequence extracted from NCBI backbone (NCBIN:81536, NCBI:81530)  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 48.4%; Score 46; DB 2; Length 355;  
Best Local Similarity 61.5%; Pred. No. 5.5;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLL 13  
| | | | |  
310 YAFIQGNFRNGFL 322

Db

RESULT 28  
B97185  
glycosyltransferase [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C:Accession: B97185  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: B97185  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-377 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK80269.1; PID:g15025320; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC2313

Query Match 47.9%; Score 45.5; DB 2; Length 377;  
Best Local Similarity 47.4%; Pred. No. 7.1;  
Matches 9; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 3 FVG---EKFRNLLVFFOK 18  
| | | | |  
227 FGIPIESFNITVFFSK 245

Db

RESULT 29  
JN0621  
G protein-coupled receptor type B - bovine  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 19-May-2000  
C:Accession: JN0621  
R;Matsuo, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.  
Biochem. Biophys. Res. Commun. 194, 504-511, 1993  
A:Title: Identification of novel members of G-protein coupled receptor superfamily expressed in rat brain.  
A:Reference number: JN0621; MUID:93326166; PMID:8392843  
A:Accession: JN0621  
A:Molecule type: mRNA  
A:Residues: 1-350 <MAT>  
A:Cross-references: GB:S63848; NID:g399710; PIDN:AA827547.1; PID:g399711  
A:Experimental source: tongue taste papillae  
C:Comment: This protein is involved in modulating taste sensitivity or regeneration of taste buds.  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein  
F:42-66/Domain: transmembrane #status predicted <TM2>  
F:80-99/Domain: transmembrane #status predicted <TM2>  
F:114-135/Domain: transmembrane #status predicted <TM3>  
F:154-175/Domain: transmembrane #status predicted <TM4>  
F:200-222/Domain: transmembrane #status predicted <TM5>  
F:242-265/Domain: transmembrane #status predicted <TM6>  
F:284-306/Domain: transmembrane #status predicted <TM7>  
F:6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.4%; Score 45; DB 2; Length 350;  
Best Local Similarity 38.9%; Pred. No. 8;  
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFOK 18  
| | | | |  
303 YFVGTSPNIMVAKK 320

Db

RESULT 30  
JCI104  
angiotensin II receptor type 1 - human  
N:Alternate names: angiotensin II receptor 1A  
C:Species: Homo sapiens (man)  
C>Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 21-Jul-2000  
C:Accession: JCI104; JQ1402; JH0267; A44014; S18983  
R;Mauzy, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.  
Biochem. Biophys. Res. Commun. 186, 277-284, 1992  
A:Title: Cloning, expression, and characterization of a gene encoding the human angiotensin II receptor.  
A:Reference number: JCI104; MUID:92337608; PMID:1378723  
A:Accession: JCI104  
A:Molecule type: DNA  
A:Residues: 1-359 <MAU>  
R;Putra, H.; Guo, D.F.; Inagami, T.  
Biochem. Biophys. Res. Commun. 183, 8-13, 1992  
A:Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type 1 receptor.  
A:Reference number: JQ1402; MUID:92181475; PMID:1543512  
A:Accession: JQ1402  
A:Molecule type: DNA  
A:Residues: 1-359 <FUR>  
A:Cross-references: EMBL:Z11162; NID:g28709; PID:g28710  
A:Experimental source: lymphocyte  
R;Bergsma, D.J.; Ellis, C.; Kumar, C.; Nuthallaganti, P.; Kersten, H.; Elshourbagy, N.; Fagan, J.; Biemann, M.P.; Res. Commun. 183, 989-995, 1992  
A:Title: Cloning and characterization of a human angiotensin II type 1 receptor.  
A:Reference number: JH0574; MUID:92231907; PMID:1567413  
A:Accession: JH0574  
A:Molecule type: mRNA  
A:Residues: 1-359 <BER>  
A:Cross-references: GB:M87290; NID:g178682; PIDN:AAA35535.1; PID:g178683  
A:Experimental source: liver  
R;Takayanagi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Hiji, M.; Inagami, T.; Fagan, J.; Biemann, M.P.; Res. Commun. 183, 910-916, 1992  
A:Title: Molecular cloning, sequence analysis and expression of a cDNA encoding human type 1 receptor.

A:Reference number: JH0267; MUID:92198490; PMID:1550596  
A:Accession: JH0267  
A:Molecule type: mRNA  
A:Residues: 1-359 <YAK>  
A:Experimental source: liver  
R:Curnow, K.M.; Pascoe, L.; White, P.C.  
Mol. Endocrinol. 6, 1113-1118, 1992  
A:Title: Genetic analysis of the human type-1 angiotensin II receptor.  
A:Reference number: A44014; MUID:92375105; PMID:1508224  
A:Accession: A44014  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-359 <CUR>  
A:Cross-references: GB:M03394; NID:G178680; PID:G178681  
A:Note: sequence extracted from NCBI backbone (NCBIN:111831, NCBIIP:111833)  
C:Genetics:  
A:Gene: GDB:AGTR1  
A:Cross-references: GDB:132359; OMIM:106165  
A:Map position: 3q21-3q25  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein  
F:30-53/Domain: transmembrane #status predicted <TM1>  
F:65-90/Domain: transmembrane #status predicted <TM2>  
F:103-124/Domain: transmembrane #status predicted <TM3>  
F:145-167/Domain: transmembrane #status predicted <TM4>  
F:194-216/Domain: transmembrane #status predicted <TM5>  
F:241-264/Domain: transmembrane #status predicted <TM6>  
F:281-305/Domain: transmembrane #status predicted <TM7>  
F:4,176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.4%; Score 45; DB 2; Length 359;  
Best Local Similarity 53.8%; Pred. No. 8.2;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13  
Db 302 YGFLGKKFKRYFL 314

Search completed: March 4, 2004, 18:04:03  
Job time : 10.1837 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 17:47:47 ; Search time 5.87755 Seconds  
(without alignments)  
159.465 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKERNLLVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query % | Match Length | ID | Description |
|------------|-------|---------|--------------|----|-------------|
| 1          | 95    | 100.0   | 352          | 1  | CKR5_CERAE  |
| 2          | 95    | 100.0   | 352          | 1  | CKR5_CERP   |
| 3          | 95    | 100.0   | 352          | 1  | CKR5_CERTO  |
| 4          | 95    | 100.0   | 352          | 1  | CKR5_GORGO  |
| 5          | 95    | 100.0   | 352          | 1  | CKR5_HUMAN  |
| 6          | 95    | 100.0   | 352          | 1  | CKR5_HYLLE  |
| 7          | 95    | 100.0   | 352          | 1  | CKR5_HYLM   |
| 8          | 95    | 100.0   | 352          | 1  | CKR5_HYLSY  |
| 9          | 95    | 100.0   | 352          | 1  | CKR5_MACMU  |
| 10         | 95    | 100.0   | 352          | 1  | CKR5_PANTR  |
| 11         | 95    | 100.0   | 352          | 1  | CKR5_PAPHA  |
| 12         | 95    | 100.0   | 352          | 1  | CKR5_PONPY  |
| 13         | 95    | 100.0   | 352          | 1  | CKR5_PYBHI  |
| 14         | 95    | 100.0   | 352          | 1  | CKR5_PYGNE  |
| 15         | 95    | 100.0   | 352          | 1  | CKR5_TRAFR  |
| 16         | 95    | 100.0   | 352          | 1  | CKR5_TRAPH  |
| 17         | 85    | 89.5    | 354          | 1  | CKR5_RAT    |
| 18         | 80    | 84.2    | 354          | 1  | CKR5_MOUSE  |
| 19         | 78    | 82.1    | 373          | 1  | CKR2_MOUSE  |
| 20         | 78    | 82.1    | 373          | 1  | CKR2_RAT    |
| 21         | 76    | 80.0    | 360          | 1  | CKR2_MACMU  |
| 22         | 65    | 68.4    | 355          | 1  | CKR3_CERAE  |
| 23         | 65    | 68.4    | 355          | 1  | CKR3_HUMAN  |
| 24         | 65    | 68.4    | 355          | 1  | CKR3_MACMU  |
| 25         | 64    | 67.4    | 353          | 1  | CKR3_MOUSE  |
| 26         | 64    | 67.4    | 359          | 1  | CKR3_MOUSE  |
| 27         | 64    | 67.4    | 359          | 1  | CKR3_RAT    |
| 28         | 63    | 66.3    | 355          | 1  | CKR8_HUMAN  |
| 29         | 63    | 66.3    | 356          | 1  | CKR8_MACMU  |
| 30         | 61    | 64.2    | 374          | 1  | CKR6_HUMAN  |
| 31         | 60    | 63.2    | 355          | 1  | CKR1_HUMAN  |
| 32         | 59    | 62.1    | 367          | 1  | CKR6_MOUSE  |
| 33         | 58    | 61.1    | 354          | 1  | C3X1_RAT    |

## ALIGNMENTS

|     |      |      |      |   |            |
|-----|------|------|------|---|------------|
| 34  | 57   | 60.0 | 354  | 1 | C3X1_MOUSE |
| 35  | 57   | 60.0 | 355  | 1 | C3X1_HUMAN |
| 36  | 57   | 60.0 | 360  | 1 | CKR4_HUMAN |
| 37  | 56   | 58.9 | 355  | 1 | CKR1_MACMU |
| 38  | 55   | 57.9 | 358  | 1 | CKR3_CAVPO |
| 39  | 53   | 55.8 | 355  | 1 | CKR1_MOUSE |
| 40  | 53   | 55.8 | 356  | 1 | CKR3_MOUSE |
| 41  | 52   | 54.7 | 360  | 1 | CKR4_MOUSE |
| 42  | 52   | 54.7 | 378  | 1 | CKR7_HUMAN |
| 43  | 50   | 52.6 | 353  | 1 | IL8B_MACMU |
| 44  | 50   | 52.6 | 353  | 1 | IL8B_PANTR |
| 45  | 50   | 52.6 | 356  | 1 | IL8B_CANFA |
| 46  | 50   | 52.6 | 359  | 1 | IL8B_MOUSE |
| 47  | 50   | 52.6 | 359  | 1 | IL8B_RAT   |
| 48  | 50   | 52.6 | 360  | 1 | IL8B_HUMAN |
| 49  | 49   | 51.6 | 322  | 1 | CXC1_MOUSE |
| 50  | 49   | 51.6 | 374  | 1 | CKR2_HUMAN |
| 51  | 47   | 49.5 | 358  | 1 | IL8B_RABIT |
| 52  | 47   | 49.5 | 367  | 1 | CKR3_MOUSE |
| 53  | 47   | 49.5 | 378  | 1 | CKR7_MOUSE |
| 54  | 47   | 49.5 | 781  | 1 | APR2_SULTO |
| 55  | 46   | 48.4 | 246  | 1 | XPT_MOUSE  |
| 56  | 46   | 48.4 | 355  | 1 | IL8A_RABIT |
| 57  | 46   | 48.4 | 360  | 1 | IL8B_BOVIN |
| 58  | 46   | 48.4 | 962  | 1 | XPT_HUMAN  |
| 59  | 45   | 47.4 | 350  | 1 | CKRB_BOVIN |
| 60  | 45   | 47.4 | 359  | 1 | AG2R_BOVIN |
| 61  | 45   | 47.4 | 359  | 1 | AG2R_CANFA |
| 62  | 45   | 47.4 | 359  | 1 | AG2R_CAVPO |
| 63  | 45   | 47.4 | 359  | 1 | AG2R_HUMAN |
| 64  | 45   | 47.4 | 359  | 1 | AG2R_MERUN |
| 65  | 45   | 47.4 | 359  | 1 | AG2R_MOUSE |
| 66  | 45   | 47.4 | 359  | 1 | AG2R_PANTR |
| 67  | 45   | 47.4 | 359  | 1 | AG2R_PIG   |
| 68  | 45   | 47.4 | 359  | 1 | AG2R_RABIT |
| 69  | 45   | 47.4 | 359  | 1 | AG2R_RAT   |
| 70  | 45   | 47.4 | 359  | 1 | AG2R_SHEEP |
| 71  | 45   | 47.4 | 359  | 1 | AG2S_MOUSE |
| 72  | 45   | 47.4 | 359  | 1 | AG2S_RAT   |
| 73  | 44   | 46.3 | 350  | 1 | CKRB_HUMAN |
| 74  | 44   | 46.3 | 375  | 1 | CML2_HUMAN |
| 75  | 44   | 46.3 | 378  | 1 | CML2_MOUSE |
| 76  | 43   | 45.3 | 259  | 1 | Y238_METJA |
| 77  | 43   | 45.3 | 333  | 1 | CXCL_HUMAN |
| 78  | 43   | 45.3 | 349  | 1 | IL8A_RAT   |
| 79  | 43   | 45.3 | 350  | 1 | OPSL_CALJA |
| 80  | 43   | 45.3 | 357  | 1 | CKR9_HUMAN |
| 81  | 43   | 45.3 | 359  | 1 | OPSR_RAT   |
| 82  | 43   | 45.3 | 362  | 1 | OPSR_CHICK |
| 83  | 43   | 45.3 | 364  | 1 | OPSG_CAVPO |
| 84  | 43   | 45.3 | 364  | 1 | OPSG_HUMAN |
| 85  | 43   | 45.3 | 364  | 1 | OPSG_RABIT |
| 86  | 43   | 45.3 | 364  | 1 | OPSG_SCICA |
| 87  | 43   | 45.3 | 364  | 1 | OPSR_CAPHI |
| 88  | 43   | 45.3 | 364  | 1 | OPSR_HUMAN |
| 89  | 43   | 45.3 | 369  | 1 | CKR9_MOUSE |
| 90  | 43   | 45.3 | 384  | 1 | CKD6_HUMAN |
| 91  | 43   | 45.3 | 1060 | 1 | NKCL_MANSE |
| 92  | 42.5 | 44.7 | 189  | 1 | YBFC_ECOLI |
| 93  | 42   | 44.2 | 309  | 1 | HTPX_FUSNN |
| 94  | 42   | 44.2 | 353  | 1 | IL8B_GORGO |
| 95  | 42   | 44.2 | 359  | 1 | OPSG_MOUSE |
| 96  | 42   | 44.2 | 361  | 1 | P2Y4_MOUSE |
| 97  | 42   | 44.2 | 361  | 1 | P2Y4_RAT   |
| 98  | 42   | 44.2 | 629  | 1 | GAP1_CAEEL |
| 99  | 41   | 43.2 | 350  | 1 | IL8A_GORGO |
| 100 | 41   | 43.2 | 350  | 1 | IL8A_HUMAN |

|                                                                                                                                                                        |                                                                              |                            |           |                         |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------|----------------------------|-----------|-------------------------|
| FT                                                                                                                                                                     | VARIANT                                                                      | 14                         | 14        | N -> Y.                 |
| ST                                                                                                                                                                     | VARIANT                                                                      | 352                        | 352       | F -> L.                 |
| SQ                                                                                                                                                                     | SEQUENCE                                                                     | 352 AA;                    | 40561 MW; | 7F52E690C72EC29A CRC64; |
| <br>Query Match 100.0%; Score 95; DB 1; Length 352;<br>Best Local Similarity 100.0%; Pred. No. 6.9e-09;<br>Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                                                              |                            |           |                         |
| QY                                                                                                                                                                     | 1                                                                            | YAFVGEKFRNYLLIVFFQK 18     |           |                         |
|                                                                                                                                                                        |                                                                              |                            |           |                         |
| DB                                                                                                                                                                     | 297                                                                          | YAFVGEKFRNYLLIVFFQK 314    |           |                         |
| <br>RESULT 2                                                                                                                                                           |                                                                              |                            |           |                         |
| CKR5_CERP_Y                                                                                                                                                            | STANDARD;                                                                    | PRT;                       | 352 AA.   |                         |
| ID                                                                                                                                                                     | C9TV42;                                                                      |                            |           |                         |
| DT                                                                                                                                                                     | 15-MAR-2004 (Rel. 43, Created)                                               |                            |           |                         |
| DT                                                                                                                                                                     | 15-MAR-2004 (Rel. 43, Last sequence update)                                  |                            |           |                         |
| DT                                                                                                                                                                     | 15-MAR-2004 (Rel. 43, Last annotation update)                                |                            |           |                         |
| DE                                                                                                                                                                     | C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).         |                            |           |                         |
| GN                                                                                                                                                                     | CCRS OR CMKBRS.                                                              |                            |           |                         |
| OS                                                                                                                                                                     | Cercopithecus pygerythrus (Vervet monkey).                                   |                            |           |                         |
| OC                                                                                                                                                                     | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;            |                            |           |                         |
| OC                                                                                                                                                                     | Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;                  |                            |           |                         |
| OC                                                                                                                                                                     | Cercopithecinae; Cercopithecus.                                              |                            |           |                         |
| OX                                                                                                                                                                     | NCBI_TaxID=60710;                                                            |                            |           |                         |
| RN                                                                                                                                                                     | [1]                                                                          |                            |           |                         |
| RP                                                                                                                                                                     | SEQUENCE FROM N.A.                                                           |                            |           |                         |
| RC                                                                                                                                                                     | STRAIN=100;                                                                  |                            |           |                         |
| RX                                                                                                                                                                     | MEDLINE=9933215; PubMed=10408730;                                            |                            |           |                         |
| RA                                                                                                                                                                     | Muller-Trutwin M.C., Corbet S., Hansen J., Georges-Courbot M.-C.,            |                            |           |                         |
| RA                                                                                                                                                                     | Diop O., Rigoulet J., Barre-Sinoussi F., Fomesgaard A.;                      |                            |           |                         |
| RT                                                                                                                                                                     | "Mutations in CCR5-coding sequences are not associated with HIV              |                            |           |                         |
| RT                                                                                                                                                                     | carrier status in African nonhuman primates.";                               |                            |           |                         |
| RL                                                                                                                                                                     | AIDS Res. Hum. Retroviruses 15:931-939(1999);                                |                            |           |                         |
| CC                                                                                                                                                                     | -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,       |                            |           |                         |
| CC                                                                                                                                                                     | MIP-1-beta and RANTES and subsequently transduces a signal by                |                            |           |                         |
| CC                                                                                                                                                                     | increasing the intracellular calcium ions level. May play a role             |                            |           |                         |
| CC                                                                                                                                                                     | in the control of granulocytic lineage proliferation or                      |                            |           |                         |
| CC                                                                                                                                                                     | differentiation.                                                             |                            |           |                         |
| CC                                                                                                                                                                     | -!- SUBCELLULAR LOCATION: Integral membrane protein.                         |                            |           |                         |
| CC                                                                                                                                                                     | -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.          |                            |           |                         |
| CC                                                                                                                                                                     |                                                                              |                            |           |                         |
| CC                                                                                                                                                                     | This SWISS-PROT entry is copyright. It is produced through a collaboration   |                            |           |                         |
| CC                                                                                                                                                                     | between the Swiss Institute of Bioinformatics and the EMBL outstation on its |                            |           |                         |
| CC                                                                                                                                                                     | the European Bioinformatics Institute. There are no restrictions on its      |                            |           |                         |
| CC                                                                                                                                                                     | use by non-profit institutions as long as its content is in no way           |                            |           |                         |
| CC                                                                                                                                                                     | modified and this statement is not removed. Usage by and for commercial      |                            |           |                         |
| CC                                                                                                                                                                     | entities requires a license agreement (See http://www.isb-sib.ch/annouce/    |                            |           |                         |
| CC                                                                                                                                                                     | or send an email to license@sb-sib.ch).                                      |                            |           |                         |
| CC                                                                                                                                                                     |                                                                              |                            |           |                         |
| DR                                                                                                                                                                     | EMBL; AF035222; AAD4015.1; -;                                                |                            |           |                         |
| DR                                                                                                                                                                     | InterPro; IPR000276; GPCK_Rhodpsn.                                           |                            |           |                         |
| DR                                                                                                                                                                     | Pfam; PF00001; 7tm.1.1.                                                      |                            |           |                         |
| DR                                                                                                                                                                     | PRINTS; PR00237; GPCRHOPOPSN.                                                |                            |           |                         |
| DR                                                                                                                                                                     | PROSITE; PS00237; G-PROTEIN RECP Fl_1; 1.                                    |                            |           |                         |
| DR                                                                                                                                                                     | PROSITE; PS00262; G-PROTEIN RECP Fl_2; 1.                                    |                            |           |                         |
| KW                                                                                                                                                                     | G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.          |                            |           |                         |
| FT                                                                                                                                                                     | DOMAIN 1 30                                                                  | EXTRACELLULAR (POTENTIAL). |           |                         |
| FT                                                                                                                                                                     | TRANSMEM 31 58                                                               | 1 (POTENTIAL).             |           |                         |
| FT                                                                                                                                                                     | DOMAIN 59 68                                                                 | CYTOPLASMIC (POTENTIAL).   |           |                         |
| FT                                                                                                                                                                     | TRANSMEM 69 89                                                               | 2 (POTENTIAL).             |           |                         |
| FT                                                                                                                                                                     | DOMAIN 90 102                                                                | EXTRACELLULAR (POTENTIAL). |           |                         |
| FT                                                                                                                                                                     | TRANSMEM 103 124                                                             | 3 (POTENTIAL).             |           |                         |
| FT                                                                                                                                                                     | DOMAIN 125 141                                                               | CYTOPLASMIC (POTENTIAL).   |           |                         |
| FT                                                                                                                                                                     | TRANSMEM 142 166                                                             | 4 (POTENTIAL).             |           |                         |
| FT                                                                                                                                                                     | DOMAIN 167 198                                                               | EXTRACELLULAR (POTENTIAL). |           |                         |
| FT                                                                                                                                                                     | TRANSMEM 199 218                                                             | 5 (POTENTIAL).             |           |                         |
| FT                                                                                                                                                                     | DOMAIN 219 235                                                               | CYTOPLASMIC (POTENTIAL).   |           |                         |
| FT                                                                                                                                                                     | TRANSMEM 236 260                                                             | 6 (POTENTIAL).             |           |                         |
| FT                                                                                                                                                                     | DOMAIN 261 277                                                               | EXTRACELLULAR (POTENTIAL). |           |                         |
| FT                                                                                                                                                                     | TRANSMEM 278 301                                                             | 7 (POTENTIAL).             |           |                         |

```

FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40558 MW; EF17D67CBCC3DB0 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKERNYLVFFQK 18
DB 297 YAFVGEKERNYLVFFQK 314

RESULT 3
CKR5_CERTO
ID CKR5_CERTO STANDARD; PRT; 352 AA.
AC O62743; O62744; O62745; O62746;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecidae;
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate 079, 085, 087, and 089;
RX MEDLINE=98321155; PubMed=9656999;
RA Chen Z., Gettie A., Ho D.D., Marx P.A.;
RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys naturally infected in west Africa: a comparison of coreceptor usage of primary SIVsm, HIV-2, and SIVmac.";
RL Virology 246:113-124(1998).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF051902; AAC39830.1; -
CC EMBL; AF051903; AAC39831.1; -
CC EMBL; AF051904; AAC39832.1; -
CC EMBL; AF051905; AAC39833.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.
CC PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
CC PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSFAM 31 58 1 (POTENTIAL).
FT DOMAIN 51 68 CYTOPLASMIC (POTENTIAL).
FT TRANSFAM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSFAM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSFAM 142 166 4 (POTENTIAL).

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FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSFAM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSFAM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSFAM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
FT VARIANT 2 2 D -> E (IN ISOLATE 087).
FT VARIANT 3 3 Y -> D (IN ISOLATE 079).
FT VARIANT 3 3 V -> G (IN ISOLATE 087).
FT VARIANT 25 25 M -> K (IN ISOLATE 079).
FT VARIANT 100 100 L -> V (IN ISOLATE 089).
FT VARIANT 107 107 L -> V (IN ISOLATE 079).
FT VARIANT 134 134 V -> G (IN ISOLATE 079).
FT VARIANT 146 146 V -> L (IN ISOLATES 085 AND 089).
FT VARIANT 340 340 T -> I (IN ISOLATE 079).
SQ SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKERNYLVFFQK 18
DB 297 YAFVGEKERNYLVFFQK 314

RESULT 4
CKR5_GORGO
ID CKR5_GORGO STANDARD; PRT; 352 AA.
AC P56439;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKR5.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains.".
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC EMBL; AF005659; AAB62553.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsn.

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DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS00262; G PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-09; Indels 0;  
 Matches 18; Conservative 0; Mismatches 0; Caps 0;

QY 1 YAFVGEKFNLYLVEFQK 18  
 |||||  
 DB 297 YAFVGEKFNLYLVEFQK 314

RESULT 5  
 CKR5 HUMAN STANDARD; PRT; 352 AA.  
 AC P51681; O14692; O14693; O14696; O14697; O14698; O14699;  
 AC O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;  
 AC O14708; O15538; Q8UP84;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)  
 DE (HIV-1 fusion co-receptor) (CHEMB13) (CD195 antigen).  
 GN CCR5 OR CMKBR5.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96241590; PubMed=8639485;  
 RA Samson M., Jabbe O., Mollereau C., Vaessart G., Parmentier M.;  
 RT "Molecular cloning and functional expression of a new human  
 RT CC-chemokine receptor gene."  
 RL Biochemistry 35:3362-3367(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96291862; PubMed=8663314;  
 RA Raport C.J., Gosling J., Schweighart V.L., Gray P.W., Charo I.F.;  
 RT "Molecular cloning and functional characterization of a novel human  
 RT CC chemokine receptor (CCR5) for RANTES, MIP-1beta, and MIP-1alpha."  
 RL J. Biol. Chem. 271:17161-17166(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96295970; PubMed=8699119;  
 RA Combadere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;  
 RT "Cloning and functional expression of CC CKR5, a human monocyte CC  
 RT chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and  
 RT RANTES."  
 RL J. Leukoc. Biol. 60:147-152(1996).  
 RN [4]

RP SEQUENCE FROM N.A.  
 RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
 RA Khan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
 RA Gnoj L., la Bastie L., Kaplan N., Greco T., Touchman J.,  
 RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,  
 RA Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E.,  
 RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,  
 RA Matanabe M., Doggett N., Garcia D., Sagripanti J.L.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98001387; PubMed=9343222;  
 RA Kuhnmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 RT implicate specific amino acids in infections by simian and human  
 RT immunodeficiency viruses."  
 RL J. Virol. 71:8642-8656(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A., AND POLYMORPHISMS.  
 RX MEDLINE=98022612; PubMed=9359654;  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism."  
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98049523; PubMed=9388201;  
 RA Mummidi S., Ahuja S.S., McDaniel B.L., Ahuja S.K.;  
 RT "The human CC chemokine receptor 5 (CCR5) gene. Multiple transcripts  
 RT with 5'-end heterogeneity, dual promoter usage, and evidence for  
 RT polymorphisms within the regulatory regions and noncoding exons."  
 RL J. Biol. Chem. 272:30662-30671(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A., AND VARIANT ARG-178.  
 RA Magierowska M., Barre-Sinoussi F., Issafras H., Theodorou I.,  
 RA Debre P.;  
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org)."  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
 RX MEDLINE=98260017; PubMed=8649511;  
 RA Deng H., Liu R., Elmeyer W., Choe S., Unutmaz D., Burkhardt M.,  
 RA di Marzio P., Marmon S., Sutton R.E., Hill C.M., Davis C.B.,  
 RA Peiper S.C., Schall T.J., Littman D.R., Landau N.R.;  
 RT "Identification of a major co-receptor for primary isolates of  
 RT HIV-1."  
 RL Nature 381:661-666(1996).  
 RN [11]  
 RP CHARACTERIZATION OF ITS HIV-1 RECEPTOR FUNCTION.  
 RX MEDLINE=98260018; PubMed=8649512;  
 RA Dragic T., Litwin V., Allaway G.P., Martin S.R., Huang Y.,  
 RA Nagashima K.A., Cayanan C., Maddon P.J., Koup R.A., Moore J.P.,  
 RA Paxton W.A.;  
 RT "HIV-1 entry into CD4+ cells is mediated by the chemokine receptor  
 RT CC-CKR-5."  
 RL Nature 381:667-673(1996).  
 RN [12]  
 RP SULFATION.  
 RX MEDLINE=99189752; PubMed=10089882;  
 RA Farzan M., Mirzabekov T., Kolchinsky P., Wyatt R., Cayabyab M.,  
 RA Gerard N.P., Gerard C., Sodroski J., Choe H.;  
 RT "Tyrosine sulfation of the amino terminus of CCR5 facilitates HIV-1  
 RT entry."  
 RL Cell 96:667-676(1999).  
 CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and rantes and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; TAS.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR GO; GO:0007125; P:invasive growth; TAS.  
DR GO; GO:0007203; P:phosphatidylinositol-4,5-bisphosphate hydro...; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHODOPSN.  
DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.  
DR PROSITE; PS0262; G PROTEIN RECP F1.2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
KW Polymorphism.  
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 2 (POTENTIAL).  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 103 124 3 (POTENTIAL).

Query Match 100.0%; Score 95; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 6.9e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGKFRNYLLVFFQK 18  
|||||

DB 297 YAFVGKFRNYLLVFFQK 314  
|||||

RESULT 6

CXRS\_HYLLE STANDARD; PRT; 352 AA.

AC O97883;  
DT 30-MAY-2000 (Rel. 39, Created)  
DD 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5) (CCR5).  
GN CXRS OR CXMR5.  
OS Hylobates leucogynus (White-cheeked gibbon).  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
OX NCBI\_TaxID=61853;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99416438; PubMed=10486970;  
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
RL "Biological evolution of the CCR5 chemokine receptor gene in primates.";  
RT Mol. Biol. Evol. 16:1145-1154(1999).  
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
MIP-1-beta and RANTES and subsequently transduces a signal by  
increasing the intracellular calcium ions level. May play a role  
in the control of granulocytic lineage proliferation or  
differentiation.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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entities requires a license agreement (See <http://www.isb-sib.ch/annouce/>)  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; AF075451; AAD19863.1; -.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHODOPSN.  
DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.  
DR PROSITE; PS0262; G PROTEIN RECP F1.2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 2 (POTENTIAL).



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FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40445 MW; 4F8E4F344CEB7C91 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 7
CKRS_HYLM
ID CKRS_HYLM STANDARD; PRT; 352 AA.
AC Q95NC0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CCR5.
OS Hylobates moloch (silvery gibbon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=81572;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF177899; AAK43382.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1.1
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G PROTEIN RECF F1.1; 1.
CC PROSITE; PS0262; G PROTEIN RECF F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40436 MW; 5623CA9340CF274 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 8
CKRS_HYLSY
ID CKRS_HYLSY STANDARD; PRT; 352 AA.
AC Q95NC5;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CCR5.
OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=9590;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF177884; AAK43367.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1.1
CC PRINTS; PR00237; GPCRHOOPS.
CC PROSITE; PS00237; G PROTEIN RECF F1.1; 1.
CC PROSITE; PS0262; G PROTEIN RECF F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 103 124 3 (POTENTIAL).

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FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40508 MW; F4P64B3AD5AF658A CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 9
ID CCR5_MACMU STANDARD; PRT; 352 AA.
AC P79436; 002746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CXCR5.
OS Macaca mulatta (Rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT SIVmac239.";
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry.";
RL J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors.";
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peliper S.C., Parmentier M., Broder C.C., Doms R.W.;

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RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U77672; AAC511109.1; -
CC EMBL; U73739; AAC511158.1; -
CC EMBL; U96762; AAC34132.1; -
CC EMBL; AF005660; AB62554.1; -
CC EMBL; AF005661; AB62555.1; -
CC EMBL; AF005662; AB62556.1; -
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00337; G_PROTEIN_RECP_F1_1; 1.
CC PROSITE; PS00462; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 278 301 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD RES 3 3 SULFATION (BY SIMILARITY).
FT MOD RES 10 10 SULFATION (BY SIMILARITY).
FT MOD RES 14 14 SULFATION (BY SIMILARITY).
FT MOD RES 15 15 SULFATION (BY SIMILARITY).
FT CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 241 241 M -> I (IN REF. 3).
FT CONFLICT 292 292 I -> M (IN REF. 3).
SQ SEQUENCE 352 AA; 40507 MW; 58B96C85909FACB2 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 10
ID CCR5_PANTR STANDARD; PRT; 352 AA.
AC P56440; 002778;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).

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GN CCR5 OR CMKRS5.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX Zimmerman P.A., Buckler-White A., Alkhatib G.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98022612; PubMed=9359654;  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism.";  
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97426118; PubMed=9282822;  
 RA Zacharova V., Zachar V., Gouatin A.S.;  
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural  
 RT HIV type 1 host.";  
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98090115; PubMed=9430250;  
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;  
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1.";  
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX Zhang Y., Ryder O.A., Zhang Y.;  
 RT "Sequence comparison of the CCR5 gene in primates and primate  
 RT phylogeny.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level. May play a role  
 CC in the control of granulocytic lineage proliferation or  
 CC differentiation.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL; AF005663; AAB62557.1; -  
 CC EMBL; U94329; AAB58446.1; -  
 CC EMBL; AF011542; AAB65742.1; -  
 CC EMBL; U97666; AAC51670.1; -  
 CC EMBL; AF011540; AAB65740.1; -  
 CC EMBL; U89797; AAC03717.1; -  
 CC EMBL; AF17894; AAK43377.1; -  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC Pfam; PF00001; 7tm 1; 1.  
 CC PRINTS; PR00237; GPCR\_Rhodopsn.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 CC PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 5 (POTENTIAL).  
 FT TRANSMEM 199 218 6 (POTENTIAL).  
 FT DOMAIN 219 235 7 (POTENTIAL).  
 FT TRANSMEM 236 260 8 (POTENTIAL).  
 FT DOMAIN 261 277 9 (POTENTIAL).  
 FT TRANSMEM 278 301 10 (POTENTIAL).  
 FT DOMAIN 302 352 11 (POTENTIAL).  
 FT DISULFID 101 178 12 (POTENTIAL).  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 FT CARBOHYD 268 268 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 123 123 T -> S (IN REF. 1).  
 SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;  
 Query Match 100.0%; Score 95; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YAFVGEKERNYLLVFFQK 18  
 Db 297 YAFVGEKERNYLLVFFQK 314  
 RESULT 11  
 CCR5 PAPA  
 ID CCR5 PAPA STANDARD; PRT; 352 AA.  
 AC PS6441;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKRS5.  
 OS Papio hamadryas (Hamadryas baboon), and  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Papio.  
 OX NCBI\_TaxID=9557, 9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX SPECIES=P.hamadryas;  
 RX MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX SPECIES=P.hamadryas;  
 RX MEDLINE=99210133; PubMed=10195758;  
 RA Saksena N.K., Wang B., Novembre F.J., Bolton W., Smit T.K., Lal R.B.;  
 RT "Species-specific changes in the CCR5 gene from African and Asian  
 RT nonhuman primates.";  
 RL AIDS Res. Hum. Retroviruses 15:479-483(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX SPECIES=P.anubis;  
 RA Benton P.A., Timanus D.K., Shearer M.H., Lee D.R., Kennedy R.C.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
 CC MIP-1-beta and RANTES and subsequently transduces a signal by

increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF005658; AAB62552.1; -  
 EMBL; AF105287; AAD20556.1; -  
 EMBL; AF105288; AAD20557.1; -  
 EMBL; AF105289; AAD20558.1; -  
 EMBL; AF105290; AAD20559.1; -  
 EMBL; AF023452; AAC63830.1; -  
 InterPro; IPR000276; GPCR\_Rhodopsin.  
 Pfam; PF00001; 7tm 1; 1.  
 PRINTS; PR00237; GPCRHOPOPSN.  
 PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 PROSITE; PS0262; G-PROTEIN RECP\_F1\_2; 1.  
 G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 31 58 1 (POTENTIAL).  
 DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 69 89 2 (POTENTIAL).  
 DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 103 124 3 (POTENTIAL).  
 DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 142 166 4 (POTENTIAL).  
 DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 199 218 5 (POTENTIAL).  
 DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 236 260 6 (POTENTIAL).  
 DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 278 301 7 (POTENTIAL).  
 DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 DISULFID 101 178 BY SIMILARITY.  
 MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 CARBOHYD 268 268 N-LINKED (GLCNAC...) (POTENTIAL).  
 SEQUENCE 352 AA; 40489 MW; 5E1504A9BA1FE882 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFNLYLVFFQK 18  
 |||||  
 DB 297 YAFVGEKFNLYLVFFQK 314

RESULT 12  
 CKR5\_PONPY  
 ID CKR5\_PONPY STANDARD; PRT; 352 AA.  
 AC 097881;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKR5.  
 OS Pongo pygmaeus (Orangutan).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
 NCBI\_TaxID=9600;  
 RN [1]  
 RP SEQUENCE FROM N.A.

MDL:99416438; PubMed=10486970;  
 Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 "Sequence evolution of the CCR5 chemokine receptor gene in primates.";  
 Mol. Biol. Evol. 16:1145-1154 (1999).

-1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha, MIP-1-beta and RANTES and subsequently transduces a signal by increasing the intracellular calcium ions level. May play a role in the control of granulocytic lineage proliferation or differentiation.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; AF075446; AAD19858.1; -  
 InterPro; IPR000276; GPCR\_Rhodopsin.  
 Pfam; PF00001; 7tm 1; 1.  
 PRINTS; PR00237; GPCRHOPOPSN.  
 PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 PROSITE; PS0262; G-PROTEIN RECP\_F1\_2; 1.  
 G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.

DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 31 58 1 (POTENTIAL).  
 DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 69 89 2 (POTENTIAL).  
 DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 103 124 3 (POTENTIAL).  
 DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 142 166 4 (POTENTIAL).  
 DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 199 218 5 (POTENTIAL).  
 DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 TRANSMEM 236 260 6 (POTENTIAL).  
 DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 TRANSMEM 278 301 7 (POTENTIAL).  
 DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 DISULFID 101 178 BY SIMILARITY.  
 MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SEQUENCE 352 AA; 40527 MW; F4E2F47135AF658A CRC64;

Query Match 100.0%; Score 95; DB 1; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFNLYLVFFQK 18  
 |||||  
 DB 297 YAFVGEKFNLYLVFFQK 314

RESULT 13  
 CKR5\_PYGBI  
 ID CKR5\_PYGBI STANDARD; PRT; 352 AA.  
 AC 097880;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKR5.  
 OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;  
 OC Pygathrix.  
 NCBI\_TaxID=61621;  
 RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF075445; AAD19857.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm 1; 1.
CC PRINTS: PR00237; GPCRHHODPSN.
CC PROSITE: PS00237; G PROTEIN RECP F1.1; 1.
CC PROSITE: PS0262; G PROTEIN RECP F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC
CC DOMAIN 1 30
CC FT EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 31 58
CC FT DOMAIN 59 68
CC FT CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 69 89
CC FT DOMAIN 90 102
CC FT EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 103 124
CC FT DOMAIN 125 141
CC FT CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 142 166
CC FT DOMAIN 167 198
CC FT EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 199 218
CC FT DOMAIN 219 235
CC FT CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 236 260
CC FT DOMAIN 261 277
CC FT EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 278 301
CC FT DOMAIN 302 323
CC FT CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 101 178
CC FT BY SIMILARITY.
CC FT MOD_RES 3 3
CC FT SULFATION (BY SIMILARITY).
CC FT MOD_RES 10 10
CC FT SULFATION (BY SIMILARITY).
CC FT MOD_RES 14 14
CC FT SULFATION (BY SIMILARITY).
CC FT MOD_RES 15 15
CC FT SULFATION (BY SIMILARITY).
CC
CC SEQUENCE 352 AA; 40585 MW; 4366f142730f938f CRC64;
Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
DB 297 YAFVGEKFRNYLLVFFQK 314
RESULT 14
CCR5_PYGNE
ID CCR5_PYGNE STANDARD; PRT; 352 AA.
AC 097882;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Pygathrix.
OC NCBI_TaxId=54133;

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[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -I- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,
CC MIP-1-beta and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level. May play a role
CC in the control of granulocytic lineage proliferation or
CC differentiation.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF075448; AAD19860.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm 1; 1.
CC PRINTS: PR00237; GPCRHHODPSN.
CC PROSITE: PS00237; G PROTEIN RECP F1.1; 1.
CC PROSITE: PS0262; G PROTEIN RECP F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC
CC DOMAIN 1 30
CC FT EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 31 58
CC FT DOMAIN 59 68
CC FT CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 69 89
CC FT DOMAIN 90 102
CC FT EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 103 124
CC FT DOMAIN 125 141
CC FT CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 142 166
CC FT DOMAIN 167 198
CC FT EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 199 218
CC FT DOMAIN 219 235
CC FT CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 236 260
CC FT DOMAIN 261 277
CC FT EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 278 301
CC FT DOMAIN 302 352
CC FT CYTOPLASMIC (POTENTIAL)..
CC FT DISULFID 101 178
CC FT BY SIMILARITY.
CC FT MOD_RES 3 3
CC FT SULFATION (BY SIMILARITY).
CC FT MOD_RES 10 10
CC FT SULFATION (BY SIMILARITY).
CC FT MOD_RES 14 14
CC FT SULFATION (BY SIMILARITY).
CC FT MOD_RES 15 15
CC FT SULFATION (BY SIMILARITY).
CC
CC SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3861 CRC64;
Query Match 100.0%; Score 95; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YAFVGEKFRNYLLVFFQK 18
DB 297 YAFVGEKFRNYLLVFFQK 314
RESULT 15
CCR5_TRAFR
ID CCR5_TRAFR STANDARD; PRT; 352 AA.
AC 097878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CCR5 OR CMKBR5.
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Trachypithecus.

```

Trachypithecus.  
NCBI\_TaxID=61618;  
[1]  
SEQUENCE FROM N.A.  
Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
MEDLINE=99416438; PubMed=10486970;  
"Sequence evolution of the CCR5 chemokine receptor gene in primates.";  
Mol. Biol. Evol. 16:1145-1154 (1999).  
-1- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-1-alpha,  
MIP-1-beta and RANTES and subsequently transduces a signal by  
increasing the intracellular calcium ions level. May play a role  
in the control of granulocytic lineage proliferation or  
differentiation.  
-1- SUBCELLULAR LOCATION: Integral membrane protein.  
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
-----  
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-----  
EMBL; AF075443; AAD19855.1; -  
InterPro; IPR000276; GPCR\_Rhodopsn.  
Pfam; PF00001; 7tm1; 1.  
PRINTS; PR00237; GPCRHDOPSN  
PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
DR PROSITE; PS02082; G-PROTEIN RECP\_F1\_2; 1.  
D G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 2 (POTENTIAL).  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 103 124 3 (POTENTIAL).  
FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 142 166 4 (POTENTIAL).  
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 199 218 5 (POTENTIAL).  
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 236 260 6 (POTENTIAL).  
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 278 301 7 (POTENTIAL).  
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
FT DISULFD 101 178 BY SIMILARITY.  
FT MOD RES 3 3 SULFATION (BY SIMILARITY).  
FT MOD RES 10 10 SULFATION (BY SIMILARITY).  
FT MOD RES 14 14 SULFATION (BY SIMILARITY).  
FT MOD RES 15 15 SULFATION (BY SIMILARITY).  
SQ SEQUENCE 352 AA; 40509 MW; 4366FF148D3A5938F CRC64;  
Query Match 100.0%; Score 95; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 6.9e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YAFVGEKFRNYLLVFFQK 18  
| | | | | | | | | | | | | | | | | |  
DDB 297 YAFVGEKFRNYLLVFFQK 314  
-----  
RESULT 17  
CCR5\_RAT  
ID CCR5 RAT STANDARD; PRT; 354 AA.  
AC 008556;  
DC 01-NOV-1997 (Rel. 35; Created)  
DT 01-NOV-1997 (Rel. 35; Last sequence update)  
DD 30-MAY-2000 (Rel. 39; Last annotation update)  
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (MIP-1  
alpha receptor).  
OS Rattus norvegicus (Rat).  
GN CCR5 OR CMKR5.







FT TRANSMEM 257 281 6 (POTENTIAL).  
 FT DOMAIN 282 298 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 299 322 7 (POTENTIAL).  
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 126 203 BY SIMILARITY.  
 FT CONFLICT 39 39 Y -> H (IN REF. 1).  
 FT CONFLICT 184 184 A -> G (IN REF. 1).  
 FT CONFLICT 264 264 V -> G (IN REF. 1).  
 SQ SEQUENCE 373 AA; 42782 MW; FA012C10F4C9325A CRC64;

Query Match 82.1%; Score 78; DB 1; Length 373;  
 Best Local Similarity 77.8%; Pred. No. 6.4e-06;  
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFNLYLVFFOK 18  
 ||||| ||| :|||  
 Db 318 YAFVGEKFNLYLVFFOK 335

## RESULT 20

CKR2 RAT  
 ID CKR2 RAT STANDARD; PRT; 373 AA.  
 AC O55193;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).  
 GN CKR2 OR CMKR2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=98318173; PubMed=9655467;  
 RA Jiang Y., Salafranca M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 RT "Chemokine receptor expression in cultured glia and rat experimental  
 allergic encephalomyelitis";  
 RL J. Neuroimmunol. 86:11-12(1998).  
 CC -!- FUNCTION: Receptor for the MCP-1 (JE), MCP-3 (PIC) and MCP-5  
 chemokines. Transduces a signal by increasing the intracellular  
 calcium ions level (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in lung, spleen, kidney, thymus and  
 macrophages.  
 CC -!- INDUCTION: In animals in which experimental allergic  
 encephalomyelitis (EAE) has been induced.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC  
 CC EMBL; U77349; AAC03242.1; -;  
 CC InterPro; IPR000276; GPCR\_Rhodopsin.  
 CC Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 61 81 POTENTIAL.  
 FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 92 112 POTENTIAL.  
 FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 129 149 POTENTIAL.  
 FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 171 191 POTENTIAL.  
 FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 221 241 POTENTIAL.  
 FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 257 277 POTENTIAL.  
 FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 302 322 POTENTIAL.  
 FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 126 203 BY SIMILARITY.  
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 82.1%; Score 78; DB 1; Length 373;  
 Best Local Similarity 77.8%; Pred. No. 6.4e-06;  
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFNLYLVFFOK 18  
 ||||| ||| :|||  
 Db 318 YAFVGEKFNLYLVFFOK 335

## RESULT 21

CKR2 MACMU  
 ID CKR2 MACMU STANDARD; PRT; 360 AA.  
 AC O18793;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE C-C chemokine receptor type 2 (C-C CKR-2) (CCR-2) (CCR2).  
 GN Monocyte chemoattractant protein 1 receptor (MCP-1-R).  
 CC CKR2 OR CMKR2.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21354176; PubMed=11461684;  
 RA Margulies B.J., Hauer D.A., Clements J.E.;  
 RT "Identification and comparison of eleven rhesus macaque chemokine  
 receptors";  
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
 CC -!- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 CC Transduces a signal by increasing the intracellular calcium ions  
 level.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Name=B;  
 CC Name=A;  
 CC IsoId=O18793-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoId=O18793-2; Sequence=Not described;

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC  
 CC EMBL; AF013958; AAD11572.1; -;  
 CC InterPro; IPR000276; GPCR\_Rhodopsin.  
 CC Pfam; PF00001; 7tm.1; 1.

DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 43 70 1 (POTENTIAL).  
 FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).

FT TRANSEM 81 100 2 (POTENTIAL).  
 FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 115 136 3 (POTENTIAL).  
 FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 154 178 4 (POTENTIAL).  
 FT DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 207 226 5 (POTENTIAL).  
 FT DOMAIN 227 243 6 (POTENTIAL).  
 FT TRANSEM 244 268 7 (POTENTIAL).  
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 286 309 7 (POTENTIAL).  
 FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT MOD RES 26 26 SULFATION (BY SIMILARITY).  
 FT DISULFID 113 190 BY SIMILARITY.  
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 80.0%; Score 76; DB 1; Length 360;  
 Best Local Similarity 77.8%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFPQK 18  
 |||||:||||:|  
 DB 305 YAFVGEKFRNVLVFPQK 322

## RESULT 22

ID\_CKR3\_CERAE STANDARD; PRT; 355 AA.  
 AC P56452;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)  
 DE (CCR3).  
 GN CCR3 OR CMKBR3.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sol N., Treboute C., Gomas E., Ferchal F., Alison M.;  
 RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RL -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin.  
 CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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EMBL; Y13775; CAA74106.1;  
 InterPro; IPR000276; GPCR\_Rhodpsn.  
 Pfam; PF00001; 7tm 1; 1.  
 PRINTS; PR00237; GPCR\_Rhodopsin.  
 DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECP FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 35 62 1 (POTENTIAL).  
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 73 93 2 (POTENTIAL).  
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 108 129 3 (POTENTIAL).  
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).

FT TRANSEM 147 171 4 (POTENTIAL).  
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 204 223 5 (POTENTIAL).  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSEM 240 264 6 (POTENTIAL).  
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).  
 FT TRANSEM 282 305 7 (POTENTIAL).  
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 106 183 BY SIMILARITY.  
 SQ SEQUENCE 355 AA; 40830 MW; 44F7A5EFE9B978FF CRC64;

Query Match 68.4%; Score 65; DB 1; Length 355;  
 Best Local Similarity 66.7%; Pred. No. 0.0011;  
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFPQK 18  
 |||||:||||:|  
 DB 301 YAFVGEKFRNVLVFPQK 318

## RESULT 23

ID\_CKR3\_HUMAN STANDARD; PRT; 355 AA.  
 AC P51677; Q15748; Q86WD2; Q9ULY8;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3) (CCR3)  
 DE (CCR3) (Eosinophil eotaxin receptor).  
 GN CCR3 OR CMKBR3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Monocytes;  
 RX MEDLINE=95348056; PubMed=7622448;  
 RA Combadiere C., Ahuja S.K., Murphy P.M.;  
 RT "Cloning and functional expression of a human eosinophil CC chemokine  
 RT receptor.";  
 RL J. Biol. Chem. 270:16491-16494 (1995).  
 RN [2]  
 RP ERRATUM.  
 RA Combadiere C., Ahuja S.K., Murphy P.M.;  
 RL J. Biol. Chem. 270:30235-30235 (1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96235044; PubMed=8642344;  
 RA Daugherty B.L., Siciliano S.J., Demartino J.A., Malkowitz L.,  
 RA Sirotina A., Springer M.S.;  
 RT "Cloning, expression, and characterization of the human eosinophil  
 RT eotaxin receptor.";  
 RL J. Exp. Med. 183:2349-2354 (1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96281895; PubMed=8676064;  
 RA Ponath P.D., Qin S., Post T.W., Wang J., Wu L., Gerard N.P.,  
 RA Newman W., Gerard C., Mackay C.R.;  
 RT "Molecular cloning and characterization of a human eotaxin receptor  
 RT expressed selectively on eosinophils.";  
 RL J. Exp. Med. 183:2737-2748 (1996).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX Xiao L., Weiss S., Qari S., Rudolph D., Hodge T., Lal R.;  
 RT "Partial resistance to infection by syncytium-inducing primary HIV-1  
 RT in exposed uninfected individuals homozygous for CCR5 32bp deletion.";  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A., AND VARIANT SER-218.  
 RX MEDLINE=21040311; PubMed=11196669;  
 RA Kato H., Tsuchiya N., Izumi S., Miyamasu M., Nakajima T., Kawasaki H.,  
 RA Hirai K., Tokunaga K.;

RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";  
 RN Genes Immun. 1:97-104(1999).  
 RP [7]  
 RX SEQUENCE FROM N.A.  
 RX MEDLINE=22074933; PubMed=12079287;  
 RX Vilh S., Dayhoff D.B., Wang C.E., Imam Z., Ehrenberg P.K.,  
 RA Michael N.L.;  
 RA "Transcription regulation of human chemokine receptor CCR3: evidence  
 RT for a rare TATA-less promoter structure conserved between Drosophila  
 RT and humans";  
 RL Genomics 80:86-95(2002).  
 RP [8]  
 RP SEQUENCE FROM N.A.  
 RA Kopatz S.A., Aronstam R.S., Sharma S.V.;  
 RA "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 RP [9]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Brain, Lung, and Testis;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshynski S., Carninci P., Prange C.,  
 RA Raba S.S., Lomellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,  
 CC eotaxin-3, MCP-3, MCP-4, RANTES and MIP-1 delta. Subsequently  
 CC transduces a signal by increasing the intracellular calcium ions  
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: In eosinophils as well as trace amounts in  
 CC neutrophils and monocytes.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -----  
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 CC -----  
 DR EMBL; U28694; AAC50469.1; -;  
 DR EMBL; U51241; AB16811.1; -;  
 DR EMBL; U45727; AB09726.1; -;  
 DR EMBL; AF026535; AB02589.1; -;  
 DR EMBL; AB023887; BA08696.1; -;  
 DR EMBL; AF247361; AA08515.1; -;  
 DR EMBL; AY221092; AA065970.2; -;  
 DR EMBL; BC033514; AB033514.1; -;  
 DR EMBL; G02436; G02436.  
 DR Genew; HGNC:1604; CCR3.  
 DR MIM; 601268; -;  
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
 DR GO; GO:0004950; P: chemokine receptor activity; TAS.  
 DR GO; GO:0007155; P: cell adhesion; TAS.  
 DR GO; GO:0006368; P: cellular defense response; TAS.

DR GO; GO:0006935; P: chemotaxis; TAS.  
 DR GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.  
 DR GO; GO:0007188; P: G-protein signaling, coupled to GMP nucleoside; TAS.  
 DR GO; GO:0006954; P: inflammatory response; TAS.  
 DR GO; GO:0007125; P: invasive growth; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm 1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Polymorphism.  
 KW DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 35 62 1 (POTENTIAL).  
 FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 73 93 2 (POTENTIAL).  
 FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 108 129 3 (POTENTIAL).  
 FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 147 171 4 (POTENTIAL).  
 FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 204 223 5 (POTENTIAL).  
 FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 240 264 6 (POTENTIAL).  
 FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 282 305 7 (POTENTIAL).  
 FT DOMAIN 306 355 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 106 183 BY SIMILARITY.  
 FT VARIANT 218 218 C->S (polymorphism found in about 7% of  
 FT the population; may show reduced  
 FT activity).  
 FT CONFLICT 276 276 S->T (IN REF. 4 AND 5).  
 FT SEQUENCE 355 AA; 41043 MW; B95DCD7A6C643874 CRC64;  
 Query Match 68.4%; Score 65; DB 1; Length 355;  
 Best Local Similarity 66.7%; Pred. No. 0.0011;  
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 YAFVGEKPRNVLVFFOK 18  
 |||||:|||||:  
 DB 301 YAFVGEKPRNVLVFFOK 318  
 RESULT 24  
 CCR3 MACMU STANDARD; PRT; 355 AA.  
 ID CCR3 MACMU STANDARD; PRT; 355 AA.  
 AC P56483;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 3 (C-C CCR-3) (CCR-3) (CCR3)  
 DE (CCR3).  
 GN CCR3 OR CCR3R3.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OC NCBI\_TaxID=9544;  
 OX [1]\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21354176; PubMed=11461694;  
 RA Margulies B.J., Hauer D.A., Clements J.E.;  
 RT "Identification and comparison of eleven rhesus macaque chemokine  
 RT receptors";  
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98118446; PubMed=9454694;  
 RA Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;  
 RT "The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor  
 RT for HIV-2, but not for HIV-1";  
 RL Virology 240:213-220(1998).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,

CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by  
 CC increasing the intracellular calcium ions level.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----  
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 CC -----

DR EMBL; AF017283; AAB70527.1; -;  
 DR EMBL; Y13776; CAA74107.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECP F1.2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 34  
 FT TRANSMEM 35 62  
 FT DOMAIN 63 72  
 FT TRANSMEM 73 93  
 FT DOMAIN 94 107  
 FT TRANSMEM 108 129  
 FT DOMAIN 130 146  
 FT TRANSMEM 147 171  
 FT DOMAIN 172 203  
 FT TRANSMEM 204 223  
 FT DOMAIN 224 239  
 FT TRANSMEM 240 261  
 FT DOMAIN 265 281  
 FT TRANSMEM 282 305  
 FT DOMAIN 306 355  
 FT DISULFID 106 183  
 FT CONFLICT 180 180 K -> E (IN REF. 2).  
 FT CONFLICT 202 202 K -> R (IN REF. 2).  
 SQ SEQUENCE 355 AA; 40805 MW; E271F1B694970D9F CRC64;

Query Match 68.4%; Score 65; DB 1; Length 355;  
 Best Local Similarity 66.7%; Pred. No. 0.0011;  
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 YAFVGEKFRNLLVFFQK 18  
 DB 301 YAFVGEKFRNLLVFFQK 318

RESULT 25  
 CKR8 MOUSE  
 ID CKR8 MOUSE STANDARD; PRT; 353 AA.  
 AC P56484;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 8 (C-C CKR-8) (CC-CKR-8) (CCR-8).  
 DE CCR8 OR CMKR8 OR TER1.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zaballos A., Goya I.I., Gutierrez J., Varona R., Marquez G.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv;  
 EX MEDLINE=98334001; PubMed=9670926;  
 RA Zingoni A., Soto H., Hedrick J.A., Stoppacciaro A., Storazzi C.T.,  
 RA Sinigaglia F., D'Ambrosio D., O'Garra A., Robinson D., Rocchi M.,

RA Santoni A., Zlotnik A., Napolitano M.;  
 RT "The chemokine receptor CCR8 is preferentially expressed in Th2 but  
 RL not Th1 cells.";  
 RL J. Immunol. 161:547-551(1998).  
 CC -1- FUNCTION: Receptor for the TCA-3 chemokine.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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 CC -----

DR EMBL; Z98206; CAB10896.1; -;  
 DR EMBL; Z98205; CAB10895.1; -;  
 DR EMBL; AF001277; AAC97598.1; -;  
 DR MGD; MGI-1201402; Ccr8.  
 DR GO; GO:0016493; F-C-C chemokine receptor activity; IDA.  
 DR GO; GO:0005515; P:protein binding; IPI.  
 DR GO; GO:0006935; P:chemotaxis; IDA.  
 DR InterPro: IPR004068; CC 8 receptor.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS; PR01530; CHEMOKINER8.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G PROTEIN RECP F1.1; 1.  
 DR PROSITE; PS0262; G PROTEIN RECP F1.2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 33  
 FT TRANSMEM 34 61  
 FT DOMAIN 62 71  
 FT TRANSMEM 72 91  
 FT DOMAIN 92 105  
 FT TRANSMEM 106 127  
 FT DOMAIN 128 144  
 FT TRANSMEM 145 169  
 FT DOMAIN 170 200  
 FT TRANSMEM 201 220  
 FT DOMAIN 221 236  
 FT TRANSMEM 237 261  
 FT DOMAIN 262 278  
 FT TRANSMEM 279 302  
 FT DOMAIN 303 353  
 FT DISULFID 104 181  
 FT CARBOHYD 8  
 FT N-LINKED (GLCNAC...); (POTENTIAL).  
 SQ SEQUENCE 353 AA; 40045 MW; 31EC4B642CDB9AE5 CRC64;

Query Match 67.4%; Score 64; DB 1; Length 353;  
 Best Local Similarity 61.1%; Pred. No. 0.0016;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 YAFVGEKFRNLLVFFQK 18  
 DB 298 YAFVGEKFRNLLVFFQK 315

RESULT 26  
 CKR3 MOUSE  
 ID CKR3 MOUSE STANDARD; PRT; 359 AA.  
 AC P51678;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CCR-3)  
 DE (CCR3) (CKR3) (Macrophage inflammatory protein-1 alpha receptor-like  
 DE 2) (MIP-1 alpha RL2).  
 GN CCR3 OR CMKR3 OR CMKR1L2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
RT receptors.";
RL J. Immunol. 155:5299-5305 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=95340546; PubMed=7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor.";
RL J. Biol. Chem. 270:17494-17501 (1995).
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in skeletal muscle and in trace
CC amounts in leukocytes.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; U29677; AAA86118.1; -.
CC EMBL; U28406; AAA89155.1; -.
CC MGD; MGI:104616; Ccr3.
CC GO; GO:0016493; F:C-C chemokine receptor activity; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC GO; GO:0006935; P:chemotaxis; IDA.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC DOMAIN 1 38
CC FT TRANSMEM 39 64 1 (POTENTIAL).
CC FT DOMAIN 65 68 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 69 95 2 (POTENTIAL).
CC FT DOMAIN 96 111 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 112 133 3 (POTENTIAL).
CC FT DOMAIN 134 150 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 151 175 4 (POTENTIAL).
CC FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 202 227 5 (POTENTIAL).
CC FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 244 268 6 (POTENTIAL).
CC FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 286 309 7 (POTENTIAL).
CC FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
CC FT DISULFID 110 187 BY SIMILARITY.
CC FT CONFLICT 270 270 R -> S (IN REF. 2).
CC SEQUENCE 359 AA; 41825 MW; AC11ED6E283CEAF CRC64;
Query Match 67.4%; Score 64; DB 1; Length 359;
Best Local Similarity 61.1%; Pred. No. 0.0016;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 YAFVGRKERNYLLVFFOK 18
Db 305 YAFVGRFRKHRLURFFHR 322

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RESULT 27
CCR3_RAT
ID_CCR3_RAT STANDARD; PRT; 359 AA.
AC 054814; O55169;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CCR-3) (CCR-3) (CCR3)
DE (CCR3).
GN CCR3 OR CMKBR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Spleen;
RX MEDLINE=98318173; PubMed=9655467;
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Peng L., Sonntag M.K.,
RA Defiebre C.M., Pennell N.A., Streit W.J., Harrison J.K.;
RT "Chemokine receptor expression in cultured glia and rat experimental
RT allergic encephalomyelitis.";
RL J. Neuroimmunol. 86:1-12 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,
CC MCP-3, MCP-4 and RANTES and subsequently transduces a signal by
CC increasing the intracellular calcium ions level (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in spleen but not in astrocytes or
CC microglia.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
CC EMBL; AF003954; AAC03337.1; -.
CC EMBL; Y13400; CAA73830.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
CC DOMAIN 1 43
CC FT TRANSMEM 44 64 1 (POTENTIAL).
CC FT DOMAIN 65 74 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 75 95 2 (POTENTIAL).
CC FT DOMAIN 96 112 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 113 133 3 (POTENTIAL).
CC FT DOMAIN 134 154 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 155 175 4 (POTENTIAL).
CC FT DOMAIN 176 206 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 207 227 5 (POTENTIAL).
CC FT DOMAIN 228 243 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 244 264 6 (POTENTIAL).
CC FT DOMAIN 265 288 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 289 309 7 (POTENTIAL).
CC FT DOMAIN 310 359 CYTOPLASMIC (POTENTIAL).
CC FT CONFLICT 164 164 F -> L (IN REF. 2).
CC SEQUENCE 359 AA; 41643 MW; 880F682984F501DA CRC64;
Query Match 67.4%; Score 64; DB 1; Length 359;

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Best Local Similarity 61.1%; Pred. No. 0.0016;  
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18  
DB 305 YAFVGEKFRNVLVFFQK 322

## RESULT 28

CC CR8 HUMAN STANDARD; PRT; 355 AA.  
AC P51685;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 8 (C-C CR8) (CC-CR8) (CCR-8) (GPR-CY6)  
DE (GPRCV6) (Chemokine receptor-like 1) (CCR-L1) (TER1) (CMKRL2) (CC-  
DE chemokine receptor CHEMRL1).  
DE CCR8 OR CMKRL2 OR CCR1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97351133; PubMed=9207005;  
RA Tiffany H.L., Lautens L.L., Gao J.-L., Pease J., Locati M.,  
RA Combiadere C., Modi W., Bonner T.I., Murphy P.M.;  
RT "Identification of CCR8: a human monocyte and thymus receptor for the  
RT C-C chemokine I-309";  
RL J. Exp. Med. 186:165-170 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98129363; PubMed=9469461;  
RA Goya I., Gutierrez J., Varona R., Kremer L., Zaballos A., Marquez G.;  
RT "Identification of CCR8 as the specific receptor for the human beta-  
RT chemokine I-309: cloning and molecular characterization of murine  
RT CCR8 as the receptor for TCA-3";  
RL J. Immunol. 160:1975-1981 (1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97040707; PubMed=8886020;  
RA Zaballos A., Varona R., Gutierrez J., Lind P., Marquez G.;  
RT "Molecular cloning and RNA expression of two new human chemokine  
RT receptor-like genes";  
RL Biochem. Biophys. Res. Commun. 227:846-853 (1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97131825; PubMed=8977299;  
RA Samson M., Stordeur P., Labbe O., Soularue P., Vassart G.,  
RA Parmentier M.;  
RT "Molecular cloning and chromosomal mapping of a novel human gene,  
RT Chem1, expressed in T lymphocytes and polymorphonuclear cells and  
RT encoding a putative chemokine receptor";  
RL Eur. J. Immunol. 26:3021-3028 (1996).  
RN [5]  
RP SEQUENCE FROM N.A.  
RA Nakajima T., Yoshida R., Harada S.;  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP LIGAND BINDING.  
RX MEDLINE=98180363; PubMed=9521068;  
RA Bernardini G., Hedrick J., Sozzani S., Luini W., Spinetti G.,  
RA Weiss M., Menon S., Zlotnik A., Mantovani A., Santoni A.,  
RA Napolitano M.;  
RT "Identification of the CC chemokines TARC and macrophage inflammatory  
RT protein-1 beta as novel functional ligands for the CCR8 receptor";  
RL Eur. J. Immunol. 28:582-588 (1998).  
CC -1- FUNCTION: Receptor for the chemokines SCY1/I-309, SCY4/MIP-1-  
CC beta and SCY17/TARC. May regulate monocyte chemotaxis and thymic  
CC cell line apoptosis. Alternative coreceptor with CD4 for HIV-1  
CC infection.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
CC  
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CC EMBL; U45983; AAB61962.1; -  
CC EMBL; U62556; AAB05542.1; -  
CC EMBL; Z79782; CAB02142.1; -  
CC EMBL; Y08456; CAA69712.1; -  
CC EMBL; D49919; BAA23387.1; -  
CC EMBL; AF005210; AAB62547.1; -  
CC PIR; JCS067; JCS067.  
CC Genew; HGNC:1609; CCR8.  
CC MIM; 601834; -  
CC GO; GO:0005887; C: integral to plasma membrane; TAS.  
CC GO; GO:0004950; F: chemokine receptor activity; TAS.  
CC GO; GO:0015026; F: coreceptor activity; TAS.  
CC GO; GO:0007155; P: cell adhesion; TAS.  
CC GO; GO:0006935; P: chemotaxis; TAS.  
CC GO; GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.  
CC GO; GO:0007186; P: G-protein coupled receptor protein signalin.; TAS.  
CC GO; GO:0006955; P: immune response; TAS.  
CC InterPro; IPR004068; CC 8 receptor.  
CC InterPro; IPR000276; GPCR Rhodopsn.  
CC Pfam; PF00001; 7tm 1; 1.  
CC PRINTS; PR01530; CHEMOKINER8.  
CC PRINTS; PR00237; GPCR RHODOPSIN.  
CC PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
CC PROSITE; PS0262; G-PROTEIN RECP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
FT DOMAIN 1 35  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 36 63  
FT DOMAIN 64 73  
FT CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 74 93  
FT DOMAIN 94 107  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 108 129  
FT DOMAIN 130 146  
FT CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 147 171  
FT DOMAIN 172 202  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 203 222  
FT DOMAIN 223 238  
FT CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 239 263  
FT DOMAIN 264 280  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 281 304  
FT DOMAIN 305 355  
FT CYTOPLASMIC (POTENTIAL).  
FT DISULFID 106 183  
FT BY SIMILARITY.  
SQ SEQUENCE 355 AA; 40844 MW; BCI4A153CF695361 CRC64;

Query Match 66.3%; Score 63; DB 1; Length 355;  
Best Local Similarity 66.7%; Pred. No. 0.0024;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18  
DB 300 YAFVGEKFRNVLVFFQK 317

## RESULT 29

CC CR8 MACMU STANDARD; PRT; 356 AA.  
AC O97665;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 8 (C-C CR8) (CCR-8) (CCR-8).  
GN CCR8.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spine;  
 RX MEDLINE=21354176; PubMed=11461684;  
 RA Margulies B.J., Hauer D.A., Clements J.E.;  
 RT "Identification and comparison of eleven rhesus macaque chemokine  
 RT receptors.";  
 RL AIDS Res. Hum. Retroviruses 17:981-986 (2001).  
 CC -!- FUNCTION: Receptor for the chemokines SCY1/I-309, SCY44/MIP-1-  
 CC beta and SCY17/TAC. May regulate monocyte chemotaxis and thymic  
 CC cell line apoptosis (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; AF100205; AAC72403.1; -;  
 DR InterPro; IPR004068; CC 8 receptor.  
 DR InterPro; IPR00276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR01530; CHEMOKINER8.  
 DR PRINTS; PR00237; GPCRHOPOPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECP F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN RECP F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 35  
 FT TRANSMEM 36 63  
 FT DOMAIN 64 73  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 74 93  
 FT TRANSMEM 94 107  
 FT EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 108 129  
 FT TRANSMEM 130 146  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 147 172  
 FT TRANSMEM 173 203  
 FT EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 204 223  
 FT TRANSMEM 224 239  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 240 264  
 FT TRANSMEM 265 281  
 FT EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 282 305  
 FT TRANSMEM 306 356  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 106 184  
 FT BY SIMILARITY.  
 SQ SEQUENCE 356 AA; 41210 MW; 1979628DEE44845B CRC64;  
 Query Match 66.3%; Score 63; DB 1; Length 356;  
 Best Local Similarity 66.7%; Pred. No. 0.0024;  
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 YAFVGEKFRNVLVFFQK 18  
 |||||:|:|  
 Db 301 YAFVGEKFKHLSEIFQK 318  
 |||||:|:|  
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 ID CKR6\_HUMAN STANDARD; PRT; 374 AA.  
 AC P51684; P78553; Q92846;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1998 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE C-C chemokine receptor type 6 (C-C CKR-6) (CC-CKR-6) (CCR-6) (IARC  
 DE receptor) (GPR-CV4) (GPCR4) (Chemokine receptor-like 3) (CCR-L3)  
 DE (DRY6).  
 GN CKR6 OR CMK6 OR SREL22 OR GPR29 OR CKRL3.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.; AND FUNCTION.  
 RX MEDLINE=97313465; PubMed=9169459;  
 RA Baba M., Imai T., Nishimura M., Kakizaki M., Takagi S., Hieshima K.,  
 RA Nomiya H., Yoshie O.;  
 RT "Identification of CCR6, the specific receptor for a novel  
 RT lymphocyte-directed CC chemokine LARC.";  
 RL J. Biol. Chem. 272:14893-14898 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Lautens L.L., Modi W., Bonner T.I.;  
 RA Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97040707; PubMed=886020;  
 RA Zaballo A., Varona R., Gutierrez J., Lind P., Marquez G.;  
 RT "Molecular cloning and RNA expression of two new human chemokine  
 RT receptor-like genes.";  
 RL Biochem. Biophys. Res. Commun. 227:846-853 (1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA McCoy R., Perlmutter D.H.;  
 RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97224503; PubMed=9070937;  
 RA Liao F., Lee H.-H., Farber J.M.;  
 RT "Cloning of STRL22, a new human gene encoding a G-protein-coupled  
 RT receptor related to chemokine receptors and located on chromosome  
 RT 6q27.";  
 RL Genomics 40:175-180 (1997).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA Warren C.N., Aronstam R.S., Sharma S.V.;  
 RT "cDNA clones of human proteins involved in signal transduction  
 RT sequenced by the Guthrie cDNA resource center ([www.cdna.org](http://www.cdna.org)).";  
 RN Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22935763; PubMed=14574404;  
 RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,  
 RA Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,  
 RA Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,  
 RA Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,  
 RA Babbage A.K., Baguley C.L., Bailey J., Banerjee R., Barker D.J.,  
 RA Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,  
 RA Blakey S., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,  
 RA Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,  
 RA Chapman J.C., Clark S.V., Clark G., Clee C.M., Clegg S., Cobley V.,  
 RA Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,  
 RA Culley K.M., Dhani P., Davies J., Dunn M., Earthrowl M.E.,  
 RA Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,  
 RA Frankland J., French L., Garner P., Garnett J., Ghori M.J.,  
 RA Gilby L.M., Gillson C.J., Griffiths R.J., Grafham D.V., Grant M.,  
 RA Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,  
 RA Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcote R.,  
 RA Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,  
 RA Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,  
 RA Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,  
 RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,  
 RA Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,  
 RA Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLean K.,  
 RA McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,  
 RA Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,  
 RA Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,  
 RA Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,  
 RA Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,  
 RA Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,  
 RA Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,  
 RA Wall M., Wallis J.M., White A.P., White S.S., Whitehead S.L.,

RA Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,  
 RA Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,  
 RA Durbin R., Hubbard T., Sulston J.B., Dunham I., Rogers J., Beck S.,  
 RT "The DNA sequence and analysis of human chromosome 6,"  
 RL Nature 425:805-811(2003).  
 RP (8)  
 RP SEQUENCE FROM N.A.  
 RC  
 RC TISSUE=Pancreas;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.I., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carminci P., Prange C.,  
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences,"  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Receptor for a C-C type chemokine. Binds to MIP-3-  
 CC alpha/LARC and subsequently transduces a signal by increasing the  
 CC intracellular calcium ions level.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Spleen, lymph nodes, appendix, and fetal  
 CC liver. Expressed in lymphocytes, T cells and B cells but not in  
 CC natural killer cells, monocytes or granulocytes.  
 CC -!- INDUCTION: By interleukin-2.  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 CC -!- CAUTION: It is uncertain whether Met-1 or Met-6 is the initiator.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 CC EMBL; U45984; AAB62714.1; -;  
 CC EMBL; Z79784; CAB02144.1; ALT\_INIT.  
 CC EMBL; U60000; AAB06949.1; -;  
 CC EMBL; U68030; AAC51124.1; -;  
 CC EMBL; U68032; AAC51125.1; -;  
 CC EMBL; AY242126; AAC92293.1; -;  
 CC EMBL; AL121935; CAB9328.1; -;  
 CC EMBL; BC037960; AAB37960.1; -;  
 CC HSSP; P34396; IDDD.  
 CC Genew; HGNC:1607; CCR6.  
 CC MIM; 601835; -;  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0004950; F:chemokine receptor activity; TAS.  
 CC GO; GO:0004872; F:receptor activity; TAS.  
 CC GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. .); TAS.  
 CC GO; GO:0006928; P:cell motility; TAS.  
 CC GO; GO:0006968; P:cellular defense response; TAS.  
 CC GO; GO:0006935; P:chemotaxis; TAS.  
 CC GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.  
 CC GO; GO:0006959; P:humoral immune response; TAS.  
 CC GO; GO:0007165; P:signal transduction; TAS.  
 CC InterPro; IPR004067; CC 6 receptor.  
 CC InterPro; IPR000276; GPCR\_Rhodpsn.  
 CC Pfam; PF00001; 7tm 1; 1.  
 CC PRINTS; PR01529; CHEMOKINER6.

DR PRINTS; PR00237; GPCR\_RHODPSN.  
 DR PROSITE; PS00237; G PROTEIN RECP FL 1; 1.  
 DR PROSITE; PS00237; G PROTEIN RECP FL 2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1 47  
 FT TRANSMEM 48 74  
 FT DOMAIN 75 83  
 FT TRANSMEM 84 104  
 FT DOMAIN 105 119  
 FT TRANSMEM 120 141  
 FT DOMAIN 142 159  
 FT TRANSMEM 160 180  
 FT DOMAIN 181 211  
 FT TRANSMEM 212 238  
 FT DOMAIN 239 254  
 FT TRANSMEM 255 279  
 FT DOMAIN 280 303  
 FT TRANSMEM 304 321  
 FT DOMAIN 322 374  
 FT TRANSMEM 374 474  
 FT DISULFID 118 197  
 FT CARBOHYD 7 7  
 FT CONFLICT 23 23  
 FT CONFLICT 60 60  
 FT CONFLICT 74 74  
 FT CONFLICT 86 86  
 FT CONFLICT 164 164  
 FT CONFLICT 182 182  
 FT CONFLICT 192 192  
 FT CONFLICT 206 206  
 FT CONFLICT 225 225  
 FT CONFLICT 370 374  
 SQ SEQUENCE 374 AA; 42494 MW; D7F963534E990BC4 CRC64;  
 Query March 64.2%; Score 61; DB 1; Length 374;  
 Best Local Similarity 76.9%; Pred. No. 0.0056;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLL 13  
 |||:|||||  
 Db 316 YAFVGEKFRNYFL 328

Search completed: March 4, 2004, 18:00:07  
 Job time : 6.07755 secs



| Result No. | Score | Query |        | DB | ID     | Description        |
|------------|-------|-------|--------|----|--------|--------------------|
|            |       | Match | Length |    |        |                    |
| 1          | 95    | 100.0 | 333    | 4  | O14694 | O14694 homo sapien |
| 2          | 95    | 100.0 | 334    | 6  | Q9TU07 | Q9TU07 erythrocebu |
| 3          | 95    | 100.0 | 339    | 4  | Q9UN24 | Q9UN24 homo sapien |
| 4          | 95    | 100.0 | 339    | 4  | Q9UN26 | Q9UN26 homo sapien |
| 5          | 95    | 100.0 | 339    | 4  | Q9UN23 | Q9UN23 homo sapien |
| 6          | 95    | 100.0 | 339    | 4  | Q9UBJ7 | Q9UBJ7 homo sapien |
| 7          | 95    | 100.0 | 339    | 4  | Q9UN25 | Q9UN25 homo sapien |
| 8          | 95    | 100.0 | 339    | 4  | Q9UN27 | Q9UN27 homo sapien |
| 9          | 95    | 100.0 | 339    | 4  | Q9UBT9 | Q9UBT9 homo sapien |
| 10         | 95    | 100.0 | 339    | 4  | Q9UN28 | Q9UN28 homo sapien |
| 11         | 95    | 100.0 | 339    | 6  | Q9TQW0 | Q9TQW0 hylobates c |
| 12         | 95    | 100.0 | 339    | 6  | Q9TUX1 | Q9TUX1 hylobates c |
| 13         | 95    | 100.0 | 339    | 6  | Q9UTU9 | Q9UTU9 ceropitheci |
| 14         | 95    | 100.0 | 339    | 6  | Q9TWS8 | Q9TWS8 gorilla gor |
| 15         | 95    | 100.0 | 339    | 6  | Q9UTU4 | Q9UTU4 macaca neme |
| 16         | 95    | 100.0 | 339    | 6  | Q9TWT9 | Q9TWT9 hylobates c |

90 95 100.0 352 6 Q9XT14  
 91 95 100.0 352 6 Q9XT76  
 92 95 100.0 352 6 Q9SNC3  
 93 95 100.0 352 6 Q9SNC3  
 94 95 100.0 352 6 Q9TV47  
 95 95 100.0 352 6 Q9SNC1  
 96 95 100.0 352 6 Q9SNC1  
 97 95 100.0 352 6 Q9SNC1  
 98 95 100.0 352 6 Q9SNC6  
 99 95 100.0 352 6 Q9SNC8  
 100 95 100.0 352 6 Q9TV44

## ALIGNMENTS

RESULT 1  
 OI4694  
 ID OI4694 PRELIMINARY; PRT; 333 AA.  
 AC OI4694;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE CCR5 receptor (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang G., Hahn B.,  
 RA Ho D.D.;  
 RT "HIV-1 subtypes, co-receptor usage, and CCR5 polymorphism.";  
 RL AIDS Res. Hum. Retroviruses 0:0-0(1997).  
 DR EMBL; AF011504; AAB65704.1; -;  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0004872; F: receptor activity; IEA.  
 DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 333 333  
 SQ SEQUENCE 333 AA; 38174 MW; AEFBA07A67893AEB CRC64;

Query Match 100.0%; Score 95; DB 4; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
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 Db 278 YAFVGEKFRNLLVFFQK 295

RESULT 2  
 Q9TUQ7  
 ID Q9TUQ7 PRELIMINARY; PRT; 334 AA.  
 AC Q9TUQ7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (fragment).  
 GN CCR5.  
 OS Erythrocybus patus (Red guenon) (Hussar).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Erythrocybus.  
 OX NCBI\_TaxID=9538;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF162049; AAD47804.1; -;  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0004872; F: receptor activity; IEA.  
 DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 334 334  
 SQ SEQUENCE 334 AA; 38460 MW; B19DOCEC667B69F0 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||  
 Db 285 YAFVGEKFRNLLVFFQK 302

RESULT 3  
 Q9UN24  
 ID Q9UN24 PRELIMINARY; PRT; 339 AA.  
 AC Q9UN24;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Fillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 species.";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF161919; AAD47676.1; -;  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0004872; F: receptor activity; IEA.  
 DR GO; GO:0001584; P: rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39066 MW; 8BAF02E19423BF79 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
 |||||  
 Db 290 YAFVGEKFRNLLVFFQK 307

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RESULT 4
Q9UN26
ID Q9UN26 PRELIMINARY; PRT; 339 AA.
AC Q9UN26
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161916; AAD47673.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39162 MW; A56369FE052994AB CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
|||||

RESULT 5
Q9UN23
ID Q9UN23 PRELIMINARY; PRT; 339 AA.
AC Q9UN23
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
|||||

RESULT 6
Q9UBJ7
ID Q9UBJ7 PRELIMINARY; PRT; 339 AA.
AC Q9UBJ7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161921; AAD47678.1; -.
DR EMBL; AF161917; AAD47674.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39128 MW; 9C3369FFFF1F2F7A CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
|||||

RESULT 7
Q9UN25
ID Q9UN25 PRELIMINARY; PRT; 339 AA.
AC Q9UN25
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161920; AAD47677.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161918; AAD47675.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; R:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 10FE05FE5371D4B3 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFOK 18
|||||
Db 290 YAFVGEKFRNLYLVFFOK 307

RESULT 8
Q9UN27 ID Q9UN27 PRELIMINARY; PRT; 339 AA.
AC Q9UN27
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161914; AAD47671.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; R:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 88AD8B4E2CB4EC2 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFOK 18
|||||
Db 290 YAFVGEKFRNLYLVFFOK 307

RESULT 9
Q9UBT9 ID Q9UBT9 PRELIMINARY; PRT; 339 AA.
AC Q9UBT9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161915; AAD47672.1; -.
DR EMBL; AF161909; AAD47666.1; -.
DR EMBL; AF161910; AAD47667.1; -.
DR EMBL; AF161911; AAD47668.1; -.
DR EMBL; AF161912; AAD47669.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 3C6369F92C9FA7 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFOK 18
|||||
Db 290 YAFVGEKFRNLYLVFFOK 307

RESULT 10
Q9UN28 ID Q9UN28 PRELIMINARY; PRT; 339 AA.
AC Q9UN28
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
DE CCR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161913; AAD47670.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
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DR GO:0004872; F:receptor activity; IEA.  
 DR GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm 1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39183 MW; 56C819F92D6DB1A6 CRC64;

Query Match 100.0%; Score 95; DB 4; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18  
 |||||  
 Db 290 YAFVGEKFRNYLLVFFQK 307

## RESULT 11

Q9TQW0  
 ID Q9TQW0 PRELIMINARY; PRT; 339 AA.  
 AC Q9TQW0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Hylobates concolor (crested gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=29089;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF162024; AAD4779.1; -  
 DR EMBL: AF161889; AAD4764.1; -  
 DR GO:00016021; C:integral to membrane; IEA.  
 DR GO:0004872; F:receptor activity; IEA.  
 DR GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO:0007186; P:G-protein coupled receptor activity; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm 1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39036 MW; 5555FEAP2614D35C CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18  
 |||||  
 Db 290 YAFVGEKFRNYLLVFFQK 307

## RESULT 12

Q9TUX1  
 ID Q9TUX1 PRELIMINARY; PRT; 339 AA.  
 AC Q9TUX1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Hylobates concolor (crested gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=29089;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF161887; AAD4764.1; -  
 DR GO:00016021; C:integral to membrane; IEA.  
 DR GO:0004872; F:receptor activity; IEA.  
 DR GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO:0007186; P:G-protein coupled receptor activity; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm 1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39075 MW; 09257FBFB834C4AE CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18  
 |||||  
 Db 290 YAFVGEKFRNYLLVFFQK 307

## RESULT 13

Q9TUU9  
 ID Q9TUU9 PRELIMINARY; PRT; 339 AA.  
 AC Q9TUU9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE C-C chemokine receptor 5 (Fragment).  
 GN CCR5.  
 OS Cercopithecus diana (Diana monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OX NCBI\_TaxID=36224;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,  
 RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;  
 RT "Sequences of the CCR5 genes from diverse simian and prosimian  
 RT species";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF161948; AAD47704.1; -  
 DR GO:00016021; C:integral to membrane; IEA.  
 DR GO:0004872; F:receptor activity; IEA.  
 DR GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO:0007186; P:G-protein coupled receptor activity; IEA.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm 1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 339 339  
 SQ SEQUENCE 339 AA; 39015 MW; 6D1A91546270F70D CRC64;

Qy 1 YAFVGEKFRNYLLVFFQK 18  
 |||||  
 Db 290 YAFVGEKFRNYLLVFFQK 307

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Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 14
Q9TUT8 ID Q9TUT8 PRELIMINARY; PRT; 339 AA.
AC Q9TUT8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 15
Q9TUT4 ID Q9TUT4 PRELIMINARY; PRT; 339 AA.
AC Q9TUT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161894; AAD47651.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39079 MW; A4A79753DA2F7AAF CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 16
Q9TUT9 ID Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (fragment).
GN CCR5.
OS Hylobates concolor (crested gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX NCBI_TaxID=29089;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161890; AAD47647.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1 339
FT NON_TER 339 339
SQ SEQUENCE 339 AA; 39024 MW; EC4CE48DEEF107E CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||||
DB 290 YAFVGEKFRNYLLVFFQK 307

RESULT 17
Q9TSQ1 ID Q9TSQ1 PRELIMINARY; PRT; 339 AA.
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AC Q9TSQ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162023; AAD47778.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 3216 MW; 847E935FA03B52D CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
=====

RESULT 18
Q9TU08
ID Q9TU08 PRELIMINARY; PRT; 339 AA.
AC Q9TU08;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 3216 MW; 847E935FA03B52D CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
=====

RESULT 18
Q9TU08
ID Q9TU08 PRELIMINARY; PRT; 339 AA.
AC Q9TU08;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161949; AAD47705.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 3216 MW; 847E935FA03B52D CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
=====

RESULT 18
Q9TU08
ID Q9TU08 PRELIMINARY; PRT; 339 AA.
AC Q9TU08;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus diana (Diana monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopithecus.
OX NCBI_TaxID=36224;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8B601D46A4 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
=====

RESULT 20
Q9TUW4
ID Q9TUW4 PRELIMINARY; PRT; 339 AA.
AC Q9TUW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

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KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39049 MW; 6D1A93F66270F3ED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
=====

RESULT 19
Q9TCW4
ID Q9TCW4 PRELIMINARY; PRT; 339 AA.
AC Q9TCW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161905; AAD47662.1; -.
DR EMBL; AF161898; AAD47655.1; -.
DR EMBL; AF161901; AAD47658.1; -.
DR EMBL; AF161904; AAD47661.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39129 MW; 4A88F8B601D46A4 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
Db 290 YAFVGEKFRNYLLVFFQK 307
=====

RESULT 20
Q9TUW4
ID Q9TUW4 PRELIMINARY; PRT; 339 AA.
AC Q9TUW4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

```

```
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161903; AAD47660.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39159 MW; 8E699B882BAC0B84 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 21
Q9TUQ7 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus nictitans (white-nosed guenon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercopitheidae.
OX NCBI_TaxID=36228;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162047; AAD47802.1; -.
DR EMBL; AF162042; AAD47797.1; -.
DR EMBL; AF162044; AAD47799.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39150 MW; 847D5F92BB03B6E2 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 22
Q9TUQ5 PRELIMINARY; PRT; 339 AA.
AC Q9TUQ5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162054; AAD47809.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1 1
FT NON TER 339 339
SQ SEQUENCE 339 AA; 39048 MW; 1A2E19E3A6A5A52A CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 23
Q9TUU3 PRELIMINARY; PRT; 339 AA.
AC Q9TUU3
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161961; AAD47716.1; -.

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DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39121 MW; AFB6E3BE4D6D3484 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
|||||
|||||

RESULT 24
Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Saguinus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=100754;
RN [1]
RP Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162015; AAD4770.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor activity; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39063 MW; 78BCE7A84B877085 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
|||||
|||||

RESULT 25
Q9TQT0 PRELIMINARY; PRT; 339 AA.
AC Q9TQT0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
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DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161954; AAD4770.1; -.
DR EMBL: AF161950; AAD4770.1; -.
DR EMBL: AF161952; AAD4770.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 339
SQ SEQUENCE 339 AA; 39097 MW; C576E7AA492D7080 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
DB 290 YAFVGEKFRNLLVFFQK 307
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|||||

RESULT 26
Q9TUT9 PRELIMINARY; PRT; 339 AA.
AC Q9TUT9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstman K., Chen Z., Korber B., Oprendeck J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF161972; AAD4772.1; -.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0004872; F: receptor activity; IEA.
DR GO: 0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: 0007186; P: G-protein coupled receptor protein signalin. . . ; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
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FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39067 MW; 5BFCHC5BA96C2F9E CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
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DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 27
Q9TSN2
ID Q9TSN2 PRELIMINARY; PRT; 339 AA.
AC Q9TSN2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF161953; AAD47709.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39137 MW; 9E62ED3288607C1 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
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DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 28
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ID Q9TUR6 PRELIMINARY; PRT; 339 AA.
AC Q9TUR6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Cercopithecus aethiops vervet.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=100936;
RN [1]

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RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162026; AAD47781.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39178 MW; 9DF2AGF446C55AED CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18
 |||||
DB 290 YAFVGEKFRNLLVFFQK 307

RESULT 29
Q9TOV6
ID Q9TOV6 PRELIMINARY; PRT; 339 AA.
AC Q9TOV6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE C-C chemokine receptor 5 (Fragment).
GN CCR5.
OS Colobus quereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheciidae; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunstan K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,
RA Shibata R., Yoder A., Pillai S., Kuiken C., Marx P., Wolinsky S.;
RT "Sequences of the CCR5 genes from diverse simian and prosimian
RT species."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF162005; AAD47760.1; -.
DR EMBL; AF162000; AAD47755.1; -.
DR EMBL; AF162001; AAD47756.1; -.
DR EMBL; AF162002; AAD47757.1; -.
DR EMBL; AF162003; AAD47758.1; -.
DR EMBL; AF162004; AAD47759.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
FT NON TER 1
FT NON TER 339
SQ SEQUENCE 339 AA; 39168 MW; 6A43F72FEBFF566F CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18  
| | | | | | | | | | | | | | | | | |  
Db 290 YAFVGEKFRNLLVFFQK 307

## RESULT 30

Q9TUM6 PRELIMINARY; PRT; 339 AA.  
AC Q9TUM6;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE C-C chemokine receptor 5 (Fragment).  
GN CCR5.  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kunstman K., Chen Z., Korber B., Orondek J., Stanton J., Agy M.,  
RA Shibata R., Yoder A., Pillai S., Kiiken C., Marx P., Wolinsky S.;  
RT "sequences of the CCR5 genes from diverse simian and prosimian  
RT species.";  
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
RL EMBL; AF161900; AAD47657.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm 1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 339 339  
SQ SEQUENCE 339 AA; 39103 MW; 4038C132D024C5A4 CRC64;

Query Match 100.0%; Score 95; DB 6; Length 339;

Best Local Similarity 100.0%; Pred. No. 1.le-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18  
| | | | | | | | | | | | | | | | | |  
Db 290 YAFVGEKFRNLLVFFQK 307

Search completed: March 4, 2004, 18:02:56

Job time : 29.0204 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2004, 17:55:22 ; Search time 11.5714 Seconds  
(without alignments)  
80.307 Million cell updates/sec

Title: US-10-084-813-15

Perfect score: 95

Sequence: 1 YAFVGEKFRNLLVFFQK 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.\*

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2: /cgn2\_6/prodata/2/iaa/5B COMB.pap.\*

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4: /cgn2\_6/prodata/2/iaa/6B COMB.pap.\*

5: /cgn2\_6/prodata/2/iaa/PCRTUS COMB.pap.\*

6: /cgn2\_6/prodata/2/iaa/backfiles!.pap.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 95    | 100.0       | 352    | 3  | US-08-466-343D-2  |
| 2          | 95    | 100.0       | 352    | 3  | US-08-087-232A-13 |
| 3          | 95    | 100.0       | 352    | 3  | US-08-861-105-14  |
| 4          | 95    | 100.0       | 352    | 3  | US-08-575-967A-2  |
| 5          | 95    | 100.0       | 352    | 3  | US-08-045-583-52  |
| 6          | 95    | 100.0       | 352    | 4  | US-09-517-605-5   |
| 7          | 95    | 100.0       | 352    | 4  | US-09-534-185-52  |
| 8          | 95    | 100.0       | 352    | 4  | US-08-833-752-5   |
| 9          | 95    | 100.0       | 352    | 4  | US-09-502-783A-2  |
| 10         | 95    | 100.0       | 352    | 4  | US-09-796-202-1   |
| 11         | 80    | 84.2        | 354    | 4  | US-08-724-984A-2  |
| 12         | 79    | 83.2        | 347    | 1  | US-08-461-244-3   |
| 13         | 79    | 83.2        | 360    | 3  | US-08-450-393A-4  |
| 14         | 79    | 83.2        | 360    | 3  | US-08-446-669-4   |
| 15         | 79    | 83.2        | 360    | 3  | US-09-045-583-50  |
| 16         | 79    | 83.2        | 360    | 4  | US-09-534-185-50  |
| 17         | 79    | 83.2        | 360    | 4  | US-09-131-827A-2  |
| 18         | 79    | 83.2        | 360    | 4  | US-09-131-827A-20 |
| 19         | 79    | 83.2        | 360    | 5  | PCT-US95-00476-4  |
| 20         | 77    | 81.1        | 360    | 4  | US-08-833-752-7   |
| 21         | 76    | 80.0        | 360    | 3  | US-09-045-583-51  |
| 22         | 76    | 80.0        | 360    | 4  | US-09-534-185-51  |
| 23         | 65    | 68.4        | 355    | 3  | US-08-575-967A-4  |
| 24         | 65    | 68.4        | 355    | 3  | US-08-847-296B-1  |
| 25         | 65    | 68.4        | 355    | 3  | US-09-045-583-54  |
| 26         | 65    | 68.4        | 355    | 4  | US-09-534-185-54  |
| 27         | 65    | 68.4        | 355    | 4  | US-08-720-565-2   |

Sequence 4, Appli  
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35 61 64.2 374 3 US-09-045-583-48  
36 61 64.2 374 4 US-09-534-185-48  
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41 60 63.2 355 4 US-09-886-319A-14  
42 60 63.2 355 5 PCT-US95-00476-5  
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44 57 60.0 355 1 US-08-153-848-28  
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48 57 60.0 355 4 US-09-088-337B-28  
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58 57 60.0 360 4 US-09-939-107-34  
59 56 58.9 355 3 US-09-045-583-53  
60 56 58.9 355 4 US-09-534-185-53  
61 55 57.9 360 4 US-08-833-752-10  
62 54 56.8 355 4 US-08-833-752-9  
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64 52 54.7 358 1 US-08-153-848-19  
65 52 54.7 358 3 US-09-299-843A-19  
66 52 54.7 358 4 US-09-088-337B-19  
67 52 54.7 358 5 PCT-US93-11153-19  
68 52 54.7 361 2 US-09-902-294-2  
69 52 54.7 361 3 US-09-178-637-2  
70 52 54.7 378 1 US-08-153-848-15  
71 52 54.7 378 3 US-09-299-843A-15  
72 52 54.7 378 3 US-09-251-545-1  
73 52 54.7 378 4 US-09-088-337B-15  
74 52 54.7 378 4 US-09-170-496D-74  
75 52 54.7 378 4 US-09-170-496D-204  
76 52 54.7 378 5 PCT-US93-11153-15  
77 52 54.7 410 1 US-08-153-848-7  
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79 52 54.7 410 4 US-09-088-337B-7  
80 52 54.7 410 5 PCT-US93-11153-7  
81 50 52.6 312 1 US-08-118-270-38  
82 50 52.6 312 5 PCT-US93-08528-38  
83 50 52.6 355 1 US-07-759-568-1  
84 50 52.6 355 2 US-08-450-393A-8  
85 50 52.6 355 1 US-08-390-000A-5  
86 50 52.6 355 3 US-08-446-669-8  
87 50 52.6 355 5 PCT-US95-00476-8  
88 50 52.6 360 1 US-08-202-056-7  
89 50 52.6 360 4 US-09-409-778-4  
90 50 52.6 378 1 US-08-383-750-2  
91 50 52.6 378 1 US-08-383-751A-2  
92 50 52.6 378 3 US-08-352-678-2  
93 50 52.6 378 3 US-09-045-583-49  
94 50 52.6 378 4 US-09-534-185-49  
95 50 52.6 378 4 US-09-536-954-2  
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97 49 51.6 329 4 US-09-502-783A-9  
98 49 51.6 344 3 US-08-466-343D-9  
99 49 51.6 374 1 US-08-450-393A-2  
100 49 51.6 374 3 US-08-446-669-2

## ALIGNMENTS

RESULT 1  
US-08-466-343D-2  
; Sequence 2, Application US/08466343D  
; Patent No. 6025154  
; GENERAL INFORMATION:  
; APPLICANT: LL, Yi  
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN  
; TITLE OF INVENTION: CHEMOKINE RECEPTOR HDGR10 (AS AMENDED)  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,343D  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1,488.1150000/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-466-343D-2

Query Match 100.0%; Score 95; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YAFVGEKFRNLLVFFQK 18  
DB 297 YAFVGEKFRNLLVFFQK 314  
|||||  
RESULT 2  
US-09-087-232A-13  
; Sequence 13, Application US/09087232A  
; Patent No. 6153431  
; GENERAL INFORMATION:  
; APPLICANT: Qullent et al.  
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR  
; TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/087,232A  
; FILING DATE: 28 MAY 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/048,057  
; FILING DATE: 30 MAY 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOLE, LISA B.  
; REGISTRATION NUMBER: 35,225  
; REFERENCE/DOCKET NUMBER: AP 31115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 408-2628  
; TELEFAX: (212) 765-2519  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 352 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-087-232A-13

Query Match 100.0%; Score 95; DB 3; Length 352;  
Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
DB 297 YAFVGEKFRNLLVFFQK 314  
|||||

RESULT 3  
US-08-861-105-14  
; Sequence 14, Application US/08861105  
; Patent No. 6258527  
; GENERAL INFORMATION:  
; APPLICANT: LITTMAN, DAN R.  
; APPLICANT: DENG, HONGKUI  
; APPLICANT: ELLMEIER, WILFRIED  
; APPLICANT: LANDAU, NATHANIEL R.  
; APPLICANT: LIU, RONG  
; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH  
; TITLE OF INVENTION: MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/861,105  
; FILING DATE:  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/666,020  
; FILING DATE: 19-JUN-1996  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,319  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 1049-1-004 N1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-08-861-105-14

Query Match 100.0%; Score 95; DB 3; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
 Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 4  
 US-08-575-967A-2  
 Sequence 2, Application US/08575967A  
 Patent No. 6265184  
 GENERAL INFORMATION:  
 APPLICANT: Gray et al.  
 TITLE OF INVENTION: Chemokine Receptor Materials and Methods  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 STREET: 6300 Sears Tower, 233 S. Wacker Drive  
 CITY: Chicago  
 STATE: Illinois  
 COUNTRY: USA  
 ZIP: 60606

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/575,967A  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 6265184 and, Greta E.  
 REGISTRATION NUMBER: 35,302  
 REFERENCE/DOCKET NUMBER: 32918  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-485-1662  
 TELEFAX: 206-485-1662

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: /= "88C amino acid sequence"  
 US-08-575-967A-2

Query Match 100.0%; Score 95; DB 3; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18

Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 5  
 US-09-045-583-52  
 Sequence 52, Application US/09045583  
 Patent No. 6287805  
 GENERAL INFORMATION:  
 APPLICANT: Graham, Gerard J. et al.  
 TITLE OF INVENTION: No. 6287805e1 Molecules of the G Protein-Coupled  
 NUMBER OF SEQUENCES: 56  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/045,583  
 FILING DATE: 20-MAR-98  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: MMI-044  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)742-4214  
 INFORMATION FOR SEQ ID NO: 52:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 US-09-045-583-52

Query Match 100.0%; Score 95; DB 3; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
 Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 6  
 US-09-517-605-5  
 Sequence 5, Application US/09517605  
 Patent No. 6391567  
 GENERAL INFORMATION:  
 APPLICANT: Littman, Dan R.  
 APPLICANT: Kwon, Douglas S.  
 APPLICANT: van Kooyk, Yvette  
 APPLICANT: Geijtenbeek, Theo  
 TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO  
 FILE REFERENCE: 1049-1-017  
 CURRENT APPLICATION NUMBER: US/09/517,605  
 CURRENT FILING DATE: 2000-03-02  
 NUMBER OF SEQ ID NOS: 17  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5

;/ LENGTH: 352  
;/ TYPE: PRT  
;/ ORGANISM: Homo sapiens  
US-09-517-605-5

Query Match 100.0%; Score 95; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
|||  
Db 297 YAFVGEKFRNLLVFFQK 314

## RESULT 7

US-09-534-185-52  
; Sequence 52, Application US/09534185  
; Patent No. 6403767

## GENERAL INFORMATION:

;/ APPLICANT: Graham, Gerard J. et al.  
;/ TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
;/ Heptahelical Receptor Superfamily and Uses  
;/ Therefor

;/ NUMBER OF SEQUENCES: 56

;/ CORRESPONDENCE ADDRESS:

;/ ADDRESSEE: LAHIVE & COCKFIELD, LLP  
;/ STREET: 28 State Street  
;/ CITY: Boston  
;/ STATE: Massachusetts  
;/ COUNTRY: USA  
;/ ZIP: 02109

;/ COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25

;/ CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/09/534,185  
;/ FILING DATE: 24-Mar-2000  
;/ CLASSIFICATION: <Unknown>

;/ PRIOR APPLICATION DATA:

;/ APPLICATION NUMBER: 09/045,583  
;/ FILING DATE: <Unknown>

;/ ATTORNEY/AGENT INFORMATION:

;/ NAME: Mandragouras, Amy E.  
;/ REGISTRATION NUMBER: 36,207

;/ REFERENCE/DOCKET NUMBER: MNI-044

;/ TELECOMMUNICATION INFORMATION:

;/ TELEPHONE: (617)227-7400  
;/ TELEFAX: (617)742-4214

;/ INFORMATION FOR SEQ ID NO: 52:

;/ SEQUENCE CHARACTERISTICS:

;/ LENGTH: 352 amino acids

;/ TYPE: amino acid

;/ TOPOLOGY: linear

;/ MOLECULE TYPE: peptide

;/ FRAGMENT TYPE: internal

;/ SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-09-534-185-52

Query Match 100.0%; Score 95; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
|||  
Db 297 YAFVGEKFRNLLVFFQK 314

## RESULT 8

US-08-833-752-5  
; Sequence 5, Application US/08833752  
; Patent No. 6448375

## GENERAL INFORMATION:

;/ APPLICANT: SAMSON, MICHEL  
;/ APPLICANT: PARMENTIER, MARC  
;/ APPLICANT: VASSART, GILBERT  
;/ APPLICANT: LIBERT, FREDERICK

;/ TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
;/ TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
;/ NUMBER OF SEQUENCES: 17

;/ CORRESPONDENCE ADDRESS:

;/ ADDRESSEE: Knobbe, Martens, Olson & Bear  
;/ STREET: 620 Newport Center Drive 16th Floor  
;/ CITY: Newport Beach  
;/ STATE: CA  
;/ COUNTRY: U.S.A.

;/ ZIP: 92660

;/ COMPUTER READABLE FORM:

;/ MEDIUM TYPE: Floppy disk

;/ COMPUTER: IBM PC compatible

;/ OPERATING SYSTEM: PC-DOS/MS-DOS

;/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

;/ CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/08/833,752

;/ FILING DATE: 9-APR-1997

;/ CLASSIFICATION: 536

;/ ATTORNEY/AGENT INFORMATION:

;/ NAME: Altman, Daniel E

;/ REGISTRATION NUMBER: 34,115

;/ REFERENCE/DOCKET NUMBER:

;/ INFORMATION FOR SEQ ID NO: 5:

;/ SEQUENCE CHARACTERISTICS:

;/ LENGTH: 352 amino acids

;/ TYPE: amino acid

;/ TOPOLOGY: linear

;/ MOLECULE TYPE: protein

US-08-833-752-5

Query Match 100.0%; Score 95; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
|||  
Db 297 YAFVGEKFRNLLVFFQK 314

## RESULT 9

US-09-502-783A-2  
; Sequence 2, Application US/09502783A  
; Patent No. 6511826

;/ GENERAL INFORMATION:

;/ APPLICANT: Li, Yi

;/ APPLICANT: Ruben, Steven M.

;/ TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR

;/ TITLE OF INVENTION: HDGR10

;/ FILE REFERENCE: 1488.1150006

;/ CURRENT APPLICATION NUMBER: US/09/502,783A

;/ CURRENT FILING DATE: 2001-08-23

;/ PRIOR APPLICATION NUMBER: 08/466,343

;/ PRIOR FILING DATE: 1995-06-06

;/ NUMBER OF SEQ ID NOS: 9

;/ SOFTWARE: PatentIn version 3.0

;/ SEQ ID NO 2

;/ LENGTH: 352

;/ TYPE: PRT

;/ ORGANISM: Homo sapiens

US-09-502-783A-2

Query Match 100.0%; Score 95; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
|||  
Db 297 YAFVGEKFRNLLVFFQK 314

Db 297 YAFVGEKFRNLLVFFQK 314

## RESULT 10

US-09-796-202-1  
; Sequence 1, Application US/09796202  
; Patent No. 6548636  
; GENERAL INFORMATION:  
; APPLICANT: Olson, William  
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
; FILE REFERENCE: 2048/61010/JWP/SHS  
; CURRENT APPLICATION NUMBER: US/09/796,202  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: human  
US-09-796-202-1

Query Match 100.0%; Score 95; DB 4; Length 352;  
Best Local Similarity 100.0%; Pred. No. 8.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

Db 297 YAFVGEKFRNLLVFFQK 314

## RESULT 11

US-08-724-984A-2  
; Sequence 2, Application US/08724984A  
; Patent No. 6388055  
; GENERAL INFORMATION:  
; APPLICANT: Derk Bergsma, Mary Brawner, and Usman Shabon  
; TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the CC-  
; TITLE OF INVENTION: CCR5 Receptor  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithline Beecham Corporation  
; STREET: 709 Swedeland Road, P.O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM 486  
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
SOFTWARE: MICROSOFT WORD  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/724,984A  
FILING DATE: October 3, 1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: William T. Han

REGISTRATION NUMBER: 34,344  
REFERENCE/DOCKET NUMBER: ATG50023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610 270 5024  
TELEFAX: 610 270 5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 354  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-724-984A-2

Query Match 84.2%; Score 80; DB 4; Length 354;  
Best Local Similarity 83.3%; Pred. No. 3.5e-06;  
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

Db 299 YAFVGEKFRNLLVFFQK 316

## RESULT 12

US-08-461-244-3  
; Sequence 3, Application US/08461244  
; Patent No. 5776729  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R.  
; APPLICANT: Yi, Li  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBER32  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
; ADDRESSEE: STUART & OLSTEIN  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,244  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-445  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 347 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-244-3

Query Match 83.2%; Score 79; DB 1; Length 347;  
Best Local Similarity 83.3%; Pred. No. 5.2e-06;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18

Db 292 YAFVGEKFRNLLVFFQK 309

## RESULT 13

US-08-450-393A-4  
; Sequence 4, Application US/08450393A  
; Patent No. 5707815  
; GENERAL INFORMATION:  
; APPLICANT: Charo, Israel  
; APPLICANT: Coughlin, Shaun  
; TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
; TITLE OF INVENTION: PROTEIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:



ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
STREET: 5 Palo Alto Square  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306-2155  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: Cooley Godward Castro Huddleson & Tatum  
FILING DATE: May 25, 1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Cserr, Luann  
REGISTRATION NUMBER: 31,922  
REFERENCE/DOCKET NUMBER: UCAL-237/02US  
TELEPHONE: 415-843-5165  
TELEFAX: 415-857-0663  
TELEX: 380816CooleyPA  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-450-393A-4

Query Match 83.2%; Score 79; DB 1; Length 360;  
Best Local Similarity 83.3%; Pred. No. 5.4e-06;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFOK 18  
|||||

Db 305 YAFVGEKFRNLLVFFOK 322

RESULT 14  
US-08-446-669-4  
Sequence 4, Application US/08446669  
Patent No. 6132987  
GENERAL INFORMATION:  
APPLICANT: Charo, Israel  
APPLICANT: Coughlin, Shaun  
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
TITLE OF INVENTION: PROTEIN RECEPTORS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum  
STREET: 5 Palo Alto Square  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94306-2155  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: Cooley Godward Castro Huddleson & Tatum  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Neeley, Richard  
REGISTRATION NUMBER: 30,092  
REFERENCE/DOCKET NUMBER: UCAL-237/01US  
TELEPHONE: 415-843-5000  
TELEFAX: 415-857-0663

TELEX: 380816CooleyPA  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-669-4

Query Match 83.2%; Score 79; DB 3; Length 360;  
Best Local Similarity 83.3%; Pred. No. 5.4e-06;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFOK 18  
|||||

Db 305 YAFVGEKFRNLLVFFOK 322

RESULT 15  
US-09-045-583-50  
Sequence 50, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT: Cooley Godward Castro Huddleson & Tatum  
FILING DATE: May 25, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Neeley, Richard  
REGISTRATION NUMBER: 30,092  
REFERENCE/DOCKET NUMBER: UCAL-237/01US  
TELEPHONE: 415-843-5000  
TELEFAX: 415-857-0663

Query Match 83.2%; Score 79; DB 3; Length 360;  
Best Local Similarity 83.3%; Pred. No. 5.4e-06;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFOK 18  
|||||

Db 305 YAFVGEKFRNLLVFFOK 322

RESULT 16  
US-09-534-185-50  
Sequence 50, Application US/09534185

Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Hepatic Helical Receptor Superfamily and Uses  
Therefor  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-09-534-185-50  
Query Match 83.2%; Score 79; DB 4; Length 360;  
Best Local Similarity 83.3%; Pred. No. 5.4e-06;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YAFVGEKFRNYLLVFFQK 18  
Db 305 YAFVGEKFRNYLLVFFQK 322  
RESULT 17  
US-09-131-827A-2  
Sequence 2, Application US/09131827A  
Patent No. 6600030  
GENERAL INFORMATION:  
APPLICANT: Dean, Michael  
APPLICANT: O'Brien, Stephen J.  
APPLICANT: Smith, Michael  
APPLICANT: Carrington, Mary  
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A  
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE  
FILE REFERENCE: 14014.0333  
CURRENT APPLICATION NUMBER: US/09/131,827A  
CURRENT FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/055,659  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 360  
TYPE: PRT

ORGANISM: Homo sapiens  
US-09-131-827A-2  
Query Match 83.2%; Score 79; DB 4; Length 360;  
Best Local Similarity 83.3%; Pred. No. 5.4e-06;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YAFVGEKFRNYLLVFFQK 18  
Db 305 YAFVGEKFRNYLLVFFQK 322  
RESULT 18  
US-09-131-827A-20  
Sequence 20, Application US/09131827A  
Patent No. 6600030  
GENERAL INFORMATION:  
APPLICANT: Dean, Michael  
APPLICANT: O'Brien, Stephen J.  
APPLICANT: Smith, Michael  
APPLICANT: Carrington, Mary  
TITLE OF INVENTION: DELAYED PROGRESSION TO AIDS BY A  
TITLE OF INVENTION: MISSENSE ALLELE OF THE CCR2 GENE  
FILE REFERENCE: 14014.0333  
CURRENT APPLICATION NUMBER: US/09/131,827A  
CURRENT FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/055,659  
PRIOR FILING DATE: 1997-08-14  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 20  
LENGTH: 360  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-131-827A-20  
Query Match 83.2%; Score 79; DB 4; Length 360;  
Best Local Similarity 83.3%; Pred. No. 5.4e-06;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YAFVGEKFRNYLLVFFQK 18  
Db 305 YAFVGEKFRNYLLVFFQK 322  
RESULT 19  
PCT-US95-00476-4  
Sequence 4, Application PC/TUS9500476  
GENERAL INFORMATION:  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT  
TITLE OF INVENTION: PROTEIN RECEPTORS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Robbins, Berliner & Carson  
STREET: 201 N. Figueroa Street, 5th Floor  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90012-2628  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/00476  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Berliner, Robert  
REGISTRATION NUMBER: 20,121  
REFERENCE/DOCKET NUMBER: 5555-291

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310-977-1001  
TELEFAX: 310-977-1003  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-00476-4

Query Match 83.2%; Score 79; DB 5; Length 360;  
Best Local Similarity 83.3%; Pred. No. 5.4e-06;  
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18  
Db 305 YAFVGEKFRNVLVFFQK 322

## RESULT 20

US-08-833-752-7  
Sequence 7, Application US/08833752  
Patent No. 6448375  
GENERAL INFORMATION:  
APPLICANT: SAMSON, MICHEL  
APPLICANT: PARMENTIER, MARC  
APPLICANT: VASSART, GILBERT  
APPLICANT: LIBERT, FREDERICK  
TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/833,752  
FILING DATE: 9-APR-1997  
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6448375e  
US-08-833-752-7

Query Match 81.1%; Score 77; DB 4; Length 360;  
Best Local Similarity 77.8%; Pred. No. 1.2e-05;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18  
Db 305 YAFVGEKFRNVLVFFQK 322

## RESULT 21

US-09-045-583-51

Sequence 51, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/045,583  
FILING DATE: 20-MAR-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-09-045-583-51

Query Match 80.0%; Score 76; DB 3; Length 360;  
Best Local Similarity 77.8%; Pred. No. 1.8e-05;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNVLVFFQK 18  
Db 305 YAFVGEKFRNVLVFFQK 322

## RESULT 22

US-09-534-185-51  
Sequence 51, Application US/09534185  
Patent No. 6403767  
GENERAL INFORMATION:  
APPLICANT: Graham, Gerard J. et al.  
TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled  
Heptahelical Receptor Superfamily and Uses  
Therefor

NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/534,185  
FILING DATE: 24-Mar-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/045,583  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragouras, Amy E.  
REGISTRATION NUMBER: 36,207  
REFERENCE/DOCKET NUMBER: MNI-044  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
US-09-534-185-51

Query Match 80.0%; Score 76; DB 4; Length 360;  
Best Local Similarity 77.8%; Pred. No. 1.8e-05;  
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18  
DB 305 YAFVGEKFRNLYLVFFQK 322

## RESULT 23

US-08-575-967A-4  
Sequence 4, Application US/08575967A  
Patent No. 6265184  
GENERAL INFORMATION:  
APPLICANT: Gray et al.  
TITLE OF INVENTION: Chemokine Receptor Materials and Methods  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/575,967A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6265184and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 32918  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-485-1900  
TELEFAX: 206-485-1662  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: /= "88-2B amino acid sequence"  
US-08-575-967A-4

Query Match 68.4%; Score 65; DB 3; Length 355;  
Best Local Similarity 66.7%; Pred. No. 0.0015;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18  
DB 301 YAFVGERFRKYLRRHFFHR 318

## RESULT 24

US-08-847-296B-1  
Sequence 1, Application US/08847296B  
Patent No. 6271347  
GENERAL INFORMATION:  
APPLICANT: DAUGHERTY, BRUCE L.  
APPLICANT: DEMARTINO, JULIE A.  
APPLICANT: SICILIANO, SALVATORE J.  
APPLICANT: SPRINGER, MARTIN J.  
TITLE OF INVENTION: EOSINOPHIL ROTAXIN RECEPTOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000, 126 E. Lincoln Ave.  
CITY: Rahway  
STATE: NJ  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/847,296B  
FILING DATE: 24-APR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/016,158  
FILING DATE: 26-APR-1996  
APPLICATION NUMBER: 60/017,113  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Thies, J. Eric  
REGISTRATION NUMBER: 35,382  
REFERENCE/DOCKET NUMBER: 19634Y  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-594-3904  
TELEFAX: 908-594-4720  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-847-296B-1

Query Match 68.4%; Score 65; DB 3; Length 355;  
Best Local Similarity 66.7%; Pred. No. 0.0015;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLYLVFFQK 18  
DB 301 YAFVGERFRKYLRRHFFHR 318

## RESULT 25

US-09-045-583-54  
Sequence 54, Application US/09045583  
Patent No. 6287805  
GENERAL INFORMATION:

```

; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,583
; FILING DATE: 20-MAR-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-045-583-54

Query Match 68.4%; Score 65; DB 3; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKPRNYLLVFFQK 18
Db 301 YAFVGERPKYLRHFFHR 318

RESULT 26
US-09-534-185-54
; Sequence 54, Application US/09534185
; Patent No. 6403767
; GENERAL INFORMATION:
; APPLICANT: Graham, Gerard J. et al.
; TITLE OF INVENTION: No. 6403767el Molecules of the G Protein-Coupled
; Hepatocellular Receptor Superfamily and Uses
; Therefor
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,185
; FILING DATE: 24-Mar-2000
; CLASSIFICATION: <Unknown>

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/045,583
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-044
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-534-185-54

Query Match 68.4%; Score 65; DB 4; Length 355;
Best Local Similarity 66.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKPRNYLLVFFQK 18
Db 301 YAFVGERPKYLRHFFHR 318

RESULT 27
US-08-720-565-2
; Sequence 2, Application US/08720565
; Patent No. 6537764
; GENERAL INFORMATION:
; APPLICANT: Gerard, Craig J.
; APPLICANT: Gerard, No. 6537764ma P.
; APPLICANT: Mackay, Charles R.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Post, Theodore W.
; APPLICANT: Qin, Shixin
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
; ANTAGONISTS THEREOF
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,565
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00608
; FILING DATE: 19-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375,199
; FILING DATE: 19-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: LKS94-05A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-720-565-2

Query Match 68.4%; Score 65; DB 4; Length 355;  
Best Local Similarity 66.7%; Pred. No. 0.0015;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
|||||:|||||:  
Db 301 YAFVGEKFRKYLRRHFHR 318

RESULT 28  
US-08-720-565-4  
; Sequence 4, Application US/08720565  
; Patent No. 6537764  
; GENERAL INFORMATION:  
; APPLICANT: Gerard, Craig J.  
; APPLICANT: Gerard, No. 6537764ma P.  
; APPLICANT: Mackay, Charles R.  
; APPLICANT: Ponath, Paul D.  
; APPLICANT: Post, Theodore W.  
; APPLICANT: Qin, Shixin  
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND  
; TITLE OF INVENTION: ANTAGONISTS THEREOF  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/720,565  
; FILING DATE: 30-SEP-1996  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/00608  
; FILING DATE: 19-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/375,199  
; FILING DATE: 19-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: LKS94-05A2  
; TELEPHONE: 617-861-6240  
; TELEFAX: 617-861-9540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 355 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-720-565-4

Query Match 68.4%; Score 65; DB 4; Length 355;  
Best Local Similarity 66.7%; Pred. No. 0.0015;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18

Db 301 YAFVGEKFRKYLRRHFHR 318  
|||||:|||||:|

RESULT 29  
US-08-567-882-7  
; Sequence 7, Application US/08567882  
; Patent No. 6512103  
; GENERAL INFORMATION:  
; APPLICANT: Dairaghi, Daniel J.  
; APPLICANT: Hara, Takahiko  
; APPLICANT: Miyajima, Atsushi  
; APPLICANT: Schall, Thomas J.  
; APPLICANT: Wang, Wei  
; APPLICANT: Yoshimura, Akihiko  
; TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/567,882  
; FILING DATE: 08-DEC-1995  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0506  
; TELEPHONE: 415-852-9196  
; TELEFAX: 415-496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 356 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-567-882-7

Query Match 68.4%; Score 65; DB 4; Length 356;  
Best Local Similarity 66.7%; Pred. No. 0.0015;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
|||||:|||||:|  
Db 302 YAFVGEKFRKYLRRHFHR 319

RESULT 30  
US-08-461-244-2  
; Sequence 2, Application US/08461244  
; Patent No. 5776729  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R.  
; APPLICANT: Yi, Li  
; APPLICANT: Ruben, Steven M.  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HGBR32  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
; ADDRESSEE: STUART & OLSTEIN  
; STREET: 6 Becker Farm Road  
; CITY: Roseland

STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,244  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferraro, Gregory D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-445  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-461-244-2

Query Match 66.3%; Score 63; DB 1; Length 355;  
Best Local Similarity 66.7%; Pred. No. 0.0034;  
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18  
||| ||| : |||  
Db 300 YAFVGEKFKHLSEIFQK 317

Search completed: March 4, 2004, 18:05:15  
Job time : 11.5714 secs

| Result No. | Score | Query |        |    | DB                | ID                 | Description |
|------------|-------|-------|--------|----|-------------------|--------------------|-------------|
|            |       | Match | Length | DB |                   |                    |             |
| 1          | 95    | 100.0 | 18     | 14 | US-10-084-813-15  | Sequence 15, Appl  |             |
| 2          | 95    | 100.0 | 18     | 14 | US-10-084-813-105 | Sequence 105, Appl |             |
| 3          | 95    | 100.0 | 332    | 14 | US-10-095-876A-2  | Sequence 2, Appl   |             |
| 4          | 95    | 100.0 | 352    | 9  | US-09-725-285-2   | Sequence 2, Appl   |             |
| 5          | 95    | 100.0 | 352    | 9  | US-09-759-841-2   | Sequence 2, Appl   |             |
| 6          | 95    | 100.0 | 352    | 9  | US-09-779-879A-2  | Sequence 2, Appl   |             |
| 7          | 95    | 100.0 | 352    | 9  | US-09-779-879A-22 | Sequence 22, Appl  |             |
| 8          | 95    | 100.0 | 352    | 9  | US-09-779-880A-2  | Sequence 2, Appl   |             |
| 9          | 95    | 100.0 | 352    | 9  | US-09-779-880A-22 | Sequence 22, Appl  |             |
| 10         | 95    | 100.0 | 352    | 9  | US-09-813-653-15  | Sequence 15, Appl  |             |
| 11         | 95    | 100.0 | 352    | 9  | US-09-813-653-17  | Sequence 17, Appl  |             |
| 12         | 95    | 100.0 | 352    | 9  | US-09-796-202-1   | Sequence 1, Appl   |             |
| 13         | 95    | 100.0 | 352    | 9  | US-09-195-662A-2  | Sequence 2, Appl   |             |
| 14         | 95    | 100.0 | 352    | 9  | US-09-339-912A-2  | Sequence 2, Appl   |             |
| 15         | 95    | 100.0 | 352    | 9  | US-09-938-719-5   | Sequence 5, Appl   |             |



Sequence 9, Appli  
Sequence 2, Appli  
Sequence 78, Appli  
Sequence 2, Appli  
Sequence 6, Appli  
Sequence 40, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 3, Appli  
Sequence 130, App  
Sequence 232, App  
Sequence 249, App

89 60 63.2 355 14 US-10-439-845-9  
90 60 63.2 355 15 US-10-452-015-2  
91 60 63.2 375 14 US-10-219-834-78  
92 59 62.1 367 14 US-10-254-089-2  
93 58 61.1 355 14 US-10-283-028-6  
94 57 60.0 67 9 US-09-993-844-40  
95 57 60.0 355 9 US-09-789-482-4  
96 57 60.0 355 9 US-09-789-486-4  
97 57 60.0 355 14 US-10-290-058A-3  
98 57 60.0 355 14 US-10-251-385-130  
99 57 60.0 355 14 US-10-251-385-232  
100 57 60.0 355 14 US-10-225-567A-249

## ALIGNMENTS

RESULT 1  
US-10-084-813-15  
; Sequence 15, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-15

Query Match 100.0%; Score 95; DB 14; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFOK 18  
Db 1 YAFVGEKFRNYLLVFFOK 18

RESULT 2  
US-10-084-813-105  
; Sequence 105, Application US/10084813  
; Publication No. US20030068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC  
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 105  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Deduced Amino Acid Sequence  
US-09-723-285-2

; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-105

Query Match 100.0%; Score 95; DB 14; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFOK 18  
Db 1 YAFVGEKFRNYLLVFFOK 18

RESULT 3  
US-10-095-876A-2  
; Sequence 2, Application US/10095876A  
; Publication No. US20030148294A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice; Bandman, Olga  
; APPLICANT: Coleman, Roger; Wilde, Craig G.  
; TITLE OF INVENTION: DNA ENCODING NOVEL CHEMOKINE RECEPTORS  
; FILE REFERENCE: PF-0060-1 CON  
; CURRENT APPLICATION NUMBER: US/10/095,876A  
; CURRENT FILING DATE: 2002-03-11  
; PRIOR APPLICATION NUMBER: US 06/638,081  
; PRIOR FILING DATE: 1996-04-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PERL Program  
; SEQ ID NO 2  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030148294A1 478861  
US-10-095-876A-2

Query Match 100.0%; Score 95; DB 14; Length 332;  
Best Local Similarity 100.0%; Pred. No. 4.1e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFOK 18  
Db 277 YAFVGEKFRNYLLVFFOK 294

RESULT 4  
US-09-725-285-2  
; Sequence 2, Application US/09725285  
; Patent No. US20010000241A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGMR10  
; FILE REFERENCE: 1488.1150003  
; CURRENT APPLICATION NUMBER: US/09/725,285  
; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: 09/339,912  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: 09/195,662  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 08/466,343  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Artificial Sequence: Genomic  
; FEATURE:  
; OTHER INFORMATION: Deduced Amino Acid Sequence  
US-09-723-285-2

Query Match 100.0%; Score 95; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18  
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 5  
US-09-759-841-2  
; Sequence 2, Application US/09759841  
; Patent No. US20010039026A1  
; GENERAL INFORMATION:  
; APPLICANT: Rickett, Graham A  
; APPLICANT: Dobbs, Susan  
; APPLICANT: Petros, Manousos  
; TITLE OF INVENTION: Assay Method  
; FILE REFERENCE: PC10348APME  
; CURRENT APPLICATION NUMBER: US/09/759,841  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: GB 0000661.9  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000663.5  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: GB 0000659.3  
; PRIOR FILING DATE: 2000-01-12  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-759-841-2

Query Match 100.0%; Score 95; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18  
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 6  
US-09-779-879A-2  
; Sequence 2, Application US/09779879A  
; Patent No. US20020048786A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.115000A  
; CURRENT APPLICATION NUMBER: US/09/779,879A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-879A-2

Query Match 100.0%; Score 95; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YAFVGEKFRNLLVFFQK 18  
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 7  
US-09-779-879A-22  
; Sequence 22, Application US/09779879A  
; Patent No. US20020048786A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.115000A  
; CURRENT APPLICATION NUMBER: US/09/779,879A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 22  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-879A-22

Query Match 100.0%; Score 95; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNLLVFFQK 18  
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 8  
US-09-779-880A-2  
; Sequence 2, Application US/09779880A  
; Patent No. US20020061834A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
; FILE REFERENCE: 1488.115000C  
; CURRENT APPLICATION NUMBER: US/09/779,880A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 2  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-880A-2

Query Match 100.0%; Score 95; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
| | | | | | | | | | | | | | | | | |  
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 9  
US-09-779-880A-22  
; Sequence 22, Application US/09779880A  
; Patent No. US20020061834A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Craig A.  
; APPLICANT: Roschke, Viktor  
; APPLICANT: Li, Yi  
; APPLICANT: Ruben, Steven, M.  
; TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCRS) HDGMR10  
; FILE REFERENCE: 1488.115000C  
; CURRENT APPLICATION NUMBER: US/09/779,880A  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,258  
; PRIOR FILING DATE: 2000-02-09  
; PRIOR APPLICATION NUMBER: US 60/187,999  
; PRIOR FILING DATE: 2000-03-09  
; PRIOR APPLICATION NUMBER: US 60/234,336  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-880A-22

Query Match 100.0%; Score 95; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
| | | | | | | | | | | | | | | | | |  
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 10  
US-09-813-653-15  
; Sequence 15, Application US/09813653  
; Patent No. US20020064770A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, John  
; APPLICANT: Wilson, Carol  
; APPLICANT: See, Raymond  
; APPLICANT: Tan Hehir, Christina  
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds  
; FILE REFERENCE: CNS-005  
; CURRENT APPLICATION NUMBER: US/09/813,653  
; CURRENT FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 60/190,946  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/190,996  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,299  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-813-653-15

Query Match 100.0%; Score 95; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
| | | | | | | | | | | | | | | | | |  
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 11  
US-09-813-653-17  
; Sequence 17, Application US/09813653  
; Patent No. US20020064770A1  
; GENERAL INFORMATION:  
; APPLICANT: Nestor, John  
; APPLICANT: Wilson, Carol  
; APPLICANT: See, Raymond  
; APPLICANT: Tan Hehir, Christina  
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds  
; FILE REFERENCE: CNS-005  
; CURRENT APPLICATION NUMBER: US/09/813,653  
; CURRENT FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: US 60/190,946  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/190,996  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: US 60/191,299  
; PRIOR FILING DATE: 2000-03-21  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-813-653-17

Query Match 100.0%; Score 95; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
| | | | | | | | | | | | | | | | | |  
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 12  
US-09-796-202-1  
; Sequence 1, Application US/09796202  
; Patent No. US20020068813A1  
; GENERAL INFORMATION:  
; APPLICANT: Dragic, Tatjana  
; APPLICANT: Olson, William  
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
; FILE REFERENCE: 2048/61010/JPW/SHS  
; CURRENT APPLICATION NUMBER: US/09/796,202  
; CURRENT FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 352  
; TYPE: PRT  
; ORGANISM: human  
US-09-796-202-1

Query Match 100.0%; Score 95; DB 9; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
| | | | | | | | | | | | | | | | | |  
Db 297 YAFVGEKFRNLLVFFQK 314

RESULT 13  
US-09-195-662A-2  
; Sequence 2, Application US/09195662A  
; Patent No. US20020076745A1

```

1 AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
2
3 NUMBER OF SEQUENCES: 17
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Knobbe, Martens, Olson & Bear
6 STREET: 620 Newport Center Drive 16th Floor
7 CITY: Newport Beach
8 STATE: CA
9 COUNTRY: U.S.A.
10 ZIP: 92660
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/09/938,719
19 FILING DATE: 24-Aug-2001
20 CLASSIFICATION: <Unknown>
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 09/626,939
24 FILING DATE: 27-JULY-2000
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Altman, Daniel E
27 REGISTRATION NUMBER: 34,115
28 REFERENCE/DOCKET NUMBER: <Unknown>
29 INFORMATION FOR SEQ ID NO: 5:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 352 amino acids
32 TYPE: amino acid
33 TOPOLOGY: linear
34 MOLECULE TYPE: protein
35 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
36
37 US-09-938-719-5
38
39 Query Match 100.0%; Score 95; DB 9; Length 352;
40 Best Local similarity 100.0%; Pred. No. 4.4e-07;
41 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
42
43 QY 1 YAFVGEKFRNYLLVFFQK 18
44 | | | | | | | | | | | | | | | | | |
45 DB 297 YAFVGEKFRNYLLVFFQK 314
46
47
48 RESULT 16
49 US-09-939-226-5
50 ; Sequence 5, Application US/09939226
51 ; Patent No. US20020110805A1
52 GENERAL INFORMATION:
53 APPLICANT: SAMSON, MICHEL
54 PARMENTIER, MARC
55 VASSART, GILBERT
56 LIBERT, FREDERICK
57
58 TITLE OF INVENTION: ACTIVE AND INACTIVE CO-CHEMOKINES RECEPTOR
59
60 NUMBER OF SEQUENCES: 17
61 CORRESPONDENCE ADDRESS:
62 ADDRESSEE: Knobbe, Martens, Olson & Bear
63 STREET: 620 Newport Center Drive 16th Floor
64 CITY: Newport Beach
65 STATE: CA
66 COUNTRY: U.S.A.
67 ZIP: 92660
68
69 COMPUTER READABLE FORM:
70 MEDIUM TYPE: Floppy disk
71 COMPUTER: IBM PC compatible
72 OPERATING SYSTEM: PC-DOS/MS-DOS
73 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
74 CURRENT APPLICATION DATA:
75 APPLICATION NUMBER: US/09/939,226
76 FILING DATE: 24-Aug-2001
77 CLASSIFICATION: <unknown>
78
79 PRIOR APPLICATION DATA:
80 APPLICATION NUMBER: 09/626,939

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1 FILING DATE: 2000-07-27  
2 ATTORNEY/AGENT INFORMATION:  
3 NAME: Altman, Daniel E  
4 REGISTRATION NUMBER: 34,115  
5 REFERENCE/DOCKET NUMBER: <Unknown>  
6 INFORMATION FOR SEQ ID NO: 5:  
7 SEQUENCE CHARACTERISTICS:  
8 LENGTH: 352 amino acids  
9 TYPE: amino acid  
10 TOPOLOGY: linear  
11 MOLECULE TYPE: protein  
12 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
13 US-09-938-703-5  
14  
15 Query Match 100.0%; Score 95; DB 9; Length 352;  
16 Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
17 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
18  
19 QY 1 YAFVGEKFRNYLLVFFQK 18  
20 |||||  
21 Db 297 YAFVGEKFRNYLLVFFQK 314  
22  
23 RESULT 17  
24 US-09-938-703-5  
25 ; Sequence 5, Application US/09938703  
26 ; Patent No. US20020110870A1  
27 ; GENERAL INFORMATION:  
28 ; APPLICANT: SAMSON, MICHEL  
29 ; PARENTIER, MARC  
30 ; VASSART, GILBERT  
31 ; LIBERT, FREDERICK  
32 ; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR  
33 ; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR  
34 ;  
35 ; NUMBER OF SEQUENCES: 17  
36 ; CORRESPONDENCE ADDRESS:  
37 ; ADDRESSEE: Knobbe, Martens, Olson & Bear  
38 ; STREET: 620 Newport Center Drive 16th Floor  
39 ; CITY: Newport Beach  
40 ; STATE: CA  
41 ; COUNTRY: U.S.A.  
42 ; ZIP: 92660  
43 ; COMPUTER READABLE FORM:  
44 ; MEDIUM TYPE: Floppy disk  
45 ; COMPUTER: IBM PC compatible  
46 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
47 ; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
48 ; CURRENT APPLICATION DATA:  
49 ; APPLICATION NUMBER: US/09/938,703  
50 ; FILING DATE: 24-Aug-2001  
51 ; CLASSIFICATION: <Unknown>  
52 ; PRIOR APPLICATION DATA:  
53 ; APPLICATION NUMBER: 09/626,939  
54 ; FILING DATE: 2000-07-27  
55 ; ATTORNEY/AGENT INFORMATION:  
56 ; NAME: Altman, Daniel E  
57 ; REGISTRATION NUMBER: 34,115  
58 ; REFERENCE/DOCKET NUMBER: <Unknown>  
59 ; INFORMATION FOR SEQ ID NO: 5:  
60 SEQUENCE CHARACTERISTICS:  
61 LENGTH: 352 amino acids  
62 TYPE: amino acid  
63 TOPOLOGY: linear  
64 MOLECULE TYPE: protein  
65 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
66 US-09-938-703-5  
67  
68 Query Match 100.0%; Score 95; DB 9; Length 352;  
69 Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
70 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
71  
72 QY 1 YAFVGEKFRNYLLVFFQK 18  
73 |||||  
74 Db 297 YAFVGEKFRNYLLVFFQK 314  
75  
76 RESULT 18  
77 US-09-502-783A-2  
78 ; Sequence 2, Application US/09502783A  
79 ; Patent No. US20020132269A1  
80 ; GENERAL INFORMATION:  
81 ; APPLICANT: Li, Yi  
82 ; APPLICANT: Ruben, Steven M.  
83 ; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein Chemokine Receptor (CCR)  
84 ; FILE REFERENCE: 1488.1150006  
85 ; CURRENT APPLICATION NUMBER: US/09/502,783A  
86 ; PRIOR FILING DATE: 2001-08-23  
87 ; PRIOR FILING DATE: 1995-06-06  
88 ; NUMBER OF SEQ ID NOS: 9  
89 ; SOFTWARE: Patent in version 3.0  
90 ; SEQ ID NO 2  
91 ; LENGTH: 352  
92 ; TYPE: PRT  
93 ; ORGANISM: Homo sapiens  
94 ; US-09-502-783A-2  
95  
96 Query Match 100.0%; Score 95; DB 9; Length 352;  
97 Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
98 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
99  
100 QY 1 YAFVGEKFRNYLLVFFQK 18  
101 |||||  
102 Db 297 YAFVGEKFRNYLLVFFQK 314  
103  
104 RESULT 19  
105 US-09-734-221A-14  
106 ; Sequence 14, Application US/09734221A  
107 ; Publication No. US20030096221A1  
108 ; GENERAL INFORMATION:  
109 ; APPLICANT: LITTMAN, DAN R.  
110 ; DENG, HONGKUI  
111 ; ELMEIER, WILFRIED  
112 ; LANDAU, NATHANIEL R.  
113 ; LIU, RONG  
114 ; TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH  
115 ; MACROPHAGE-TROPIC HIV, AND DIAGNOSTIC AND THERAPEUTIC  
116 ; USES THEREOF  
117 ;  
118 ; NUMBER OF SEQUENCES: 14  
119 ; CORRESPONDENCE ADDRESS:  
120 ; ADDRESSEE: David A. Jackson, Esq.  
121 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
122 ; Floor  
123 ; CITY: Hackensack  
124 ; STATE: New Jersey  
125 ; COUNTRY: USA  
126 ; ZIP: 07601  
127 ; COMPUTER READABLE FORM:  
128 ; MEDIUM TYPE: Floppy disk  
129 ; COMPUTER: IBM PC compatible  
130 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
131 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
132 ; CURRENT APPLICATION DATA:  
133 ; APPLICATION NUMBER: US/09/734,221A  
134 ; FILING DATE: 11-Dec-2000  
135 ; CLASSIFICATION: <Unknown>  
136 ; PRIOR APPLICATION DATA:  
137 ; APPLICATION NUMBER: US 08/666,020  
138 ; FILING DATE: 19-JUN-1996  
139 ; APPLICATION NUMBER: US 08/227,319  
140 ; FILING DATE: 13-APR-1994  
141 ; ATTORNEY/AGENT INFORMATION:  
142 ; NAME: Jackson Esq., David A.  
143 ; REGISTRATION NUMBER: 26,742  
144  
145 QY 1 YAFVGEKFRNYLLVFFQK 18  
146 |||||

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;
; REFERENCE/DOCKET NUMBER: 1049-1-004 N2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-734-221A-14

Query Match 100.0%; Score 95; DB 10; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 20
US-09-826-509-477
; Sequence 477, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 477
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-477

Query Match 100.0%; Score 95; DB 11; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 21
US-10-106-623-2
; Sequence 2, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Report, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
```

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;
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020150888A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-106-623-2

Query Match 100.0%; Score 95; DB 13; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YAFVGEKFRNYLLVFFQK 18
Db 297 YAFVGEKFRNYLLVFFQK 314

RESULT 22
US-10-106-623-20
; Sequence 20, Application US/10106623
; Publication No. US20020150888A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; APPLICANT: Report, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/106,623
; FILING DATE: 26-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/771,276
; FILING DATE: <Unknown>
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ATTORNEY/AGENT INFORMATION:  
NAME: No. US20020150888aland, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/33670  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-474-6300  
TELEFAX: 312-474-0448  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-106-623-20

Query Match 100.0%; Score 95; DB 13; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 23  
US-10-232-686-2  
Sequence 2, Application US/10232686  
Publication No. US20030023044A1  
GENERAL INFORMATION:  
APPLICANT: Li, Yi  
APPLICANT: Ruben, Steven M.  
TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGMR10  
FILE REFERENCE: 1488.115000N  
CURRENT APPLICATION NUMBER: US/10/232,686  
CURRENT FILING DATE: 2002-09-03  
PRIOR APPLICATION NUMBER: 09/339,912  
PRIOR FILING DATE: 1999-06-25  
PRIOR APPLICATION NUMBER: 09/195,662  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 08/466,343  
PRIOR FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 2  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-232-686-2

Query Match 100.0%; Score 95; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 24  
US-10-086-814-1  
Sequence 1, Application US/10086814  
Publication No. US20030092632A1  
GENERAL INFORMATION:  
APPLICANT: Dragic, Tatjana  
APPLICANT: Olson, William C.  
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION  
FILE REFERENCE: 61010-AB-1  
CURRENT APPLICATION NUMBER: US/10/086,814  
CURRENT FILING DATE: 2002-02-28  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 1

LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-086-814-1

Query Match 100.0%; Score 95; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 25  
US-10-067-800-2  
Sequence 2, Application US/10067800  
Publication No. US20030100058A1  
GENERAL INFORMATION:  
APPLICANT: Roschke, Viktor  
APPLICANT: Rosen, Craig A.  
APPLICANT: Ruben, Steven, M.  
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
FILE REFERENCE: 1488.115000I  
CURRENT APPLICATION NUMBER: US/10/067,800  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: PCT/US01/04153  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 09/779,880  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/297,257  
PRIOR FILING DATE: 2001-06-12  
PRIOR APPLICATION NUMBER: 60/310,458  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: 60/328,447  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/341,725  
PRIOR FILING DATE: 2001-12-21  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 2  
LENGTH: 352  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-067-800-2

Query Match 100.0%; Score 95; DB 14; Length 352;  
Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNLLVFFQK 18  
DB 297 YAFVGEKFRNLLVFFQK 314

RESULT 26  
US-10-067-800-22  
Sequence 22, Application US/10067800  
Publication No. US20030100058A1  
GENERAL INFORMATION:  
APPLICANT: Roschke, Viktor  
APPLICANT: Rosen, Craig A.  
APPLICANT: Ruben, Steven, M.  
TITLE OF INVENTION: Human G-protein Chemokine Receptor (CCR5) HDGMR10  
FILE REFERENCE: 1488.115000I  
CURRENT APPLICATION NUMBER: US/10/067,800  
CURRENT FILING DATE: 2002-02-08  
PRIOR APPLICATION NUMBER: PCT/US01/04153  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 09/779,880  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/297,257  
PRIOR FILING DATE: 2001-06-12

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: ORGANISM: Homo sapiens
US-10-025-567A-352

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||
Db 297 YAFVGEKFRNYLLVFFQK 314
 |||

RESULT 29
US-10-323-314-1
; Sequence 1, Application US/10323314
; Publication No. US20030139571A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010-1/JPW/WAF/DJK
; CURRENT APPLICATION NUMBER: US/10/323,314
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: human
US-10-323-314-1

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
 |||
Db 297 YAFVGEKFRNYLLVFFQK 314
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RESULT 30
US-10-072-301-1
; Sequence 1, Application US/10072301
; Publication No. US20030152913A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shao-bing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST CORECEPTORS FOR HUMAN I
; FILE REFERENCE: 25636-718
; CURRENT APPLICATION NUMBER: US/10/072,301
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-301-1

Query Match 100.0%; Score 95; DB 14; Length 352;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YAFVGEKFRNYLLVFFQK 18
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Db 297 YAFVGEKFRNYLLVFFQK 314
 |||

Search completed: March 4, 2004, 18:22:53
Job time : 24.0612 secs

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